```
                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      November 18, 2004, 13:06:00 ; Search time 188.365 Seconds
                                     (without alignments)
                                     4355.452 Million cell updates/sec

Title:         US-09-611-257A-24
Perfect score: 12028
Sequence:      1 MLPHRVPRCVRTPPLRGSAR........KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:        2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     A_Geneseq_23Sep04:*
           1:  geneseqp1980s:*
           2:  geneseqp1990s:*
           3:  geneseqp2000s:*
           4:  geneseqp2001s:*
           5:  geneseqp2002s:*
           6:  geneseqp2003as:*
           7:  geneseqp2003bs:*
           8:  geneseqp2004s:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                            SUMMARIES
```

Result No.	Score	* Query Match	Length	DB	ID	Description
1	12028	100.0	2287	4	AAB66475	Aab66475 Rat alpha
2	11657	96.9	2254	2	AAY14590	Aay14590 Rat T-typ
3	11626	96.7	2272	2	AAY14592	Aay14592 Rat T-typ
4	11610.5	96.5	2265	2	AAY14591	Aay14591 Rat T-typ
5	11606.5	96.5	2247	2	AAY14593	Aay14593 Rat T-typ
6	11542.5	96.0	2428	3	AAY70720	Aay70720 Rat pancr
7	10857	90.3	2250	2	AAY14586	Aay14586 Human T-t
8	10833	90.1	2268	2	AAY14588	Aay14588 Human T-t
9	10820.5	90.0	2273	4	AAE01019	Aae01019 Human T-t
10	10810.5	89.9	2261	2	AAY14587	Aay14587 Human T-t
11	10806.5	89.8	2243	2	AAY14589	Aay14589 Human T-t
12	10806.5	89.8	2243	7	ADJ68819	Adj68819 Human hea
13	10533	87.6	2266	4	AAB66481	Aab66481 Human alp
14	6226.5	51.8	2359	4	AAB66476	Aab66476 Rat alpha
15	6222	51.7	2353	7	AAY06299	Aay06299 Human act
16	6222	51.7	2353	6	ABP72254	Abp72254 Human T-t
17	6222	51.7	2353	7	ADJ69322	Adj69322 Human hea
18	6221	51.7	2353	7	AAY06298	Aay06298 Human act
19	6195.5	51.5	2353	5	ABG30840	Abg30840 Human vol
20	5872	48.8	1207	4	AAU00474	Aau00474 Human T-t
21	5835	48.5	2044	2	AAY14594	Aay14594 Human T-t
22	5827	48.4	2038	2	AAY14595	Aay14595 Human T-t
23	5718.5	47.5	2034	2	AAY06300	Aay06300 Human act
24	5409	45.0	2175	5	AAU10535	Aau10535 Human T-t
25	5409	45.0	2175	6	ABU08511	Abu08511 Human T-t
26	5409	45.0	2175	8	ADH69265	Adh69265 Human TCC
27	5405.5	44.9	2188	5	AAU10536	Aau10536 Human T-t
28	5405.5	44.9	2188	6	ABU08512	Abu08512 Human T-t
29	5405.5	44.9	2188	8	ADH69267	Adh69267 Human TCC
30	5345	44.4	1835	2	AAY14597	Aay14597 Rat T-typ
31	5345	44.4	1835	8	ADH69268	Adh69268 Rat T-typ
32	5342.5	44.4	1823	2	AAY14596	Aay14596 Human T-t
33	5179.5	43.1	1792	4	AAB66477	Aab66477 Rat brain
34	4807	40.0	982	2	AAM23743	Aam23743 Human EST
35	3950	32.8	1854	2	AAW79161	Aaw79161 Human cal
36	3950	32.8	1854	4	AAB66472	Aab66472 Protein e
37	3397	28.2	2435	4	ABB60448	Abb60448 Drosophil
38	3125	26.0	644	4	AAB66478	Aab66478 Human alp
39	2975	24.7	1859	4	ABG10954	Abg10954 Novel hum
40	1911.5	15.9	853	4	AAM93437	Aam93437 Human pol
41	1911.5	15.9	853	8	ADL31041	Adl31041 Human pro
42	1686.5	14.0	518	4	AAB66479	Aab66479 Human alp
43	1682	14.0	2339	2	AAR33549	Aar33549 Sequence
44	1680.5	14.0	2264	8	ADM31026	Adm31026 Human cal
45	1678	14.0	2343	2	AAY31809	Aay31809 N-type ca

```
                            ALIGNMENTS

RESULT 1
AAB66475
ID   AAB66475 standard; protein; 2287 AA.
XX
AC   AAB66475;
XX
DT   09-APR-2001  (first entry)
XX
DE   Rat alpha-1G calcium channel protein.
XX
KW   Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW   hypotensive; cardiant; nootropic; T-type calcium channel subunit;
KW   cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW   epilepsy; alpha-1G calcium channel.
XX
OS   Rattus sp.
XX
PN   WO200102561-A2.
XX
PD   11-JAN-2001.
XX
PF   04-JUL-2000; 2000WO-CA000794.
XX
PR   02-JUL-1999;   99US-00346794.
XX
PA   (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI   Snutch TP,  Baillie DL;
XX
DR   WPI; 2001-123111/13.
DR   N-PSDB; AAF31677.
XX
PT   Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT   cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT   epilepsy.
XX
PS   Disclosure; Page 63-72; 103pp; English.
XX
CC   The present sequence is given in a specification providing sequences and
CC   partial sequences for three types of mammalian (human and rat) T-type
CC   calcium channel subunits. An expression cassette has been generated which
CC   comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC   subunit operably linked to control sequences to effect its expression.
CC   The novel calcium channel nucleic acids and proteins are useful for
CC   treating conditions characterised by undesirable levels of T-type calcium
CC   channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC   hypertension, sleep disorder and epilepsy
XX
```

```
SQ   Sequence 2287 AA;

Query Match      100.0%;   Score 12028;   DB 4;   Length 2287;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 2287;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1  MLPHRVPRCVRTPPLRGSARPSSDDPPGPRLARGWTRRRMERAPRSRDSPVASRSSTTCPG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLPHRVPRCVRTPPLRGSARPSSDDPPGPRLARGWTRRRMERAPRSRDSPVASRSSTTCPG  60

Qy    61  PGAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSM  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  PGAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSM  120

Qy   121  LVIILLNCVTLGMFRPCEDTACDSQRCRIILQAPDDFIFAFFAVEMVVKMVALGIFGKKCYL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  LVIILLNCVTLGMFRPCEDTACDSQRCRIILQAPDDFIFAFFAVEMVVKMVALGIFGKKCYL 180

Qy   181  GDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTL  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTL  240

Qy   241  PMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLPLSVDLEPYYQTENEDESP  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLPLSVDLEPYYQTENEDESP  300

Qy   301  FICSQPRENGMRSCRSVPTLRGEGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEH 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  FICSQPRENGMRSCRSVPTLRGEGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEH 360

Qy   361  NPFKGAINFDNIGYAWIAIFQVITLBGWDIMYFVMDAHSFYNFIYFILLIIVGSFFMIN  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  NPFKGAINFDNIGYAWIAIFQVITLBGWDIMYFVMDAHSFYNFIYFILLIIVGSFFMIN  420

Qy   421  LCLVVIATQFSETKQRESQLMREQRVRFLSNASTIASFSEPGSCYBELLKYLVYILRKAA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  LCLVVIATQFSETKQRESQLMREQRVRFLSNASTIASFSEPGSCYBELLKYLVYILRKAA  480

Qy   481  RRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  RRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLG  540

Qy   541  NGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  NGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRC  600

Qy   601  QAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGP  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  QAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGP  660

Qy   661  FSSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDS  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  FSSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDS  720

Qy   721  DSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLLCDTFRKIVDSKYFGR  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  DSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLLCDTFRKIVDSKYFGR  780

Qy   781  GIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPY  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPY  840

Qy   841  NIFDGVIVVISVWELVGQQQGGGLSVLRTFRIMRVLKLIVRFLPALQRQLVLVMLKTMDNVAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  NIFDGVIVVISVWELVGQQQGGGLSVLRTFRIMRVLKLIVRFLPALQRQLVLVMLKTMDNVAT 900

Qy   901  FCMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVPQILTQEDWNK  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  FCMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVPQILTQEDWNK  960

Qy   961  VLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSV 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  VLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSV 1020

Qy  1021  DGDGDRKRLALVALGEHAELRKSLLPPLIIHTAATMSHPXSSSTGVGEALGSGSRTS  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  DGDGDRKRLALVALGEHAELRKSLLPPLIIHTAATMSHPXSSSTGVGEALGSGSRTS  1080

Qy  1081  SSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERR 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  SSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERR 1140

Qy  1141  SLLSGEQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSPDLPDTLQVPGLHRTASG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  SLLSGEQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASG  1200

Qy  1201  RSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWTVRSRLPACCR 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  RSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCR 1260

Qy  1261  ERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPKIDDPHSAERIF 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  ERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPKIDDPHSAERIF 1320

Qy  1321  LTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYIRSSWNVLDGLLVLLSVIDILIVSMVSDS 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  LTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYIRSSWNVLDGLLVLLSVIDILIVSMVSDS 1380

Qy  1381  GTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAPFIIFGIL 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  GTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAPFIIFGIL 1440

Qy  1441  GVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWV  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWV  1500

Qy  1501  DIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFPVLNMFVGVVVENFHKCRQHEE  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  DIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFPVLNMFVGVVVENFHKCRQHEE  1560

Qy  1561  BEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTTGV 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  BEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTTGV 1620

Qy  1621  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFEKLVAFAPRRFFQDRWNQLDL 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFEKLVAFAPRRFFQDRWNQLDL 1680

Qy  1681  AIVLLSIMGITILEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQAL 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  AIVLLSIMGITILEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQAL 1740

Qy  1741  PQVGNLGLLFMLLFFIFPAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  PQVGNLGLLFMLLFFIFPAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST 1800

Qy  1801  GDNWNGIMKDPSRDCQESTCYNTVLSPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GDNWNGIMKDPSRDCQESTCYNTVLSPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE  1860

Qy  1861  AKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  AKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASG  1920

Qy  1921  FSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTADRSLGHRGWG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  FSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTABRSLGHRGWG 1980

Qy  1981  LPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPL 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  LPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPL 2040

Qy  2041  RRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKH 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  RRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKH 2100
```

```
Qy   2101  IRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVET  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  IRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVET  2160

Qy   2161  QSCRRRPGFWLDEQRRHSIAVSCLDSGSGQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSI 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  QSCRRRPGFWLDEQRRHSIAVSCLDSGSGQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSI 2220

Qy   2221  SIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSD  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  SIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSD  2280

Qy   2281  PTDMDPZ  2287
           |||||||
Db   2281  PTDMDPZ  2287
```

RESULT 2
AAY14590

```
ID   AAY14590   standard; protein; 2254 AA.
XX
AC   AAY14590;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCaV1a).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO992984 7/33.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998; 98WO-US023161.
XX
PR   05-DEC-1997; 97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83485.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 67-76; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCaV1a. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2254 AA;
```

Query Match   96.9%; Score 11657; DB 2; Length 2254;
Best Local Similarity 99.7%; Pred. No. 0;

```
Matches  2219;  Conservative  0;  Mismatches  0;  Indels  6;  Gaps  0;

Qy     62  GAAGAGSTEKDPGASADSEABGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML  121
           |              ||||||||||||||||||||||||||||||||||||||||||||||
Db     30  GRQGPGSTEKDPGASADSEABGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML  89

Qy    122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  149

Qy    182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP  241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP  209

Qy    242  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  269

Qy    302  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYTNCSAGEHN  361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    270  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYTNCSAGEHN  329

Qy    362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  389

Qy    422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR  481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYIIRKAAR  449

Qy    482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHYHLGN  541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    450  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHYHLGN  509

Qy    542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ  601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    510  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ  569

Qy    602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    570  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  629

Qy    662  SSMHKLLETQSTGACHSSCKISSPCKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630  SSMHKLLETQSTGACHSSCKISSPCKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  689

Qy    722  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  749

Qy    782  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN  841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    750  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN  809

Qy    842  IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    810  IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  869

Qy    902  CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV  961
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870  CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV  929

Qy    962  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    930  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  989

Qy   1022  GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVEALGSGSRRTSS  1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990  GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVEALGSGSRRTSS  1049

Qy   1082  SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS  1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050  SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS  1109
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Qy   2222  IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP  2281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190  IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP  2249

Qy   2282  TDMDP  2286
           |||||
Db   2250  TDMDP  2254
```

RESULT 3
AAY14592
ID   AAY14592 standard; protein; 2272 AA.
XX
AC   AAY14592;
XX
DT   07-DEC-1999 (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavTlc).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83487.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 85-94; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCavTlc. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2272 AA;

Query Match   96.7%; Score 11626; DB 2; Length 2272;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;
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Qy    62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML  121
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    30  GRQGPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML   89

Qy   122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  181
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130
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Qy  1142  LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSFDLPTLQVPGLHRTASGR  1201
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1110  LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSFDLPTLQVPGLHRTASGR  1169

Qy  1202  SSASEHQDCNGKSAGRLARTLRTDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE  1261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1170  SSASEHQDCNGKSAGRLARTLRTDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE  1229

Qy  1262  RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1230  RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1289

Qy  1322  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSG  1381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1290  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSG  1349

Qy  1382  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG  1441
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1350  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG  1409

Qy  1442  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1501
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1410  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1469

Qy  1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1561
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1470  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1529

Qy  1562  EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI  1621
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1530  EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI  1589

Qy  1622  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA  1681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1590  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLA  1649

Qy  1682  IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP  1741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1650  IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP  1709

Qy  1742  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG  1801
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1710  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG  1769

Qy  1802  DNWNGIMKDPSRDCDDQRSTCYNTVISPIYFVGFVLTAQFVLVNVVIAVLMKHLEESNKEA  1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1770  DNWNGIMKDTLRDCDQRSTCYNTVISPIYFVGFVLTAQFVLVNVVIAVLMKHLEESNKEA  1829

Qy  1862  KEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1921
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1830  KEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1889

Qy  1922  SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1981
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1890  SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1949

Qy  1982  PKAQSGSILSVHSQOPADTSCIILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR  2041
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1950  PKAQSGSILSVHSQOPADTSCIILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR  2009

Qy  2042  RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVCQRSGIQSKVSKHI  2101
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2010  RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVCQRSGIQSKVSKHI  2069

Qy  2102  RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLLKKCYSVETQ  2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2070  RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLLKKCYSVETQ  2129

Qy  2162  SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS  2221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2130  SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS  2189
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Qy  1262  RDSWSAYIFPPQQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1230  RDSWSAYIFPPQQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1289

Qy  1322  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG   1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1290  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG   1349

Qy  1382  TKIIGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG   1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1350  TKIIGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG   1409

Qy  1442  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD   1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1410  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD   1469

Qy  1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE   1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1470  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE   1529

Qy  1562  EARRREEKRLRRLEKKRRSKEKQMA------------EAQCKPYYSDYSRFRLL         1603
          |||||||||||||||||||||||||            ||||||||||||||||
Db  1530  EARRREEKRLRRLEKKRRSKEKQMADLMLDDVIASGSSASAASEAQCKPYYSDYSRFLL    1589

Qy  1604  VHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVFESVFKLV   1663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1590  VHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVFESVFKJV   1649

Qy  1664  AFAFRRFFQDRWNQLDLAIVLLSIMGTILEEIEVNLSLPINPTIIRIMRVLRIARVLKLL   1723
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1650  AFGFRRFFQDRWNQLDLAIVLLSIMGTILEEIEVNLSLPINPTIIRIMRVLRIARVLKLL   1709

Qy  1724  KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA   1783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1710  KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA   1769

Qy  1784  TFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLV   1843
          |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db  1770  TFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLV   1829

Qy  1844  NVVIAVLMKHLEESNKEAKEEAELEALELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDS   1903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1830  NVVIAVLMKHLEESNKEAKEEAELEALELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDS   1889

Qy  1904  PKPGAPHTTAHIGAAASGFSLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYM   1963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1890  PKPGAPHTTAHIGAAASGFSLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYM   1949

Qy  1964  CRNGSTAERSLGHRGWGLPKAQSGSIILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA  2023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1950  CRNGSTAERSLGHRGWGLPKAQSGSIILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA  2009

Qy  2024  IPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGS   2083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2010  IPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGS   2069

Qy  2084  SIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQ   2143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2070  SIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQ   2129

Qy  2144  EEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDDSGSQPRLCPSPSSLGQP   2203
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2130  EEPLFPRDLKNCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDDSGSQPRLCPSPSSLGQP   2189

Qy  2204  LGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAA   2263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2190  LGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAA   2249

Qy  2264  SPSPKKDTLSLSGLSSDPTDMDP  2286
          |||||||||||||||||||||||
Db  2250  SPSPKKDTLSLSGLSSDPTDMDP  2272
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Db    90  VILLNCVTLGMFRPCEDIACDSQRCRIILQAFDFIFAFFAVEMVKMVALGIFGKKCYLG    149

Qy   182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDTLP      241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDTLP      209

Qy   242  MLGNVLLLCFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF   301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   210  MLGNVLLLCFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF   269

Qy   302  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN   361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN   329

Qy   362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  389

Qy   422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVILRKAAR   481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVILRKAAR   449

Qy   482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGGCTRSHRRLSVHHLVHHHHHHYHLGN     541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   450  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGGCTRSHRRLSVHHLVHHHHHHYHLGN     509

Qy   542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPPSGGPPRGAESVHSFYHADCHLEPVRCQ   601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPPSGGPPRGAESVHSFYHADCHLEPVRCQ   569

Qy   602  APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF   661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570  APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF   629

Qy   662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   630  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  689

Qy   722  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   690  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  749

Qy   782  IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLIVYGPFGYIKNPYN  841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   750  IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLIVYGPFGYIKNPYN  809

Qy   842  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMVLKLVRFLPALQRQLVVLMKTMDNVATF    901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   810  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMVLKLVRFLPALQRQLVVLMKTMDNVATF    869

Qy   902  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKV  961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKV  929

Qy   962  LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   930  LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  989

Qy  1022  GDGDRKKRLAIVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGRRTSS   1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   990  GDGDRKKRLAIVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGRRTSS   1049

Qy  1082  SGSAEPGAAHIEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRS  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1050  SGSAEPGAAHIEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRS  1109

Qy  1142  LLSGEGEQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1110  LLSGEGEQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy  1202  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE  1261
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  1170  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERRQAWVRSRLPACCRE  1229
```

```
RESULT 4
AAY14591
ID    AAY14591 standard; protein; 2265 AA.
XX
AC    AAY14591;
XX
DT    07-DEC-1999  (first entry)
XX
DE    Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b).
XX
KW    Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW    activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS    Rattus sp.
XX
PN    WO929847-A1.
XX
PD    17-JUN-1999.
XX
PF    98WO-US023161.
XX
PR    30-OCT-1998;
XX
PR    05-DEC-1997;   97US-00985809.
XX
PA    (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI    Perez-Reyes E,  Cribbs LL;
XX
DR    WPI; 1999-394972/33.
DR    N-PSDB; AAX83486.
XX
PT    New T-type voltage-gated calcium channels.
XX
PS    Disclosure; Page 76-85; 138pp; English.
XX
CC    This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC    alpha-1-G designated rCavT1b. Voltage gated channels are membrane bound
CC    glycosylated proteins formed of several subunits. The large alpha
CC    subunits form a pore in the membrane that is selective for a given ionic
CC    species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC    each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC    -type Ca channels are activated at a lower voltage than L- or N-type
CC    channels. Characteristics of T-type channels include short current time,
CC    slow activation kinetics near threshold, fast inactivation kinetics and
CC    slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC    voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC    -channels contains a putative IVS4 region comprising the amino acid
CC    sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC    channel proteins can be used to screen for drugs which affect calcium
CC    channels. Methods are also disclosed for treating a disease or disorder
CC    associated with a deficiency in a native T-type calcium channel nucleic
CC    acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ    Sequence 2265 AA;

Query Match             96.5%;  Score 11610.5;  DB 2;  Length 2265;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 2213    Conservative    1; Mismatches   11; Indels   11; Gaps     1;
```

```
Qy      62 GAAGAGSTEKDPGSADSEABGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              ||| | || |||| ||||||  ||||||||||||||||||||||||||||||||||||||
Db      30 GRQGPGSTEKDPGSADSEABGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy     122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy     182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy     242 MLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 MLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269
```

```
Qy     302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVAWNQYYTNCSAGEHN 361
           ||| |  |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVAWNQYYTNCSAGEHN 329

Qy     362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMNL 389

Qy     422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     390 CLVVIATQFSETKQRESQLMRBQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy     482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 509

Qy     542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     510 GTLRVPRASPEIQDRDANGSRRLMLPPSTPPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy     602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy     662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy     722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy     782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy     842 IFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     810 IFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy     902 CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy     962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

Qy    1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVEALGSGSRRTSS 1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVEALGSGSRRTSS 1049

Qy    1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy    1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy    1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSLPACCRE 1261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSLPACCRE 1229

Qy    1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVIIFNCITIAMERPKIDPHSAERIFL 1289

Qy    1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349
```

XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83488.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 94-103; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCavT1d. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2247 AA;

Query Match   96.5%; Score 11606.5;   DB 2;   Length 2247;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 2211;   Conservative   1; Mismatches   6; Indels   7; Gaps   1;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVFVFYLSQDSRPRSWCLRTVCNPWFERVSML 121
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVFVFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy   122 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy   182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy   242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy   302 ICSQPRENGMRSCRSVPTLRGEGGGGPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 ICSQPRENGMRSCRSVPTLRGEGGGGPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy   362 PFKGAINFDNIGYAWIAIFQVTTLEGWVDIMYFVMDAHSFYNFIYFLLLIVGSFFMINL 421
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1382 TKILGMLRVLRLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 TKILGMLRVLRLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy   1442 VQLFKGKFFVCQGGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 VQLFKGKFFVCQGGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy   1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVENFHKCRQHQEEE 1561
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVENFHKCRQHQEEE 1529

Qy   1562 EARRREEKRLRRLEKKKR----------SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
                |||||||||||||||||| :||||||||||||||||||||||||
Db   1530 EARRREEKRLRRLEKKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTS 1589

Qy   1611 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRF 1670
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRF 1649

Qy   1671 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMR 1730
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMR 1709

Qy   1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLLECDETHPCEGLGRHATFRNFGM 1790
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLLECDETHPCEGLGRHATFRNFGM 1769

Qy   1791 AFLTLFRVSTGDNWNGIMKDPSRDCDDESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1850
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 AFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1829

Qy   1851 MKHLEESNKEAKEAELEAELEAELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPH 1910
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830 MKHLEESNKEAKEAELEAELEAELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPH 1889

Qy   1911 TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1970
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890 TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1949

Qy   1971 ERSLGHRGWGLPKAQGSGILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPP 2030
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1950 ERSLGHRGWGLPKAQGSGILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPP 2009

Qy   2031 GRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR 2090
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010 GRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR 2069

Qy   2091 SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPR 2150
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070 SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPR 2129

Qy   2151 DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSDSLGGOPLGGPGSR 2210
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2130 DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSDSLGGOPLGGPGSR 2189

Qy   2211 PKKKLSPPSISIDPPESQGSRRPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKD 2270
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190 PKKKLSPPSISIDPPESQGSRRPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKD 2249

Qy   2271 TLSLSGLSSSDPTDMDP 2286
                |||||||||||||||||
Db   2250 TLSLSGLSSSDPTDMDP 2265

RESULT 5
AAY14593
ID   AAY14593 standard; protein; 2247 AA.
XX
AC   AAY14593;
XX
DT   07-DEC-1999 (first entry)

```
Db  1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1561
Qy  1470  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1529
Db  1562  EARRREEKRLRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI   1621
Qy  1530  EARRREEKRLRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI    1582
Db  1622  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLA  1681
Qy  1583  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLA  1642
Db  1682  IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKAVGMRALLHTVMQALP   1741
Qy  1643  IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKAVGMRALLHTVMQALP   1702
Db  1742  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG  1801
Qy  1703  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG  1762
Db  1802  DNWNGIMKDPSRDCDQESTCVNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA  1861
Qy  1763  DNWNGIMKDTLRDCDQESTCVNTVISPIYFVVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1822
Db  1862  KEEAELBAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1921
Qy  1823  KEEAELBAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1882
Db  1922  SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1981
Qy  1883  SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1942
Db  1982  PKAQSGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPGRSPLAQRPLR   2041
Qy  1943  PKAQSGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPGRSPLAQRPLR   2002
Db  2042  RQAAIRTDSLDVQLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI   2101
Qy  2003  RQAAIRTDSLDVQLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI   2062
Db  2102  RLPAPCPGLEPSWAKDPPETRSSLEDLTDELSWTSGDLLPSSQBEPLFPRDLKKCCYSVETQ 2161
Qy  2063  RLPAPCPGLEPSWAKDPPETRSSLEDLTDELSWTSGDLLPSSQBEPLFPRDLKKCCYSVETQ 2122
Db  2162  SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGRPKKKLSPPSIS   2221
Qy  2123  SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGRPKKKLSPPSIS   2182
Db  2222  IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP  2281
Qy  2183  IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP  2242
Db  2282  TDMDP  2286
Qy  2243  TDMDP  2247
```

```
RESULT 6
AAY70720
ID   AAY70720 standard; protein; 2428 AA.
XX
AC   AAY70720;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Rat pancreatic T-type calcium channel.
XX
KW   Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;
KW   pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;
KW   antidiabetic; calcium influx; L type calcium channel; NIDDM;
KW   type II diabetes; non-insulin dependent diabetes mellitus.
XX
```

```
Db  330   PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  389
Qy  422   CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEBLLKYLIVYILRKAAR 481
Db  390   CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEBLLKYLIVYILRKAAR 449
Qy  482   RLAQYSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN     541
Db  450   RLAQYSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN     509
Qy  542   GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ  601
Db  510   GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ  569
Qy  602   APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  661
Db  570   APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  629
Qy  662   SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721
Db  630   SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  689
Qy  722   SEAVVEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  781
Db  690   SEAVVEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  749
Qy  782   IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN   841
Db  750   IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN   809
Qy  842   IFDGVIVVISVNEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901
Db  810   IFDGVIVVISVNEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  869
Qy  902   CMLLMLFIFIFSILGMHLFGCKFPASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDMNKV 961
Db  870   CMLLMLFIFIFSILGMHLFGCKFPASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDMNKV 929
Qy  962   LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  1021
Db  930   LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  989
Qy  1022  GDGDRKKRLALVALGEHAELRKSLLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS   1081
Db  990   GDGDRKKRLALVALGEHAELRKSLLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS   1049
Qy  1082  SGSAEPGAAHHEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRS  1141
Db  1050  SGSAEPGAAHHEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRS  1109
Qy  1142  LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR  1201
Db  1110  LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR  1169
Qy  1202  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE   1261
Db  1170  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE   1229
Qy  1262  RDSWSAYIFPPQSRFRLLCHRIITHKQMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
Db  1230  RDSWSAYIFPPQSRFRLLCHRIITHKQMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289
Qy  1322  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVMVSDSG      1381
Db  1290  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVMVSDSG      1349
Qy  1382  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG  1441
Db  1350  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG  1409
Qy  1442  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1501
Db  1410  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1469
```

```
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1..52
FT                   /note= "Region upstream to pancreatic T-type calcium
FT                   channel protein"
FT   Misc-difference 4
FT                   /note= "Encoded by in-frame stop codon TGA"
FT   Protein         53..2428
FT                   /label= Pancreatic_T-type_calcium_channel_alpha1_subunit
FT                   /note= "This region is claimed as SEQ ID NO: 2"
FT   Region          53..86
FT                   /note= "Unique region that differs from amino acid
FT                   sequence of neuronal T-type calcium channel alpha1
FT                   subunit (alpha1G)"
FT   Region          1023..1046
FT                   /label= Intracellular loop I(II-III)
FT                   /note= "Unique region that differs from amino acid
FT                   sequence of neuronal T-type calcium channel alpha1
FT                   subunit (alphaIG)"
FT   Region          1622..1640
FT                   /label= Intracellular loop_L(III-IV)
FT                   /note= "Unique region that differs from amino acid
FT                   sequence of neuronal T-type calcium channel alpha1
FT                   subunit (alphaIG)"
FT   Misc-difference 2341
FT                   /note= "Encoded by in-frame stop codon TGA"
FT   Misc-difference 2371
FT                   /note= "Encoded by in-frame stop codon TAA"
XX
PN   WO200015845-A1.
XX
PD   23-MAR-2000.
XX
PF   26-AUG-1999;   99WO-US019675.
XX
PR   26-AUG-1998;   98US-0098004P.
PR   27-JAN-1999;   99US-0117399P.
XX
PA   (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
PI   Li M;
XX
DR   WPI; 2000-271475/23.
DR   N-PSDB; AZ52309.
XX
PT   Novel nucleic acids encoding pancreatic T-type calcium channels used for
PT   regulation of T-type calcium channels and treatment of type II diabetes.
XX
PS   Example 1; Page 120; 124pp; English.
XX
CC   The present sequence is a protein that includes pancreatic T-type calcium
CC   channel alpha1 subunit derived from rat insulin secreting beta cell line,
CC   INS-1. The protein shows 96.3 % identity to the neuronal T-type calcium
CC   channel alpha1 subunit (alphaIG). The T-type Ca2+ channel from INS-1
CC   (alphaIG-INS) and neuronal alphaIG are alternative splice isoforms of the
CC   same gene. The INS-1 isoform is also expressed in brain, neonatal heart
CC   and kidney besides pancreatic beta cells. T-type Ca2+ channel belongs to
CC   the family of low voltage activated Ca2+ channels. The present sequence
CC   is used for treating diseases associated with abnormal expression or
CC   function of T-type calcium channels. They are especially used for
CC   treating type II diabetes. Modulators of pancreatic T-type Ca2+ channel
CC   e.g. antisense oligonucleotides, ribozymes and inhibitors are used in
CC   methods for modifying insulin secretion by pancreatic beta cells, basal
CC   calcium levels, potential L type calcium channel activity, pancreatic
CC   cell death, pancreatic beta cell proliferation and calcium influx through
CC   L type calcium channels in cells
XX
SQ   Sequence 2428 AA;
```

```
Qy      3  PHRVPRCVRTPPLRGSARPSSDDPPCGPRLARGWTRRMERAPRSRDSPVASRS------   54
                 ||     |              :::||
Db     22  PTGVPRLREDTSSEGLRSPLFGPPGAPAG-------QRMDEEEDGAGAEESGQPRSFTQ   73

Qy     55  -STTCPGPGAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNP  113
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74  LNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNP  133

Qy    114  WFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGI  173
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134  WFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVRMVALGI  193

Qy    174  FGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILV  233
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194  FGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILV  253

Qy    234  TLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQT  293
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254  TLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQT  313

Qy    294  ENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYT  353
                ||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    314  ENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYT  373

Qy    354  NCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIV  413
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374  NCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIV  433

Qy    414  GSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLV  473
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434  GSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLV  493

Qy    474  YILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHH  533
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    494  YILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHH  553

Qy    534  HHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADC  593
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554  HHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADC  613

Qy    594  HLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTS  653
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614  HLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTS  673

Qy    654  FNIPPGPFSSMHKLLETQSTGACHSSCCKISSPCSKADSGACGPDSCPYCARTGAGEPSA  713
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674  FNIPPGPFSSMHKLLETQSTGACHSSCCKISSPCSKADSGACGPDSCPYCARTGAGEPSA  733

Qy    714  DHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIV  773
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734  DHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIV  793

Qy    774  DSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPF  833
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794  DSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPF  853

Qy    834  GYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMK  893
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854  GYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMK  913

Qy    894  TMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQIL  953
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914  TMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQIL  973

Qy    954  TQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE--------- 1003
                |||||||||||||||||||||||||||||||||||||||||||||||||
Db    974  TQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEIGKREDASG 1033

Qy   1004  ------------GDATKSESEPDFFSPSVDGDDRKKRLALVALGEHAELRKSLLPPLI 1050
                            |||||||||||||||||||||||||||||||||||||||||||
Db   1034  QLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDDRKKRLALVALGEHAELRKSLLPPLI 1093
```

```
Query Match       96.0%;   Score 11542.5;  DB 3;  Length 2428;
Best Local Similarity   95.4%;   Pred. No. 0;
Matches 2219;   Mismatches  3;  Conservative  3;  Mismatches  54;  Indels  51;  Gaps  4;
```

```
Qy  1051  IHTAATPMSHPKSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSA  1110
          ||||||||| ||||||||||||||||||||||||||||||||||| |||||||||||||
Db  1094  IHTAATPMSLPKSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKSPPSARSSPHSPWSA  1153

Qy  1111  ASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPAGSDHR  1170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1154  ASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPAGSDHR  1213

Qy  1171  HRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQL  1230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1214  HRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQL  1273

Qy  1231  DGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFD  1290
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1274  DGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFD  1333

Qy  1291  HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQ  1350
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1334  HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQ  1393

Qy  1351  AYLRSSWNVLDGLLVLISVIDIIVSMVSDSGTKILGMLRVIRLLRTLRPLRVISRAQGLK  1410
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1394  AYLRSSWNVLDGLLVLISVIDIIVSMVSDSGTKILGMLRVIRLLRTLRPLRVISRAQGLK  1453

Qy  1411  LVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS  1470
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1454  LVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS  1513

Qy  1471  YRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFIS  1530
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1514  YRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFIS  1573

Qy  1531  FLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEKRLRKKRR-------------  1579
          |||||||||||||||||||||||||||||||||||||||||||||
Db  1574  FLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEKRLRKKRRNLMLDDVIASG  1633

Qy  1580  SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIL  1639
          : : ::  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1634  SSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIL  1693

Qy  1640  DEALKICNYIFTVIFVIFVFVESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNL  1699
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||| |
Db  1694  DEALKICNYIFTVIFVIFVFVESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNA  1753

Qy  1700  SLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAA  1759
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  1754  SLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAA  1813

Qy  1760  LGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQES  1819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  1814  LGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQES  1873

Qy  1820  TCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLS  1879
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db  1874  TCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAEELEAELELEMKTLS  1933

Qy  1880  PQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPL  1939
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  1934  PQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPL  1993

Qy  1940  GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT  1999
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1994  GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT  2053

Qy  2000  SCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSR  2059
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2054  SCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSR  2113

Qy  2060  EDLLSEVSGPSCPLTRSSSFWGGSSIQVQRSGIQSKVSKIHRLPAPCPGLEPSWAKDPP  2119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2114  EDLLSEVSGPSCPLTRSSSFWGGSSIQVQRSGIQSKVSKIHRLPAPCPGLEPSWAKDPP  2173

Qy  2120  ETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSI  2179
          |||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||
Db  2174  ETRSSLELDTELSWISGDLLPSSQEEPLSPRDLKKCYSVETQSCRRRPGSWLDEQRRHSI  2233

Qy  2180  AVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKKLSPPSISIDPPESQGSRPPCSPGVC  2239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2234  AVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKKLSPPSISIDPPESQGSRPPCSPGVC  2293

Qy  2240  LRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP  2286
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  2294  LRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP  2340
```

RESULT 7
AAY14586
ID   AAY14586 standard; protein; 2250 AA.
XX
AC   AAY14586;
XX
DT   07-DEC-1999 (first entry)
XX
DE   Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83481.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 31-40; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2250 AA;

Query Match   90.3%;   Score 10857;   DB 2;   Length 2250;
Best Local Similarity   93.6%;   Pred. No. 0;
Matches 2084;   Conservative 32;   Mismatches 104;   Indels 6;   Gaps 4;

```
Qy  62  GAACAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML  121
        |  |||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  30  GRPGPGSAEKDPGSADSEAEGLPYPALAPVFFFYLSQDSRPRSWCLRTVCNPWFERISML  89
```

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Qy   122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFPGKKCYLG  181
Db    90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG   149

Qy   182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDLTLP      241
Db   150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDLTLP      209

Qy   242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF   301
Db   210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF   269

Qy   302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTCVNWNQYYTNCSAGEHN    361
Db   270 ICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNTCVNWNQYYTNCSAGEHN    329

Qy   362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL   421
Db   330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL   389

Qy   422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTIASFSEPGSCYEELLKYLVVILRKAAR   481
Db   390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTIASFSEPGSCYEELLKYLVVILRKAAR   449

Qy   482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN    541
Db   450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHYHIGN    509

Qy   542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSPYHADCHLEPVRCQ   601
Db   510 GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQ    569

Qy   602 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPDGPF    661
Db   570 APPPRSPSEASGRTVGSGKVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPGPY    629

Qy   662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD   721
Db   630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD   689

Qy   722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   781
Db   690 SEAVYEFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   748

Qy   782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN   841
Db   749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN   808

Qy   842 IFDGVIVISTVWEIVGQGQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901
Db   809 IFDGVIVISTVWEIVGQGQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  868

Qy   902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV   961
Db   869 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV   928

Qy   962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVEGFQAEGDATKSESEPDFFSSVD       1021
Db   929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVEGFQAEGDANKSESEPDFFSSLD       988

Qy  1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
Db   989 GDGDRKKCCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSS 1048

Qy  1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
Db  1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSAAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1107

Qy  1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFPDLPDTLQVPGLHRTASGR 1201
Db  1108 LLSGEGQESQDEEESSEEERASPAGSDHRHRGSLEREAKSSFPDLPDTLQVPGLHRTASGR 1167


Qy  1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE   1261
Db  1168 GSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGEVRAWIRARLPACCLE   1227

Qy  1262 RDSWSAYIFPPQSRFLLCHRIITHKMFDHVVLIIFLNCITIAMERPKIDPHSAERIFL    1321
Db  1228 RDSWSAYIFPPQSRFLLCHRIITHKMFDHVVLIIFLNCITIAMERPKIDPHSAERIFL    1287

Qy  1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSG 1381
Db  1288 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSG 1347

Qy  1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILG  1441
Db  1348 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILG  1407

Qy  1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1501
Db  1408 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1467

Qy  1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISPLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1561
Db  1468 IMYDGLDAVGVDQQPIMNHNPWMLLYFISPLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1527

Qy  1562 EARRREEKRLRRLEKKRRSKEKQMAEAAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1621
Db  1528 EARRREEKRLRRLEKKRRSKEKQMAEAAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1587

Qy  1622 GLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA  1681
Db  1588 GLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVFLESVFKLVAFGFRRFFQDRWNQLDLA  1647

Qy  1682 IVLLSIMGITLBEIEVNLSLPINPTTIIRIMRVLRIARVLKLKMAVGMRALLHTVMQALP  1741
Db  1648 IVLLSIMGITLBEIEVNASLPINPTIIRIMRVLRIARVLKLKMAVGMRALLDTVMQALP   1707

Qy  1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG  1801
Db  1708 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLLFRVSTG   1767

Qy  1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA  1861
Db  1768 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA  1827

Qy  1862 KEBAELEAELELEMKTLSPQPHSPLGSPPLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1921
Db  1828 KEBAELEAELELEMKTLSPQPHSPLGSPPLWPGVEGPDSPDSPKPGALHPAAHARSASHF  1887

Qy  1922 SLEHPTMVPHPEBVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1991
Db  1888 SLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGL  1944

Qy  1982 PKAQSGSILSVHSQOPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
Db  1945 PKAQSGSVLSVHSQPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLR  2004

Qy  2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSEFWGGGSSIQVQQRSGIQSKVSKHI 2101
Db  2005 RQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHM  2064

Qy  2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSOEEPLFPRDLKKCYSVET  2160
Db  2065 TPPAPCPGPEPNWGKGPFPETRSSLELDTELSWISGDLLPPGGGQEEPSPRDLKKCYSVEA  2124

Qy  2161 QSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGGQPLGGPGSRPKKKLSPPSI 2220
Db  2125 QSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSI  2184

Qy  2221 SIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSD  2280
Db  2185 TIDPPESQGPRTPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSD   2244

Qy  2281 PTTMDP  2286
```

```
Db     2245 PADLDP 2250
             |:|
            PADLDP

Qy      242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy      302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
            ||||||||||||||||||||:|||||||:|:||||||||||||||||||||||||||||||
Db      270 ICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy      362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMNL 421
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMNL 389

Qy      422 CLVVIATQFSETKQRSQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVILRKAAR 481
            ||||||||||||||||:|||||:||||||||||||||||:|:|||||||||||||||||
Db      390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVILRKAAR 449

Qy      482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGGSCTRSHRRLSVHHLVHHHHHHYHLGN 541
            ||||||||||||||||:|||||||||||:|||:|||||||:||||||||||||||||||
Db      450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVHHLVHHHHHHYHLGN 509

Qy      542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAEBVHSFYHADCHLEPVRCQ 601
            |||||||||||||||||||||||||||||:||||:|||||||||:||||||||||||||
Db      510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAEBVHSFYHADCHLEPVRCQ 569

Qy      602 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
            ||||:|||||:|||||||||||||||||:|||:|||||||:||||||||||:||||||:
Db      570 APPRSPEASGRTVGSGKVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

Qy      662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
            |||||||||||||||:|||||||:|||||||||||:||||:|||:|||||||:|:||||
Db      630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Qy      722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
            ||||||||||||||||||||:|:|||||||:|||||||||||||||||||||||||||||
Db      690 SEAVYEFTQDAQHSDLRDPHS-RQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 748

Qy      782 IMIAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
            ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db      749 IMIAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 808

Qy      842 IFPDGVIVISVSVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
            |||||||||:||||||||||||:||||||||||||||||||||||||||||||||||||||
Db      809 IFPDGVIVISVSVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 868

Qy      902 CMLLMFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
            |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db      869 CMLLMFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 928

Qy      962 LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
            ||||||||||||||||||||||||||||||||||||||||:|||||:|||||||||:||
Db      929 LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDANKSESEPDFFSPSLD 988

Qy     1022 GDGDRKKRLALAVLALGEHAELRKSLLPPLIHTAATPMSHPKSSSTGVGEALGSGRRTSS 1081
            ||||||||:|||||||:||||||||||||||||||||||||:|||||||||||:||||||
Db      989 GDGDRKKCLALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSS 1048

Qy     1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
            ||||||||| |||||||||||||:|||||||||||||||||:||||:||||||:|||||||
Db     1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1107

Qy     1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
            |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db     1108 LLSGEGQESQDEEESSEEERASPPGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1167

Qy     1202 SSASEHQDCNGKSASGRLARTLRTDDPQLGDGDNDEGNLSKGERIQAWVRSRLPACCRE 1261
            |||||||||||||||||||||||||||||||||||||:|||||:|:||||||||:||||
Db     1168 GSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLE 1227

Qy     1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1287
```

RESULT 8

AAY14588

ID   AAY14588 standard; protein; 2268 AA.

XX

AC   AAY14588;

XX

DT   07-DEC-1999   (first entry)

XX

DE   Human T-type voltage-gated Ca channel alpha-1-G (hCavT1c).

XX

KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

XX

OS   Homo sapiens.

XX

PN   WO9929847-A1.

XX

PD   17-JUN-1999.

XX

PF   30-OCT-1998;   98WO-US023161.

XX

PR   05-DEC-1997;   97US-00985809.

XX

PA   (LOYO) UNIV LOYOLA CHICAGO.

XX

PI   Perez-Reyes E, Cribbs LL;

XX

DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83483.

XX

PT   New T-type voltage-gated calcium channels.

XX

PS   Disclosure; Page 49-58; 138pp; English.

XX

CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCavT1c. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX

SQ   Sequence 2268 AA;

Query Match   90.1%; Score 10833; DB 2; Length 2268;
Best Local Similarity   92.8%; Pred. No. 0;
Matches 2083; Conservative 32; Mismatches 105; Indels 24; Gaps   5;

```
Qy       62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy      122 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       90 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy      182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLLDTLP 241
            |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db      150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLLDTLP 209
```

```
AC   AAE01019;
XX
DT   17-JUL-2001 (first entry)
XX
DE   Human T-type low voltage activated calcium channel alpha1G-c protein.
XX
KW   Human T-type low voltage activated calcium channel alpha1G-c; stress;
KW   epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
KW   endocrine disorder; respiratory disorder; peripheral muscle disorder;
KW   muscle excitability; fertilisation; contraception; hypertension;
KW   neuronal firing regulation; cardiovascular disorder; gene therapy;
KW   forensic analysis; epidemiological study; neuroleptic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1138
FT                   /note= "Encoded by GAG"
FT   Misc-difference 1142
FT                   /note= "Encoded by GAA"
FT   Misc-difference 1680
FT                   /note= "Encoded by ACG"
FT   Misc-difference 1683
FT                   /note= "Encoded by GAA"
XX
PN   WO200130844-A1.
XX
PD   03-MAY-2001.
XX
PF   06-OCT-2000; 2000WO-US027761.
XX
PR   26-OCT-1999;   99US-00426998.
XX
PA   (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI   Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX
DR   WPI; 2001-300486/31.
DR   N-PSDB; AAD04756.
XX
PT   New nucleic acid encoding human calcium channel protein, useful for
PT   identifying specific modulators and potential pharmaceuticals for
PT   treating e.g. epilepsy.
XX
PS   Claim 11; Page 81-99; 115pp; English.
XX
CC   The invention relates to isoform of human T-type low voltage activated
CC   calcium channel (alpha1G-c) cDNA and protein. Cells transformed with
CC   calcium channel DNA to express calcium alpha1G-c channel protein are used
CC   to identify specific modulators (antagonists or agonists). These
CC   modulators are useful as therapeutic agents and are used for treating
CC   wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress
CC   epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
CC   endocrine disorders, respiratory disorder, peripheral muscle disorder,
CC   muscle excitability, fertilisation, contraception, disorders involving
CC   hypertension, neuronal firing regulation, potentiation of synaptic
CC   signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
CC   hypertrophy, angina pectoris). Calcium alpha1G-c channel DNA is useful
CC   for isolating and identifying related molecule mutations. It is also
CC   optionally used as antisense sequences, in gene therapy. Calcium channel
CC   alpha1G-c DNA, protein and antibodies are useful for forensic analysis,
CC   diagnosis and epidemiological studies, by standard hybridisation or
CC   immunological assays. The present sequence is T-type low voltage
CC   activated calcium channel alpha1G-c protein
XX
SQ   Sequence 2273 AA;
```

```
Query Match             90.0%;  Score 10820.5;  DB 4;  Length 2273;
Best Local Similarity   92.5%;  Pred. No. 0;
Matches 2080;  Conservative   35;  Mismatches  105;  Indels   29;  Gaps    5;

Qy    62 GAAGAGSTEKDPGSADSEAEGLPYPAIAPVVFFYLSQDSRPRSWCLRTVCNPWFEERVSML 121
```

```
Qy 1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1288 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1347

Qy 1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1348 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1407

Qy 1442 VQLFKGKFPFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1408 VQLFKGKFPFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1467

Qy 1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE 1561
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1468 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE 1527

Qy 1562 EARRREBKRLRRLEKKKRSKEKQMA------------------EAQCKPYYSDYSRRFLL 1603
         |||||||||||||||||||||||||                  |||||||||||||||
Db 1528 EARRREBKRLRRLEKKKRSKEKQMADLMLDDVIASGSASAASEAQCKPYYSDYSRRFLL 1587

Qy 1604 VHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVESVFKLV 1663
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1588 VHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVLESVFKLV 1647

Qy 1664 AFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIVNLSLPINPTIIRIMRVLRIARVLKLL 1723
         || ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 1648 AFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIVNASLPINPTIIRIMRVLRIARVLKLL 1707

Qy 1724 KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFPAALGVELFGDLECDETHPCEGLGRHA 1783
         |||||||||| |||||||||||||||||||||| ||||||||||||||||||||||||||
Db 1708 KMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA 1767

Qy 1784 TFRNFGMAFLTLFRVSFGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLV 1843
         ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db 1768 TFRNFGMAFLTLFRVSFGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLV 1827

Qy 1844 NVVIAVLMKHLEESNKEAKEBAELEABLELEMKTLSPQHSPLGSSPFLWPGVEGVNSTDS 1903
         |||||||||||||||||||||||||| ||||||||||||||||||||||| :|:  ||
Db 1828 NVVIAVLMKHLEESNKEAKEBAELEAELELEMKTLSPQHSPLGSSPFLWPGVEGPDSPDS 1887

Qy 1904 PKPGAPHTTAHIGAAGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1963
         ||||| | :|| |||||||| | ||||| |||   |||||||||||||||||||||||
Db 1888 PKPGALHPAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYM 1944

Qy 1964 CRNGSTAERSLGHRGWGLPKAQSGSIISVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA 2023
         ||:||||  ||||||||||||||||:|||||||||| ||||||| | ||||||.|||| 
Db 1945 CRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGT 2004

Qy 2024 IPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGS 2083
         ||||||||||||||||||||||||||||||||||||||| ||||||  | ||| |||.|
Db 2005 IPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQS 2064

Qy 2084 SIQVQQRSGIQSKVSXHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSS 2142
         | : || : | |:  |:  ||||||||||| |:. ||||||||||||||||||||| .|
Db 2065 STQAQQHSRSHSKISKHMTPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGG 2124

Qy 2143 QEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQ 2202
         |||| .|||||||||||.|||:||| .|||||||||||||||||||||.|  .||||||
Db 2125 QEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQ 2184

Qy 2203 PLGGPGSRPKKKLSPPSISIDDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTA 2262
         |||||||||||||||||:.||||||||| | |.|| ||||||||.||||||  :|| |:|
Db 2185 PLGGPGSRPKKKLSPPSITIDPPESQGPRTPSPGICLRRRAPSSDSKDPLASGPPDSMA 2244

Qy 2263 ASPSPKKDTLSLSGLSSDPTDMDP 2286
         ||||||||.|||||||||| |:||
Db 2245 ASPSPKKDVLSLSGLSSDPADLDP 2268
```

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RESULT 9
AAE01019
ID   AAE01019 standard; protein; 2273 AA.
XX
```

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Qy   1179 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRIARTLRTDDPQLDGDDNDE 1238
          ||||||||||||||||||||||||||||||||||||::|:.:|||||:||||::|
Db   1168 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDE 1227

Qy   1239 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1298
          |||||||:.||:|:.||||||.|||||||||||||||||||||||||||||||||||||
Db   1228 GNLSKGERVRAWIRARLPACCLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1287

Qy   1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1358
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347

Qy   1359 VLDGLIVLISVIDILVSMVSDSGTKIIGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1418
          ||||||||||||||||||||||||||.|||||||||||||||||||||||||||||||||
Db   1348 VLDGLIVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1407

Qy   1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASYRWVRHKY 1478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASYRWVRHKY 1467

Qy   1479 NFDNLGQALMSLFVLASKDGWDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468 NFDNLGQALMSLFVLASKDGWDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1527

Qy   1539 VLNMFVGVVVENFHKCRQHQEEEAARRREEKRLRLEKKRRSKEKQMAEAQCKPYYSDYS 1598
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1528 VLNMFVGVVVENFHKCRQHQEEEAARRREEKRLRLEKKRRSKEKQMAEAQCKPYYSDYS 1587

Qy   1599 RPFLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFES 1658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||.||
Db   1588 RPFLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLES 1647

Qy   1659 VFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIAR 1718
          |||||||.||||||||||||||||||||||||.||.|||.|||||||||||||||||||
Db   1648 VFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGIPLEQIEVNASLPINPTIIRIMRVLRIAR 1707

Qy   1719 VLKLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG 1778
          ||||||||||||||.|||||||||||||||||||||||||||||||||||||||||||
Db   1708 VLKLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG 1767

Qy   1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTA 1838
          |||||||||||||||||||||||||||||||||.:|||||||||||||||||||||||||
Db   1768 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTA 1827

Qy   1839 QFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGV 1898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   1828 QFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGP 1887

Qy   1899 NSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP 1958
          :.|||||||:||.||.:|||:|||||||||.||||::.        :|||||||||||||
Db   1888 DSFDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLP 1944

Qy   1959 NDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSYILQPKDVHYLLQPHGA 2018
          |||||||||||||.|||||||||||||||.|||||||||||||||||.|.|:|:|||.|
Db   1945 NDSYMCRNGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQPHLLQPHSA 2004

Qy   2019 PTWGAIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSS 2078
          ||||:|||||||||||||||||||||||||||||||||||||||:|||||.||.:|.:|
Db   2005 PTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYS 2064

Qy   2079 FWGGSSIQYQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDL 2138
          ||| ||:| ||:|:||:||||:.|.|||||| ||.|.|.|||||||||||||||||||||
Db   2065 FWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDL 2124

Qy   2139 L-PSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPS 2197
          | | .:|||:.||||||||||.|||.|||..:|||||||||||||||||||||:|..:|| 
Db   2125 LPPGGGOEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPS 2184

Qy   2198 SLGGQPLGGPGSRPKKKLGPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSP 2257
          .|||||||||||||||||.|||:.||||||||||| .||.|||||||..||||||.|:.|
Db   2185 NLGGQPLGGPGSRPKKKLSPPSITIDPPESQGSRPTPPSPGICLRRRAPSSDSKDPLASGP 2244
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Db     30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVFFYYLSQDSRPRSWCLRTVCNPWFERISML 89

Db    122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Db    182 DTWNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    150 DTWNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Db    242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
          |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy    210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Db    302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
          |||||||||||||||||||||||.||||| ||.|.||||||||||||||||||||||||||
Qy    270 ICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYBAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Db    362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Db    422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKLVIYILRKAAR 481
          |||||||||||||||.|||||||||||||||||||||||||||||||||.|:|||||||
Qy    390 CLVVIATQFSETKQRSQLMREQRVRFLSNASTLASFSEPGSCYEELLKYIVYILRKAAR 449

Db    482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 541
          |||||||.||||.||||||.|.|||||.|||.|.|||||||||||||||||||||||||
Qy    450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCCSRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Db    542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
          |||||||||||||||||||||||||||||||..||||||||||||||||||||||||||
Qy    510 GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ 569

Db    602 APPPRCPSEASGRTVGSGKVPTVTHSPPPBILKDRALVEVAPSPGPPTLTSFNIPPGPF 661
          |||||.|||||||||||||||||||||||||:|:||||||||..||||||:|.|||||:
Qy    570 APPPRSPSEASGRTVGSGKVPTVTHSPPPETLKEKALVEVAASSGGPPTLISLNIPPGPY 629

Db    662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
          ||||||||||||||||:||||||||.||||||||||||||||||.|||||:|.|||||||
Qy    630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Db    722 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
          |||||||||||||||||||||.|||||||||||||||||||||||||||||||||||||
Qy    690 SEAVYEFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 748

Db    782 IMIAILVNTLSWGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
          |||||||||||||||||.|||||||||||||||||||||||||||||||||||||||||
Qy    749 IMIAILVNTLSWGIEYHQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 808

Db    842 IFDGVIVSWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATF 901
          ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Qy    809 IFDGVIVSWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 868

Db    902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    869 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 928

Db    962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE----------1003
          ||||||||||||||||||||||||||||||||||||||||||
Qy    929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEEISKREDASGQLSCIQLP 988

Db   1004 ----GDATKSEBEPDFFSPSVDGDDRKKRIALVAIGEHAELRKSLLPPLIIHTAATPM 1058
              .||:|||.||||||.||.||.|||| ||||:.|||.||||||||||||||||||||
Qy    989 VDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPM 1048

Db   1059 SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRR 1118
          |.|||||||:|||||..||||||||||||||| |||||.||||||||||||||||||||||
Qy   1049 SLPKSTSTGLGEALGPASRRTSSSGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRR 1107

Db   1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPAGSDHRHRGSLERE 1178
          |||||||||||||||||||||||||||||.:|||:||||||.|||||||||||||||||
Qy   1108 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQOSQDQEESSEEERASPAGSDHRHRGSLERE 1167
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Qy  2258  LDSTAASPSPKKDTLSLSGLSSDPTDMDP  2286
          |||  |||||||| |||||||||| : |
Db  2245  PDSMAASPSPKKDVLSLSGLSSDPADLDP  2273
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RESULT 10
AAY14587

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ID   AAY14587  standard; protein; 2261 AA.
XX
AC   AAY14587;
XX
DT   07-DEC-1999   (first entry)
XX
DE   Human T-type voltage-gated Cc channel alpha-1-G (hCaVT1b).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
OS   Homo sapiens.
XX
PN   WO992994 7-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998; 98WO-US023161.
XX
PR   05-DEC-1997; 97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83482.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 40-49; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCaVT1b. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2261 AA;
```

Query Match   89.9%; Score 10810.5; DB 2; Length 2261;
Best Local Similarity   92.9%; Pred. No. 0;
Matches 2078; Conservative   33; Mismatches 109; Indels   17; Gaps   5;

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Qy   62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML  121
Db   30  GRPGPGSAAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISML  89

Qy  122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  181
Db   90  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  149

Qy  182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP  241
Db  150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP  209
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Db  150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP  209

Qy  242  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  301
Db  210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPY  269

Qy  302  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETNSSSNTTCVNWNQYYTNCSAGEHN   361
Db  270  ICSQPRENGMRSCRSVPTLRGDGDGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN  329

Qy  362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVWDAHSFYNFIYFILLIIVGSFFMINL  421
Db  330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVWDAHSFYNFIYFILLIIVGSFFMINL  389

Qy  422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEEGSCYEELLKYLYVILRKAAR  481
Db  390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLYVILRKAAR  449

Qy  482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN   541
Db  450  RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGN   509

Qy  542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ  601
Db  510  GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQ   569

Qy  602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  661
Db  570  APPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY  629

Qy  662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721
Db  630  SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD  689

Qy  722  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  781
Db  690  SEAVYEFTQDAQHSDLRDPHS-RQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   748

Qy  782  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN  841
Db  749  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN  808

Qy  842  IFDGVIVIVSVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901
Db  809  IFDGVIVIVSVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  868

Qy  902  CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV   961
Db  869  CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV   928

Qy  962  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
Db  929  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDANKSESEPDFFSPSLD  988

Qy 1022  GDGDRKKRLALAVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVEALGSSGSRRTSS 1081
Db  989  GDGDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPASRRTSS  1048

Qy 1082  SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
Db 1049  SGGAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1107

Qy 1142  LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
Db 1108  LLSGEGQESQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1167

Qy 1202  SSASEHQDCNGKSASGRLARTLRTDDPLQGDGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
Db 1168  GSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVARWIRARLPACCLE 1227

Qy 1262  RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1228  RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1287
```

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XX
AC   AAY14589;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human T-type voltage-gated Ca channel alpha-1-G (hCaVT1d).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;        98WO-US023161.
XX
PR   05-DEC-1997;        97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83484.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 58-67; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCaVT1d. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2243 AA;
```

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Query Match          89.8%;   Score 10806.5;  DB 2;  Length 2243;
Best Local Similarity  93.3%;   Pred. No. 0;
Matches 2076;   Conservative 33;   Mismatches 104;   Indels 13;   Gaps 5;
```

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Qy    1322  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1288  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1347

Qy    1382  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1348  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1407

Qy    1442  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1408  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1467

Qy    1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1468  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1527

Qy    1562  EARRREEKRLRRLEKKRR------------SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
            ||||||||||||||||||                  ||||||||||||||||||||||||
Db    1528  EARRREEKRLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTS 1587

Qy    1611  HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVPESVFKIVAFAFRRF 1670
            ||||||||||||||||||||||||||||||||||||||||| ||||||||:| |||||
Db    1588  HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVLESVFKIVAFGFRRF 1647

Qy    1671  FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1648  FQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1707

Qy    1731  ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1790
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1708  ALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1767

Qy    1791  AFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1850
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1768  AFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1827

Qy    1851  MKHLEESNKEAKEAABLEAELEAELLEMKTLSPQQHSPLGSPF:WPGVEGVNSTDSPKPGAPH 1910
            |||||||||||||||||||||||||||||||||||||::||||||||||| ||||||||
Db    1828  MKHLEESNKEAKEAABLEAELEAELLEMKTLSPQQHSPLGSPFLWPGVEGPSDPSPKPGALH 1887

Qy    1911  TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1970
            |||||||||||| |||||||||||||||||  |||||||||||||||||||||||||
Db    1888  PAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTA 1944

Qy    1971  ERSLGHRGWGLPKAQSGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPP 2030
            |||||||||||||||||||||||||||| :||||||||||||||||||:|||||||||
Db    1945  EGPLGHRGWGLPKAQSGSVLSVHSQPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPP 2004

Qy    2031  GRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR 2090
            |||||||||||||||||||||||||||||||||||||:|||| ||||||||||||||
Db    2005  GRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSTQAQQH 2064

Qy    2091  SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEFLPSP 2149
            ||||||||||||||| ||||||||| ||||||||||||||||||||  |||||||| :
Db    2065  SRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPDGGQEEPSP 2124

Qy    2150  RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGS 2209
            ||||||| ||:| |||||||||||||||||||||||||||||||||||||||||||||
Db    2125  RDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSPHLGTDPSNLGGQPLGGPGS 2184

Qy    2210  RPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPGPKK 2269
            |||||| ||||||||||||||  ||||||||||||  |||||||| |||||||:|||||
Db    2185  RPKKKLSPPSITITDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKK 2244

Qy    2270  DTLSLSGLSSDPTDMDP 2286
            |  ||||| ||| :|
Db    2245  DVLSLSGLSSDPADLDP 2261
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Qy     62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
           ||| |  ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     30  GRPGPGSAEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy    122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy    182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy    242  MLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210  MLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy    302  ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
           |||||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
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RESULT 11
AAY14589
.  ID  AAY14589 standard; protein; 2243 AA.
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Db    270 ICSQPRENGMRSCRSVPTLRGDGGGGPCGLDYEAYNSSNTTCVNWNQYYTNCSAGEHN 329

Qy    362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFIYFILLIIVGSFFMINL 389

Qy    422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy    482 RLAQVSRAIGVRAGLLSSPVARSGQEFQPSGSCTRSHRRLSVHHLVHHLHHHHHYHLGN 541
          |||||||||||||||||||||||||     :|||||||||||||||  |||||||||
Db    450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHLHHHHHYHLGN 509

Qy    542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
          |||| |||||||||||||||||||||||| || |||||||||||||||||||||||||||
Db    510 GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ 569

Qy    602 APPPRCPSEASGRTVGSCKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
          ||||| |:||||||||||||||||||||||:|||  |:||||| ||||||||:|||||:
Db    570 APPPRSPSEASGRTVGSGKVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

Qy    662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
          |||||||||||||||| ||||||||||||||||||||||| |||||| ||||||:|||
Db    630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Qy    722 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDFTFRKIVDSKYFGRG 781
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    690 SEAVYEFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDFTFRKIVDSKYFGRG 748

Qy    782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPPGYIKNPYN 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPPGYIKNPYN 808

Qy    842 IFDGVIVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 IFDGVIVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 868

Qy    902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKV 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKV 928

Qy    962 LYNGMASTSSWAALYFIALMFGNYVLFNLLVAILVEGFQABGDATKSESEPDFFSPSVD 1021
          |||||||||||||||||||||||||||||||||||||||||||||:||||:|||||||
Db    929 LYNGMASTSSWAALYFIALMFGNYVLFNLLVAILVEGFQAEGDANKSESEPDFFSPSLD 988

Qy   1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
          |||||||:||||||||||||||||||||||||||||||||||:|||||:||||| |||||
Db    989 GDGDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEAIGPASRRTSS 1048

Qy   1082 SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
          |||||| | :||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1107

Qy   1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1108 LLSGEGQESQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1167

Qy   1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWRSRLPACCRE 1261
          |||||||||||||||||||||:|||||||:|:|||||:||||||||:|||||||||||
Db   1168 GSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLE 1227

Qy   1262 RDSWSAYIFPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228 RDSWSAYIFPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1287

Qy   1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSG 1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1288 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSG 1347

Qy   1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1348 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1407
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Db   1442 VQLFKGKFFVCQGEDTRNITNKSDCAEAASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1501

Qy   1442 VQLFKGKFFVCQGEDTRNITNKSDCAEAASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 VQLFKGKFFVCQGEDTRNITNKSDCAEAASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1467

Qy   1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1527

Qy   1562 EARRREEKRLRLEKKRRSKEKQMAEAQCKPYYSDYSYRFLLVHHLCTSHYLDLFITGVI 1621
          ||||||||||||||||||     :|||||||||||||||||||||||||||||||||||
Db   1528 EARRREEKRLRLEKKRR-----KAQCKPYYSDYSYRFLLVHHLCTSHYLDLFITGVI 1580

Qy   1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFFVFESVFKLVAFARFRFFQDRWNQLDLA 1681
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db   1581 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLA 1640

Qy   1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 IVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALP 1700

Qy   1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1760

Qy   1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
          ||||||||| ||||:|||||||||||||||||||||||||:|||||||||||||||||||
Db   1761 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1820

Qy   1862 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
          ||||||||||||||||||||||||||||||||||||| ||:||||||||  |||:|||
Db   1821 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHF 1880

Qy   1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
          ||||||| |||| ::|||:||   |||||:|||||||||||||||| :|| |||||||||
Db   1881 SLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGL 1937

Qy   1982 PKAQSGSILSVHSQPADTSCIILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
          ||||||:|||||||||||:|| |||||||:|||:|||||||:|||||||||||||||||||
Db   1938 PKAQSGSVLSVHSQPADTSYIILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLR 1997

Qy   2042 RQAAIRTDSLDVQLGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
          |||||||||||||||||||||||:|||||||||||||||||||||||:||:||||:||:|
Db   1998 RQAAIRTDSLDVQLGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHM 2057

Qy   2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVET 2160
          |:|||||||||:|||| ||||:|||||:|||||||||||  |||:|||||:||||||::
Db   2058 TPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYSVEA 2117

Qy   2161 QSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSI 2220
          |||||||:|||||||||||||||||||||:||||| |||||||||||||||||||||||||
Db   2118 QSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSI 2177

Qy   2221 SIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSD 2280
          :|||||||||||| :|||||||||||:|||| || | |||: |  || |||:||||||||
Db   2178 TIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSD 2237

Qy   2281 PTDMDP 2286
          |:| ||
Db   2238 PADLDP 2243
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RESULT 12
ADJ68819
ID   ADJ68819   standard; protein; 2243 AA.
XX
AC   ADJ68819;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID625.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;

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KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200308768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0399987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 625; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 2243 AA;

Query Match             89.8%;  Score 10806.5;  DB 7;  Length 2243;
Best Local Similarity   93.3%;  Pred. No. 0;
Matches 2076;  Conservative  33;  Mismatches  104;  Indels  13;  Gaps  5;

Qy         62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVFPFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVFPFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy        122 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVKMVALGIFGKKCYLG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVKMVALGIFGKKCYLG 149

Qy        182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy        242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy        302 ICSQPRENGMRSCRSVPTLRGEGGGPPCGLDYETNSSSNTTCVNMNQYYINCSAGEHN 361
              |||||||||||||||||||||||||||||||||| :||||||||:||||||||||||||
Db        270 ICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy        362 PFKGAINFDNIGYAWTAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMNL 421
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 PFKGAINFDNIGYAWTAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMNL 389

Qy        422 CLVVIATQFSETKQRESQLMEQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CLVVIATQFSETKQRESQLMRRQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy        482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN 541
              |||||||||||||||||||||||||||||||||::||||||||:|||||||||||||||
Db        450 RLAQVSRAAGVRVGLLSSPAPLGGQEFTQPSSSCSRSHRRLSVHHLVHHHHHHYHLGN 509

Qy        542 GTLRVPRASPEIQDRDANGSRRLMLPPSSTPPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
              ||| |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ 569

Qy        602 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSPNIPPGPF 661
              |||||||||||||||||||||||||||| :||||||||||||||||||||||:||||||:
Db        570 APPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

Qy        662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGPESADHVMPDSD 721
              ||||||||||||||||||||||||||||||||||||||||||||||: |||||||||||
Db        630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Qy        722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        690 SEAVYEFTQDAQHSDLRDPHS--RQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 748

Qy        782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 808

Qy        842 IFPDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 IFPDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 868

Qy        902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIILTQEDWNKV 961
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIILTQEDWNKV 928

Qy        962 LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
              |||||||||||||||||||||||||||||||||||||||||||||::||||||||||:|||
Db        929 LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDANKSESEPDFFSPSLD 988

Qy       1022 GDGDRKKRLALVALGEHAELRKSLLPPLLIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
              |||||||:||:||:||| :|||:|||||||||||||||||||:||||:|||||||||||
Db        989 GDGDRKKCLALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSS 1048

Qy       1082 SGSAEPGAAHHEMKCPDSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
              |||||||||| ||||:|||||||||||||||||||||||||||||||||||||||||||||
Db       1049 SGSAEPGAA-HEMKSPFSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1107

Qy       1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
              |||||||||||||||:||||:||||||||||||||||||||||||||||||||||||||||
Db       1108 LLSGEGQESQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1167

Qy       1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
              |||||||||||||||||||:|||||||||:|||||:||||||||||:||||:||||| :|
Db       1168 GSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLE 1227

Qy       1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db       1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1287

Qy       1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1347

Qy       1382 TKIIGMLRVLRLLRTLRPLRVISRAQGLKLVVETIMSSLKPIGNIVIVCCAFFIIFGILG 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db                                                                   1441
```

KW   Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;
KW   T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
KW   hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.
XX
OS   Homo sapiens.
XX
PN   WO20102561-A2.
XX
PD   11-JAN-2001.
XX
PF   04-JUL-2000; 2000WO-CA000794.
XX
PR   02-JUL-1999; 99US-00346794.
XX
PA   (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI   Snutch TP, Baillie DL;
XX
DR   WPI; 2001-123111/13.
DR   N-PSDB; AAF31684.
XX
PT   Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT   cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT   epilepsy.
XX
PS   Example 3; Fig 6; 103pp; English.
XX
CC   The present sequence is given in a specification providing sequences and
CC   partial sequences for three types of mammalian (human and rat) T-type
CC   calcium channel subunits. An expression cassette has been generated which
CC   comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC   subunit operably linked to control sequences to effect its expression.
CC   The novel calcium channel nucleic acids and proteins are useful for
CC   treating conditions characterised by undesirable levels of T-type calcium
CC   channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC   hypertension, sleep disorder and epilepsy
XX
SQ   Sequence 2266 AA;

Query Match   87.6%; Score 10533; DB 4; Length 2266;
Best Local Similarity   91.2%; Pred. No. 0;
Matches 2050; Conservative   38; Mismatches 125; Indels   36; Gaps   6;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
             :||| ||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy 122 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFPDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
             ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||:||
Db   90 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFPDFIFAFFAVEMVVKNVALGIFGKKCYIG 149

Qy 182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLLLDTLP 241
             ||:||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db 150 DTNNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy 242 MLGNVLLLCFFVFFIFGIVGVGVMAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
             ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db 210 MLGNVLLLCFFVFFIFGIVGVGVMAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy 302 ICSQPRENGMRSCRSVPTLRGEGGGGPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
             |||||||||||||||||||||:||||||:|||| ||||: :|||||||||||||||||
Db 270 ICSQPRENGMRSCRSVPTLRGDGGGGPCGLDYEAYNSSSKTTCVNWNQYYTNCSAGEHN 329

Qy 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy 422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy 482 RLAQVSRAIGVRAGLLSSPVARSGQPEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN 541

Db 1348 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1407
Qy 1442 VQLFKGKFPFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1408 VQLFKGKFPFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1467

Qy 1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVINMFVGVVVENFHKCRQHQEEE 1561
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1468 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVINMFVGVVVENFHKCRQHQEEE 1527

Qy 1562 EARRREEKRLRRLEKKRSKEKQMAEAQCKPYYSDYSGRFRLLVHHLCTSHYLDLFITGVI 1621
              |||||||||||||||||| :|||||||| ||||||||||||||||||||||||
Db 1528 EARRREEKRLRRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1580

Qy 1622 GLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA 1681
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1581 GLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA 1640

Qy 1682 IVLLSIMGITLEEIEVNSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||:|||||||
Db 1641 IVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALP 1700

Qy 1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1701 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1760

Qy 1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
              |||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||
Db 1761 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1820

Qy 1862 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
              |||||||||||||||||||||||||||||||||||||| ||: :||||||| :| |||
Db 1821 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSSPKPGALHPAAHARSASHF 1880

Qy 1922 SLEHPTMVPHEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
              |||||| || || ||||||||||||||||||||||||||||||:||||||| |||||||
Db 1881 SLEHPTMQPHPTELP--GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGL 1937

Qy 1982 PKAQGSSILSVHSQPADTSCIIQLPKDVHLYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
              |||||||:||||||||||| ::|||||| ||||||| ||||| ||||||||||||||||||
Db 1938 PKAQGSSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLR 1997

Qy 2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGGSIQVVQRSGIQSKVSKHI 2101
              |||||||||||||||||||||| ||||||: || ||| ||| : ||| |||:||:
Db 1998 RQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHM 2057

Qy 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVET 2160
               ||||||| |:| |||||||||||||||||||||||| | |||| |||||||||||
Db 2058 TPPAPCPGPENWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYSVEA 2117

Qy 2161 QSCRRRPGFWLDEQRRHSIAVSCLDSGSQOPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSI 2220
              |||:||| |||||||||||||||||||||| || ::|||| ||| ||||||||||||||
Db 2118 QSCQRRPTSWLDEQRRHSIAVSCLDSGSQOPHLGTDPSNLGQOPLGQPGSRPKKKLSPPSI 2177

Qy 2221 SIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSD 2280
              :||||||| | ||||:|||||||:|| |||| ||| |||||||||||:|||||||||
Db 2178 TIDPPESQGPRTPPSPGICLRRRAPSDSSKDPLASGPPDSMAASPSPKKDVLSLSGLSSD 2237

Qy 2281 PTDMDP 2286
              | |:||
Db 2238 PADLDP 2243

RESULT 13
AAB66481
AAB66481 standard; protein; 2266 AA.
XX
AC   AAB66481;
XX
DT   09-APR-2001 (first entry)
XX
DE   Human alpha-IG T-type calcium channel protein.
XX

```
Db   450  RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVNHLVHHHNHMHNHYHLGN   509

Qy   542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ   601
          |||:|||||||||||||||||||||||||||:  |||:|||||||||||||:|||||||
Db   510  GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCMLEPVRCQ   569

Qy   602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSGPPTLTSFNIPPGPF   661
          |||||.||.||||||||||||||||.||||||.|::|||||||.:|||||||.|||||:
Db   570  APPPRSPSRASGRTVGSGKVYPTVNTSPPPETLKERALVEVAASSGPPTLTSLNIPPGPY   629

Qy   662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD   721
          |||||||||||||||:|||||||||.||||||||||||||||| |||| | || :|||||
Db   630  SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD   689

Qy   722  SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   781
          |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db   690  SEAVYEFTQDAQHSDLRDPHS--RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  748

Qy   782  IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN   841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   749  IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN   808

Qy   842  IFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF   901
          |||||||||| :|||||||||||||||||||||||||||||||||||||||||||||||
Db   809  IFDGVIVISVNEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF   868

Qy   902  CMLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV   961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869  CMLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV   928

Qy   962  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE----------          1003
          |||||||||||||||||||||||||||||||||||||||||||
Db   929  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEEISKREDASGQLSCIQLP  988

Qy  1004  -----GDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM  1058
               |||.||||||||||||||.|||||||:|||.|.|||.|||||||||||||||||||
Db   989  VDSQQGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPM  1048

Qy  1059  SHPKSSSTGVGEALGSGSRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRR   1118
          |.||:|||.||||| .|||.|||||||||||  |||.|||||||||||||||||||||||
Db  1049  SLPKSTSTGLGEALGPASRRTSSSGSAEPGAA--HEMKSPPSARSSPHSPWSAASSWTSRR 1107

Qy  1119  SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPAGSDHRRGSLERE   1178
          |||||||||||||||||||||||||||||||||||||||||.||||||||||:|||||
Db  1108  SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEERASPAGSDHRNRGSLERE   1167

Qy  1179  AKSSFPLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDE  1238
          ||||||||||||||||||||||||||||||||||||||||||:.|| |||||||||.|:|
Db  1168  AKSSFPLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDE  1227

Qy  1239  GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRITTHKMPDHVVLVIIF  1298
          ||||||||:.||:|:||||| .||||||||||||||||||||||| |:||||||||||||
Db  1228  GNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITNKMPDHVVLVIIF  1287

Qy  1299  LNCITIAMERPKIDPHSAERIFITLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN  1358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1288  LNCITIAMERPKIDPHSAERIFITLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN  1347

Qy  1359  VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS  1418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1348  VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS  1407

Qy  1419  SLKPIGNIVVICCAFFIIFGIILGVQLFKGKFYVCQGEDTRNITNKSDCAEASYRWVRHKY  1478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db  1408  SLKPIGNIVVICCAFFIIFGIILGVQLFKGKFYVCQGEDTRNITNKSDCAEASYRWVRMKY  1467

Qy  1479  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF  1538
          ||||||||||||||||||||||||||||||||||||||||||||||.|||||||||||||
Db  1468  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPNMLLYFISFLLIVAFF  1527

Qy  1539  VLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRRSKEKQMABAAQCKPYYSDYS 1598
          |||||||||||||||||||||||||||||||||||||||||       ||||||||||||
Db  1528  VLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRR------KAQCKPYYSDYS   1580
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Qy  1599  RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIDEALKICNYIFTVIFVFES   1658
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||.||
Db  1581  RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIDEALKICNYIFTVIFVFLES  1640

Qy  1659  VFKLVJAFAFRFFQDRWNQLDLAIVLLSIMGITLBEIEVNLSLPINPTIIRIMRVLRIAR  1718
          ||||| || |||||||||||||||||||||||||||||||.:|||||||||||||||||
Db  1641  VFKLVAFGFRFFQDRWNQLDLAIVLLSIMGITLBEIEVNASLPINPTIIRIMRVLRIAR   1700

Qy  1719  VIKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLRCDETHPCEG  1778
          |||||||||||||||.|||||||||||||||||||||||||||||||||||.||||||||
Db  1701  VIKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG  1760

Qy  1779  LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTA  1838
          |||||||||||:||||||||||||||:|||||.:|||||||||:||||||||||||||||
Db  1761  LGRHATFRNFGWAFLTLFRVSTGDNWEGIMKDTLRDCDQESTCYFTVISPIYFVSFVLTA  1820

Qy  1839  QFVLVNVVIAVLMKHLEESNKEAKEAEAELELEMKTLSPQHPSLGSPFLWPGVEGV      1898
          |||||.|||||||||||||||||||||||||||||||||||||||||||:|||||.
Db  1821  QFVLVMVVIAVLMKHLEESNKEAKEAEAELELEMKTLSPQHPSLGSPFLNPGVEGP     1880

Qy  1899  NSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP  1958
          :|.||||||| :..||: ||||||||||||.|||| :|   |||||||||||||||:|||
Db  1881  DSPDSPKPGALMPAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTMSLP  1937

Qy  1959  NDSYMCRNGSTAERSLGHRGWGLPKAQSGSIISVHSQPADTSCILQLPKDVHYLLQPHGA  2018
          |||||||.|||| .|||||||||||||||| .||||||||||.|||||||..||||.:|
Db  1938  NDSYMCRRGSTABGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPMSA  1997

Qy  2019  PTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSS  2078
          ||||:|||||||||||||||||||||||||||||||||||||||.||||||.||.|. |
Db  1998  PTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYS  2057

Qy  2079  FWGGSSIQVQRRSGIQSKVSKHIRLAPCPGLEPSWAKDPPETRSSLELDTELSWIGGDL   2138
          |||.||.|.|: |.:|||.|||.   ||| |.| . |||||||||||||||||.|.|||
Db  2058  FWGQSSTQAQQHSRSHSKISKHHTPAPCAGPEPNMGKGPPETRSSLELDTELSNISGDL   2117

Qy  2139  L-PSSQEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLLDSGSGQPRLCFSPS  2197
          | |..||| .||||||||||| :||.||| .||||||||||||||||||||||| |  .||
Db  2118  LPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLLDSGSGQPHLGTDPS  2177

Qy  2198  SLGGQPLGGPGGPGSRPKKKLSPPSISDPPESQGSRRPCSPGVCLRRRAPASDSKDPSVSSP  2257
          .||||||||||||||||||||||||: :|||||||.|.||| .|||||||.|||||| ..||
Db  2178  NLGGQPLGGPGGPGSRPKKKLSPPSTTIDDPPESQGPRTPSPGICLRRRAPSSDSKDPLASGP  2237

Qy  2258  LDSTAASPSPRKDTLSLSGLSSDPTDMDP        2286
          ||.:|||||.|||.|||||||||||.|.||
Db  2238  PDSMAASPSPKKDVLSLSGLSSDPADLDP        2266
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PR   02-JUL-1999;
XX
PA   (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI   Snutch TP, Baillie DL;
XX
DR   WPI; 2001-123111/13.
DR   N-PSDB; AAF31678.
XX
PT   Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT   cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT   epilepsy.
XX
PS   Disclosure; Page 75-85; 103pp; English.
XX
CC   The present sequence is given in a specification providing sequences and
CC   partial sequences for three types of mammalian (human and rat) T-type
CC   calcium channel subunits. An expression cassette has been generated which
CC   comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC   subunit operably linked to control sequences to effect its expression.
CC   The novel calcium channel nucleic acids and proteins are useful for
CC   treating conditions characterised by undesirable levels of T-type calcium
CC   channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC   hypertension, sleep disorder and epilepsy
XX
SQ   Sequence 2359 AA;

Query Match   51.8%; Score 6226.5; DB 4; Length 2359;
Best Local Similarity   56.1%; Pred. No. 0;
Matches 1357; Conservative 246; Mismatches 506; Indels 311; Gaps 59;

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Qy    30  LARGWTRRRMERAPRSRDSPV-ASRSSTTCPG---PGAAGAG-STEKDPGS---AD---S   78
Db     6  LAADEVRVPLGASPAPAAPVRASPASPGAGREEQGGSGGVLAPESPGTECGADLGAD      65

Qy    79  EAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSMILVILLNCVTLGMFRPCED  138
Db    66  EEQPVPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCED  125

Qy   139  IACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLE  198
Db   126  VECRSERCSILEAFDDFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVMAGMME  185

Qy   199  YSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFG  258
Db   186  YSLDGHKVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFG  245

Qy   259  IVGVQLFMAGLLRNRCFLPENFSLPLSVD-LBPYYQTENEDESPFICSQPRENGMRSCRSV  317
Db   246  IVGVQLFMAGLLRNRCFLDSAFVRNNNLLTFLRPYYQTBEGEENPFICSSRRDNGMQKCSHI  305

Qy   318  PT--LRGEGGGGPPCSLDYETY------NSSSNTTCVNWNQYYTNCSAGEHNPFKGAI  367
Db   306  PSRRELRVQ------CTLGWEAYGQPQAEDGGAGRNACINWNQYYNVCRSGEFNPHNGAI  359

Qy   368  NFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIA  427
Db   360  NFDNIGYAWIAIFQVITLEGWVDIMYYMDAHSFYNFIYFILLIIMGSFFMINLCLVVIA  419

Qy   428  TQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVS  487
Db   420  TQFSETKQRENQLMREQRARYLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLY  479

Qy   488  RAIGVRAGLLSSPVAR-----SGQEPQPSGSCTRSHRRLSVHRLHLV-HHHHHHHHYHLGN  541
Db   480  ARWQSRWRKKVDPSSTVHGQQGPGRRPRRAG----RRTASVHHLVYHHHHHHHHHHYHFSH  534

Qy   542  GTLRVPRASPEIQDRDANGSRRLM-LPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVR  599
Db   535  GGPR--RPSPE---PGAGDNRLVRACAPPSPPSPGHGPP-DSESVHSIYHADCHVEGPQ  587

Qy   600  CQAPPPRCPSEASGRTVGSG---KVYPTV------HTSPPPEILKDKALVEVAPSP  646
Db   646
```

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Db   588  ERARVAHSIATAASLKLASGLGTMNYPTILPSGTVNSKGGTSSRPKGLRG----AGAP   641
Qy   647  GPPTLTSFNI-PPGPFSSMKLLETQSTGACHSSCK-ISSPC----SKADSGACGPDSCP  700
Db   642  GAAVHSPLSLGSPRPYEKIQDVVGEQGLGRASSHLSGLSVPCPLPSPQAGTLTCELKSCP  701

Qy   701  YCARTGAGEP--ESADHVMPDSDSEAVYEFTQDAQHSDLRDP-------HSRRRQR      747
Db   702  YCA-SALEDPEFEFSGSESGSDSDAHGVYEFTQDVRHGCRDPVQQPHEVGTPGHSNERRR  760

Qy   748  S-LGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTN   806
Db   761  TPLRKASQPGGIGHLWASFSGKLRRIVDSKYFNRGIMAAILVNTLSMGVEYHEQPELTN  820

Qy   807  ALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVL  866
Db   821  ALEISNIVFTSMFALEMLLKILACGPLGYIRNPYNIFDGIVVVISVWEIVGQADGGQSVL  880

Qy   867  RTFRIMRVLKLVRFLPALORQLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS  926
Db   881  RTFRLLRVLKLVRFLPALRRQLVVLMRTMDNVATFCMLLMLFIFIFSILGMHLFGCKFSL  940

Qy   927  ERD-GDTLPDRKNFDSLLWAIVTVFQILLTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
Db   941  KTDSGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGN 1000

Qy   986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRL-------ALVALG 1036
Db  1001  YVLFNLLVAILVEGFQAEGDATRSDTDEDKYISTQLEGDFXLRDLRATEMKMYSLAVTPN 1060

Qy  1037  EHAELRKSLLPPLLIHTAATPMSHPKSS--STGVGEALGSGSRRTSSSGSAEPGAAHHEMK 1095
Db  1061  GHLEGRGSLGPPLLITHTAATPMPTPKSSPNLDVAHAL-LDSRR-SSSGSVDPQLG--DQK 1116

Qy  1096  CPESARSSPHSPWSAASWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEE     1155
Db  1117  SLASLRSSPCTPWGPNSAGSSRRSSWNSLGRAPSLKRRSQCGERESLLSGEGKGSTDDE- 1175

Qy  1156  SSEEDRAS---------PAGSDHRHRGSLERERAKSSPDL-------PDTLQVPGLHRTAS 1199
Db  1176  -AEDSRPSTGTHPGASPGPRATPLRRAESLDH--RSTLDLCPPRPAPPAVQV-------  1224

Qy  1200  GRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACC  1259
Db  1225  --------HDCNGQMVALPSEFFLRIDSHKEDAAEFDDDIEDSCCFRLHKVLEPYAPQWC  1276

Qy  1260  RERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERI  1319
Db  1277  RSRESWALYLFPPQNRLRVSCQKVIAHKMFDHVVLVFIFLNCITIALERPDIDPGSTERA  1336

Qy  1320  FLTLSNYIFTAVPLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILLVSMVSD 1379
Db  1337  FLSVSNYIFTAIFVVEMMVKVKVVALGLLMGEHAYLQSSWNVLDGLLVLLVSLVDFIVAMASA 1396

Qy  1380  SGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGI  1439
Db  1397  GGAKILGVLRVVRLLRTLRPLRVISRAPGLKLVVETLLSSLRPIGNIVLICCAFFIIFGI  1456

Qy  1440  LGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGW  1499
Db  1457  LGVQLFKGKFYYCEGTDTRNITTKAECHAAHYRWVRKYNFDNLGQALMSLFVLSSKDGW  1516

Qy  1500  VDIMYDGLDAVGVDQQPIMNNNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQE  1559
Db  1517  VNIMYDGLDAVGIDQQPVQNHNPWMLLYFISPLLIVSFFVLNMFVGVVVENHKCRQHQE  1576

Qy  1560  EEEARREEKLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRILVHHLCTSHYLDLFITG  1619
Db  1577  AEEAARREEKLRRLERRRR-------KAQRRPYIADYSHTRRSIHSLCTSHYLDLFITF  1629

Qy  1620  VIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVPESVFKLVAFARFRFFQDRWNQLD  1679
Db  1630  IICLNVITMSMEHYNQPKSLDEALKYCNYVFTIIFVFVFEAAILKLVAFGFRRFFKDRWNQLD 1689
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Qy   1680  LAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQA  1739
                |||||||||||  |||||| : :||||| |:|| |||  ||||: ||||    ||:|
Db   1690  LAIVLLSIMGIALEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQA  1749

Qy   1740  LPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVS  1799
                ||||||||||||||||||:   ||||||  |||||||||||||||||||||||||
Db   1750  LPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFTNFGMAFLTLFRVS  1809

Qy   1800  TGDNWNGIMKDPSRDC---DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEE  1856
                ||||||||   |:|:  :  ||:|  :| ||:|:|:|  |||||||||||||||
Db   1810  TGDNWNGIMKDTLRECTREDKHICLSYLPALSPVYFVTFMLVAQFVLVNVVVAVLMKHLEE  1869

Qy   1857  SNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIG  1916
                |||:|||  ||||:|||||
Db   1870  SNKRAREDAEMDAEIELEM----------------------------AQGSTAQPPFTAQES----  1903

Qy   1917  AASGFSLEHFTMVPHPEEVPVPLGPLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH  1976
                :                     |::|
Db   1904  ----------------------QGTQPDTPNLLVVRKVSVSRMLSLPNDSYMFRPVAPAAAPHSH  1946

Qy   1977  RGWGLP------KAQSGSSLSVHSQPADTSCILQLP----------KDVHYLLQPHGAPTW  2021
                : |:|                      : |||:
Db   1947  ----PLQEVEMETYTGPVISAHSPLEPRASFQVPSAASSPARVSDPLCALSPRGTP--  1999

Qy   2022  GAIPKLPPPGRSPLAQPRLRRQAAIRTDSLD--VQGLGSREDLLSEVSGPSCPLTRSSSF  2079
                :       | :|:                  |::|   |  ||  |::| :::
Db   2000  ------------RSLSLSRLCRQEAMHSESLEGKVDDVGG--DSIPDYTEPAENMSTSQAS  2047

Qy   2080  WGG------------SSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDT  2129
                ::     :|||: | |||
Db   2048  TGAPRSPPCSPRPASVRTRKHTFGQRCISSR-----PPTLGGDEARAADP--------ADE  2095

Qy   2130  ELSWISGDLLPSSQEPLFP-----------RDLKKCYSVETQSCRRRPGFWLDE  2173
                :|:|                        :| |:
Db   2096  EVSHTTSSAHPWATEPHSPEASPTASPVKGTMGSGRDPRRPCSVDAQSFLDKPG-RPDA  2154

Qy   2174  QRRHSIAV----SCLDSGS-------QPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS  2221
                |:||     :|:|                | :|:    | | | ::  ||||||||
Db   2155  QRWSSVELDNGESHLESGEVRGRASELEPAL------------GSRRKKKMSPPCIS  2199

Qy   2222  IDPP--ESQGSRPPCSPG--VCLRRRAPASDS--KDPSVSSPLDSTAASP-----------  2265
                |||    :|:| | | :|  ||:|:|:|||:
Db   2200  IEPPTKDEGSSRPPAAEGGNTLRRRTPSCEAALHRDCPEPTEGPGTGGDPVAKGERWGQ  2259

Qy   2266  -SPKKDTLSLSGLSLSSDPTDM  2284
                :|: |:| |:|:|  ::|:|
Db   2260  ASCRAEHLTVPNFAFEPLDM  2279
```

```
RESULT 15
AAY06299
ID   AAY06299  standard; protein; 2353 AA.
XX
AC   AAY06299;
XX
DT   23-AUG-1999  (first entry)
XX
DE   Human activated calcium channel alpha 1H-1 subunit.
XX
KW   Calcium channel subunit 1H-1; human; neurological disorder;
KW   endocrinological disorder; cardiovascular disorder; urological disorder;
KW   hepatic disorder; respiratory disorder; vascular disorder.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Region         420..794
FT                  /note="intracellular loop"
FT   Region         520..528
FT                  /note="poly-His region"
XX
PN   WO9928342-A2.
```

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XX
PD   10-JUN-1999.
XX
PF   03-DEC-1998;  98WO-US025671.
XX
PR   03-DEC-1997;  97US-00984709.
PR   10-NOV-1998;  98US-00188932.
XX
PA   (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI   Williams M, Stauderman K, Harpold M, Hans M, Urrutia A;
PI   Washburn MS;
XX
DR   WPI; 1999-371096/31.
DR   N-PSDB; AAX59081.
XX
PT   Subunits of calcium channels.
XX
PS   Example 1; Page 151-161; 171pp; English.
XX
CC   The present sequence represents the the alpha 1H-1 subunit of a human low
CC   -voltage activated calcium channel. The sequence was deduced from cDNA
CC   (see AAX59080) isolated from a TT cell cDNA library. The invention
CC   provides calcium channel subunits, including 2 splice variants of alpha
CC   1H-1 (see also AAY06298), and isoform alpha 1H-2 (see AAY06300). The 1H-1
CC   splice variants were detected by RT-PCR in multiple tissues. They differ
CC   only at amino acid 2230, being either Asp or Glu. 1H-2 has a 319-amino
CC   acid deletion in the I-II intracellular loop relative to 1H-1. Cells and
CC   vectors containing nucleic acids encoding these subunits, and methods for
CC   identifying compounds that modulate the activity of calcium channels that
CC   contain the subunits are provided by the invention. Such compounds are
CC   used to treat calcium channel mediated disorders, including neurological,
CC   endocrinological, cardiovascular, urological, hepatic, respiratory and
CC   vascular disorders
XX
SQ   Sequence 2353 AA;
```

```
Query Match           51.7%;   Score  6222;   DB  2;   Length 2353;
Best Local Similarity 56.7%;   Pred. No. 0;
Matches 1370;  Conservative  208;  Mismatches  529;  Indels 310;  Gaps  62;

Qy   25   PPGPRLARGWTRRRMERAPRSRDSP--VASRSTTCPGPGAAGAGSTEKDPGSADSEAEG  82
               |||||                      |||
Db   19   PPGPAALVG---------ASPESPGAPGREAERGSELGVSPSESPAAERGAELGA--DEEQR  69

Qy   83   LPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACD  142
               :||:||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   70   VPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVECG  129

Qy   143  SQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLD  202
               |||||:||  ||||||||||||||||||||||:|||||||||||||||:|||:||:|||
Db   130  SERCNILEAFDAFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVVAGMMEYSLD  189

Qy   203  LQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMIGNVLLCFFVFFIFGIVGV  262
               :||||:|:|||||||||||||||||||||||||||||||:||||||||||||||||||
Db   190  GHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGV  249

Qy   263  QLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENEDESPFICSQPRENGMRSCRSVPTLR  321
               ||||||||||||           :||||:|||||:| | ::|
Db   250  QLWAGLLRNRCFLDSAFVRNNNLJFLRPYYQTEGEENPFICSSRRDNGMQKCCSHIP---  306

Qy   322  GEGGGGPPCSLDYETYN-------SSSNTTCVMNQYYTNCSAGEHNPFKGAINFDNIGY  374
                :                     ||:||||||||||||||||:||||||
Db   307  GRRELRMPCTLGWEAYTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGY  366

Qy   375  AWIAIFQVITLEGWVDIMYFVMDAHSFYNPIYFILLIIVGSFFMINLCLVVIATQFSETK  434
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   367  AWIAIFQVITLEGWVDIMYYVMDAHSFYNPIYFILLIIVGSFFMINLCLVVIATQFSETK  426

Qy   435  QRESOLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRA  494
               ||||||||||||                ||||||||||||||||||:|||| ||||:| |
Db   427  QRESOLMREQRARHISNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLYARWQSRW  486
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Qy   495  GLLSSPVARSGQEPQPSGSCTRSHRR------LSVHHLIV-HHHHHHHHYHLGNGTLRV      546
Db   487  RKKVDPSAVQGQGP--------GHRQRRAGRHTASVHHLVYHHHHHHHYHSHGSPRR        538

Qy   547  PRASPEIQDRDANGSRRIML--PPPSTPTPSGGPPRGAESVHSFYHADCHLE--PVRCQA     602
Db   539  PGPEPGACD------TRLVRAGAPPSPPSPGRGPP-DAESVHSIYHADCHIEGPQERARv     591

Qy   603  PPPRCPSEASGR-TVGSSKV-YPTV--------HTSPPPEILKDKALVEVAPSP----       646
Db   592  AHAAATAAASLRLATGLGTMNYPTILPSGVGSGKGSTSPGPK------GKWAGGPPGTG     644

Qy   647  --GPPTLTSFNIPPGPFSSMHKLLETQSTGAC--HSS-----CKISSPCSKADSGACGPD    697
Db   645  GHGPLSLNS----PDPYEKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP--PAGTLTCELK    698

Qy   698  SCPYCART-GAGEPESADHVMPDSDSRAVYEFTQDAQHSDLRDP---------            740
Db   699  SCPYCTRALEDPEGELSGSESGDSDRGVYEFTQDVRRGDRWDPTRPPRATDTPGPGPGS     758

Qy   741  HSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ    800
Db   759  PQRRAQQRAAP-GEPGWMGRLWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGVEYHEQ    817

Qy   801  PEELTNALEISNIVFTSLFALEMLLKLLVYGPPGYIKNPYNIFDGVIVVISVWEIVGQQG    860
Db   818  PEELTNALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIIVVISVWEIVGQAD    877

Qy   861  GGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLF    920
Db   878  GGLSVLRTFRLLRVLKLVRFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLF    937

Qy   921  GCKFASERD-GDTLLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSWAALYFIA    979
Db   938  GCKFSLKTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVLYNGMASTSSWAALYFVA    997

Qy   980  LMTFGNYVLFNLLVAILVEGFQAEGDATKSESSEPDFFSPSVDGDGDRKKRLALVAL----  1035
Db   998  LMTFGNYVLFNLLVAILVEGFQAEGDANRSDTDEDKTSVHFEEDFHKLRELQTTELKMCS   1057

Qy  1036  -----GEHAELRKSLLPPLIIHTAATPMSHPKSSS-TGVGEALGSGSRRTSSSGSAEPGA   1089
Db  1058  LAVTPNGHLERGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGSSSSGDPPLG-   1116

Qy  1090  AHHEMKCCPPSARSSPHSPWSAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE   1149
Db  1117  --DQKPPASLRSSPCAPWGPSGAWSSRRSSWSSLGRAPSLKRRGQCGERESLLSGEGKG   1173

Qy  1150  SQDEESSEEDRASPA--GSDHRHRGSLEREAKSSFDLPDTU----QVPGLH----R      1196
Db  1174  STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDGQVVALPSDFFLR   1231

Qy  1197  TASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLP   1256
Db  1232  IDSHREDAAELDDDSEDSCCLRLHKVLEPYKPQ------------W----            1265

Qy  1257  ACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSA   1316
Db  1266  --CRSREAWALYLFSPQNRFRVSCQKVITHKMFDHVVLVLFIFLNCVTIALERPDIDPGST  1323

Qy  1317  ERIFLTLSNYIFTAVFLAEMTVKVKVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSM 1376
Db  1324  ERVFLSVSNYIFTAIFVAEMMVKVKVVALGLLSGEHAYLQSSWNLLDGLLVLVSLVDIVVAM 1383

Qy  1377  VSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFII   1436
Db  1384  ASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFII   1443

Qy  1437  FGILGVQLFKGKFFVCQGEDTRNIITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASK   1496
Db  1444  FGILGVQLFKGKFYCEGPDTRNISTKAQCRAAHYRWRRKYNFDNLGQALMSLFVLSSK    1503

Qy  1497  DGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQ   1556
Db  1504  DGWVNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQ   1563

Qy  1557  HQEEEARRREEKLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFPLLVHHLCTSHYLDLF     1616
Db  1564  HQEAEARRREEKLRRLRERRRRSTFPS-PEAQRRPYYADYSPTRRSIHSLCTSHYLDLF    1622

Qy  1617  ITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWN   1676
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Qy  1677  QLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTV   1736
Db  1683  QLDLAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTV   1742

Qy  1737  MQALPQVGNLGLLFMLLFFIFAALGVELFGDLCEDETHPCEGLGRHATFRNFGMAFLTLF   1796
Db  1743  VQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLTLF   1802

Qy  1797  RVSTGDNWNGIMKDPSRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKH    1853
Db  1803  RVSTGDNWNGIMKDTLRECSREDHCLSYLPALSPVYFVTFVLVAQFVLVNVVAVLMKH    1862

Qy  1854  LEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTA   1913
Db  1863  LEESNKEAREDAELDAEIELEMA------------QGPGSARRVDADRP------       1899

Qy  1914  HIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA---  1970
Db  1900  ----------PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVPVPASAP       1943

Qy  1971  -----ERSLGHRGWGLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEV------YLLQP 2015
Db  1944  HPRPLQEVEMETYGAGTP--LGSVASVHSPPAESCASLQIPLAVSSPARSGEPLHALSP    2000

Qy  2016  HGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEV----SGPSC   2071
Db  2001  RGT------ARSPSLSRLLCRQEAVHTDSLEGK-IDSPRDTLDPAEPGEKTPVR         2047

Qy  2072  PLTRSSSFWGGSSIQVQQRSGIQSKV-SKH----IRLPAPCGPLEPSWAKDPPETRS     2123
Db  2048  PVTQ-----GGSLQSPPRSPRPASVRTRKHTFGQHCVSSRRAAPGGEEABASDP----    2096

Qy  2124  SLELDTELSWISGDLLP-SSQEEPLFP------RDLKKCYSVETQSCRRRPGFWLDE     2173
Db  2097  --ADEEVSHITTSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGFLDKPG-RADE   2152

Qy  2174  QRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGP--GSRPKKKLSPPSISIDPP-ESQGS   2230
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Qy  2231  -RPPCSPG--VCLRRRAPA------SDSKDPGVSSPLDSTAAS------PSPKKDTLSL   2274
Db  2204  ARPSAAEGGSTTLRRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGQASCRAEHLTV  2263

Qy  2275  SGLSSDPTDM------DP     2286
Db  2264  PSFAFEPLDLGVPSGDP      2280
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Search completed: November 18, 2004, 13:23:47
Job time : 201.365 secs

OM protein - protein search, using sw model

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                Copyright (c) 1993 - 2004 Compugen Ltd.
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GenCore version 5.1.6

Run on: November 18, 2004, 13:14:41 ; Search time 40.6868 Seconds
                                         (without alignments)
                                         3727.727 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR.........KKDTLSLSGLSSDFTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6618000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
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                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	10820.5	90.0	2273	3	US-09-426-998-5	Sequence 5, Appli
2	6221	51.7	2353	3	US-08-984-709A-50	Sequence 50, Appli
3	5872	48.8	1207	4	US-09-398-522-52	Sequence 52, Appl
4	5409	45.0	2175	3	US-09-404-650-2	Sequence 2, Appli
5	5409	45.0	2175	3	US-09-935-541-2	Sequence 2, Appli
6	5405.5	44.9	2188	3	US-09-404-650-4	Sequence 4, Appli
7	5405.5	44.9	2188	3	US-09-935-541-4	Sequence 4, Appli
8	5345	44.4	1835	4	US-09-404-650-5	Sequence 5, Appli
9	5345	44.4	1835	4	US-09-935-541-5	Sequence 5, Appli
10	1678	14.0	2343	3	US-09-268-163-4	Sequence 4, Appli
11	1677	13.9	2337	3	US-08-713-118-2	Sequence 2, Appli
12	1677	13.9	2337	3	US-09-452-007-2	Sequence 2, Appli
13	1676	13.9	2339	3	US-08-455-543A-47	Sequence 47, Appl
14	1676	13.9	2339	2	US-08-223-305C-47	Sequence 47, Appl
15	1674	13.9	2339	3	US-09-268-163-6	Sequence 6, Appli
16	1642.5	13.7	2237	1	US-08-455-543A-48	Sequence 48, Appl
17	1642.5	13.7	2237	3	US-08-223-305C-48	Sequence 48, Appl
18	1642.5	13.7	2336	3	US-09-268-163-10	Sequence 10, Appl
19	1642	13.7	1985	4	US-09-495-714C-6	Sequence 6, Appli
20	1640.5	13.6	2237	3	US-09-268-163-8	Sequence 8, Appli
21	1634.5	13.6	1984	3	US-08-836-325-10	Sequence 10, Appl
22	1634.5	13.6	1984	4	US-09-457-571-10	Sequence 10, Appl
23	1628.5	13.5	1977	4	US-09-495-714C-4	Sequence 4, Appli
24	1628	13.5	1873	1	US-08-435-675B-4	Sequence 4, Appli
25	1625.5	13.5	1989	3	US-08-836-325-12	Sequence 12, Appl
26	1625.5	13.5	1989	4	US-09-457-571-12	Sequence 12, Appl
27	1625	13.5	2161	1	US-08-455-543A-51	Sequence 51, Appl
28	1625	13.5	2161	2	US-08-223-305C-51	Sequence 51, Appl
29	1622	13.5	2161	1	US-07-745-206A-2	Sequence 2, Appli
30	1622	13.5	2161	1	US-08-455-543A-49	Sequence 49, Appl
31	1622	13.5	2161	2	US-08-223-305C-49	Sequence 49, Appl
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33	1617.5	13.4	1969	3	US-08-836-325-16	Sequence 16, Appl
34	1617.5	13.4	1969	4	US-09-457-571-16	Sequence 16, Appl
35	1616	13.4	1873	1	US-08-336-257A-7	Sequence 7, Appli
36	1614.5	13.4	1977	4	US-09-976-594-757	Sequence 757, App
37	1614.5	13.4	1977	4	US-09-919-039-367	Sequence 367, App
38	1614	13.4	1872	6	5386025-6	Patent No. 5386025
39	1595.5	13.3	1912	4	US-09-495-714C-2	Sequence 2, Appli
40	1589.5	13.2	2516	3	US-08-374-477C-2	Sequence 2, Appli
41	1589.5	13.2	2516	3	US-08-895-590-2	Sequence 2, Appli
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43	1588.5	13.2	2016	4	US-09-514-907A-2	Sequence 2, Appli
44	1588.5	13.2	2016	4	US-09-896-994-2	Sequence 2, Appli
45	1585.5	13.2	2016	3	US-09-634-920-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match   90.0%;
Best Local Similarity   92.5%; Score 10820.5; DB 3; Length 2273;
Matches 2080; Conservative 35; Mismatches 105; Indels 29; Gaps 5;

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Qy   62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
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Qy  122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
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Qy  182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy  242  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy  302  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
             |||||||||||||||||||| |||||| |||| |||||||||||||||||||||||||
Db  270  ICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy  362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEBLLKYLVIVILRKAAR   481
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Qy   482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN        541
Db   450  RLAQVSRAACVRVGLLSSPAPLGGGETQPFSSCSRSHRRLSVHHLVHHHHHHYHLGN        509

Qy   542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ    601
Db   510  GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ    569

Qy   602  APPPRCPSEASGRITVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF    661
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Qy   722  SEAVYEFTQDAQHSLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG     781
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Qy   782  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN   841
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Qy   842  IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLVVLMKTMDNVATF 901
Db   809  IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLVVLMKTMDNVATF 868

Qy   902  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKV   961
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Qy   962  LYNGMASTSSWAALYFIALMTFGNYLFNLLVAILVEGFQAE----------           1003
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Qy  1004  -----GDATKSESEPDFFSPSVDGDGDRKKRIALVALGEHAELRKSLLPPLLIHTAATPM  1058
Db   989  VDSQGGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPLLIHTAATPM 1048

Qy  1059  SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRR  1118
Db  1049  SLPKSTSTGLGEALGPASRRTSSSGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRR  1107

Qy  1119  SSRNSLGRAPSLKRRPSGEERRSLLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLERE  1178
Db  1108  SSRNSLGRAPSLKRRSPSGEERRSLLSGEGQQSQDQEESSEEERASPAGSDHRHRGSLERE 1167

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Qy  1239  GNLSKGERIQAWVRSRLPACCERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF   1298
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Db  1348  VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS  1407

Qy  1419  SLKPIGNIVVICCAFFIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAASYRWVRHKY  1478
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Qy  1479  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF  1538
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Qy  1539  VLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRSKEKQMAEAQCKPYYSDYS    1598
Db  1528  VLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRRSKEKQMAEAAQCKPYYSDYS  1587

Qy  1599  RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFES  1658
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Qy  1659  VFKLVAFARRFFQDRWNQLDLAIVLLSIMGTTLEEIEVNLSLPINPTIIRIMRVLRIAR   1718
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Qy  1719  VLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLFFIFAALGVELFGDLSCDETHPCEG   1778
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Qy  1839  QFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMKTLSPQPHSPLGSPLWPGVEGV    1898
Db  1828  QFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMKTLSPQPHSPLGSPLWPGVEGP    1887

Qy  1899  NSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP  1958
Db  1888  DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLP  1944

Qy  1959  NDSYMCRNGSTAERSLGHRGWGLPKAQSGSIILSVHSQPADTSCILQLPKDVHYLLQPHGA 2018
Db  1945  NDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAFHLLQPHSA  2004

Qy  2019  PTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSVSGPSCPLTRSSS   2078
Db  2005  PTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYS  2064

Qy  2079  FWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDL  2138
Db  2065  FWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDL  2124

Qy  2139  L-PSSQEEPLFPRDLKKCYSVEFQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPS  2197
Db  2125  LPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPS  2184

Qy  2198  SLGGQPLGGPGSGRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSP 2257
Db  2185  NLGGQPLGGPGSGRPKKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGP 2244

Qy  2258  LDSTAASPSPKKDTLSLSLGLSSDPTDMDP  2286
Db  2245  PDSMAASPSPKKDVLSLSLGLSSDPADLDP  2273
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;    ZIP: 92037
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette
;    COMPUTER: IBM Compatible
;    OPERATING SYSTEM: DOS
;    SOFTWARE: FastSEQ Version 1.5
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/984,709A
;    FILING DATE: 02-DEC-1997
;    CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Seidman, Stephanie L.
;    REGISTRATION NUMBER: 33,779
;    REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (619) 450-8400
;    TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 50:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2353 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
;   ORIGINAL SOURCE:
US-08-984-709A-50

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Db    19 PPGPAALVG------ASPESGPAGREAERGSELGVSPSSSPAAERGAELGA--DEEQR 69

Qy    83 LPYPALAPVVPFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACD 142
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Db    70 VPYPALAATVFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVECG 129

Qy   143 SQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLD 202
            |:||::|| | ||||||||||||||||:|| ||||||||||||||:|||||||||:||||
Db   130 SERCNILEAFDAFIFAFFAVEMVIKMWALGLFGQKCYLGDTWNRLDFFIVVAGMMEYSLD 189

Qy   203 LQNVSPSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGV 262
            |:|||:|:|||||:||||||||||||:||||||||||||||||:||||||||||||||||
Db   190 GHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGV 249

Qy   263 QLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENEDESPFICSQPRENGMRSCRSVPTLR 321
            ||||||||||||:|:     |:|:  :|||| |: ||:| ||| :| |:| |
Db   250 QLWAGLLRNRCFLDSAFVRNNNLTFLRPYYQTEEGENPFICSSRRDNGMQKCSHIP--- 306

Qy   322 GEGGGGPPCSLDYETYN------SSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGY 374
            |: | | :|   | |         :|::| |::||:||:| ||||||| || ||||||||
Db   307 GRRELRMPCTGWBAVTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGY 366

Qy   375 AWIALFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINLCLVIIATQFSETK 434
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   367 AWIALFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINLCLVIIATQFSETK 426

Qy   435 QRESQLMREQRVRFLSNASTILASFSEPGSCYEELLKYLIVILRKAARRLAQVSRAIGVRA 494
            ||||||||||||: ||::||:||||||||||||||||| |: :|:|::|  | : :   :
Db   427 QRESQLMREQRARHLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRSRLRLYARWQSRW 486

Qy   495 GLLSSPVARSGQEPQPSGSCTRSHRR-------LSVHHLV-HHHHHHHHYHLGNGTLRV 546
            |   |:|: : |:|         : |       :|| |||  ||||||||||  | | ||
Db   487 RKKVDPSAVQGQGP------GHRQRRAGRHTASVHHLVYHHHHHHHHYHFSHGSPRR 538

Qy   547 PRASPEIQDRDANGSRRLML--PPPSTPTPSGGPPRGAESVHSFYHADCHLE--PVRCQA 602
            |  |: |  |  || :|:|    ||| |  || | | |  | | ||||| :|   ||::|
Db   539 PGPEPGACD------TRLVRAGAPPSPPSGPGRGPP-DAESVHSIYHADCHIEGPQERARV 591

Qy   603 PPPRCPSEASGR-TVGSGKV-YPTV--------HTSPPEILKDKALVEVAPSP---- 646
            :  ||| |:| | ||||| |     |        ::  | |   || |:| |
Db   592 AHAAATAAASLRLATGLGTMNYPTILPSGVGSGKGSTSPGPK------GKWAGGPPGTG 644

Qy   647 --GPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSS---CKISSPCSKADSGACGPD 697
              |   |:|  :|  | | |       |:  | |:|   | :|| ||:||| ||| |
Db   645 GHGPLSLNS---PDPYEKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP--PAGTLTCELK 698

Qy   698 SCPYCART-GAGPEPESADHVMPDSDSEAVYEFTQDAQHSDLRDP-------- 740
            |||||  | ||| | ||:||||||||:||||||||||||:||||
Db   699 SCPYCTRALEDPEGELSGSESGDSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGS 758

Qy   741 HSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ 800
            :||||||: || ||||::| :| ||: |: ||||||||:|||:|||||||||||:|||||
Db   759 PQRRAQQRAAP-GEPGWMGRLWVTFSGKLRRIVDSKYFSRGIMAAILVNTLSMGVEYHEQ 817

Qy   801 PEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQG 860
            |||||||||||||||||:|||||||||| ||:|||:||||||||:||||||||||||||
Db   818 PEELTNALEISNIVFTSMFALEMLKLLACGPLGYIRNPYNIFDGIIVVISVWEIVGQAD 877

Qy   861 GGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSILGMHLF 920
            ||||||||||| ||||||||||| |||||::|||||||||| ||||||||||||||||||
Db   878 GGLSVLRTFRLLKLVRFLPALRRQLVLVLVKTMDNVATFCTLLMLFIFIFSILGMHLF 937

Qy   921 GCKFASERD-GDTLPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIA 979
            ||||: ||  |||:|||||||||||||||||||||||||| ||||||||||||||||| |
Db   938 GCKFSLKTDTGDTVPDRKNFDSLLWAIVTVFQIITQEDWNVVLYNGMASTSSWAALYFVA 997

Qy   980 LMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDRKRLALVAL-- 1035
            |||||||||||||||||||||||||||.:    ||                 :
Db   998 LMTFGNYVLFNLLVAILVEGFQAEGDANRSDTDEDKTSVHFEEDFHKLRELQTTELKMCS 1057

Qy  1036 ------GEHAELRKSLLPPLIIHTAATPMSHPKSSS-TGVGEALGSGSRRTSSSGSAEPGA 1089
                   |||:|| |||||:| :||||| | ||||   |    :| |||| ||:|   | |
Db  1058 LAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGSSSSSGDPPLG- 1116

Qy  1090 AHHEMKCPPSARSSPHSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1149
               : ||||: |||  | | : |||: || ||||||||||| :  ||| |||||||:
Db  1117 --DQKPPASLRSSPCAPWGPSGAWSSRRSSWSSLGRAPSLKRRGQCGERESLLSGEGKG 1173

Qy  1150 SQDEEESSEEDRASPA--GSDHRHRGSLEREAKSSFDLPDTL----QVPGLH----R 1196
            | |:|  :|   |  |  | |     ||  ||:|  | |  |
Db  1174 STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDGQVVALPSDFFLR 1231

Qy  1197 TASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRIP 1256
                |||:||: |      |  ||| |:||:|  | :: : | ::    : : |:
Db  1232 IDSHREDAAELDDDSEDSCCLRLHKVLEPYXPQ------------W---- 1265

Qy  1257 ACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFFLNCITIAMERPKIDPHSA 1316
              || | ||:||||| ||||||  ||:|||||||||||| |||||:|||:|||:||| |
Db  1266 --CRSREAWALYLFSPQNRFRVSCQKVITHKMFDHVVLVFFFLNCVTIALERPDIDPGST 1323

Qy  1317 ERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLVISVIDILVSM 1376
            ||:||::|||||||:|:||||:||||||| | ||:||:|||:|||||||| | ||:|::| |
Db  1324 ERVFLSVSNYIFTAIFVAEMMVKVVALGLLSGEHAYLQSSWNLLDGLLVLVSLVDIVVAM 1383

Qy  1377 VSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFII 1436
              : | |||| |||||||||||||||||||:|||||||||:|||:|||||||:|||||||
Db  1384 ASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFII 1443

Qy  1437 FGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASK 1496
            |||||||||||||: |: | |||| .|: | |: |||||:||||||||||||||||||:|
Db  1444 FGILGVQLFKGKFYYCEGPDTRNISTKAQCRAAHYRWVRKYNFDNLGQALMSLFVLSSK 1503

Qy  1497 DGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMVGVVENFHKCRQ 1556
            |||::|||||||||||||||: ||||||||||||||||:|||||| :||| ||||||||
Db  1504 DGWVNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQ 1563

Qy  1557 HQEEEEARRREEKRLRLEKKKRSKEKQMAEAAQCKPYYSDYSRFRLLVHHLCTSHYLDLF 1616
            |||  |||||||||||||:::|:      :    ||:|:|||: |  |||::|||||||||
Db  1564 HQEAEARRRREEKRLRLERRRRSTFPS-PEAQRRFYYADYSPTRRSIHSLCTSHYLDLF 1622
```

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Query Match          48.8%;   Score 5872;   DB 4;   Length 1207;
Best Local Similarity 95.2%;   Pred. No. 0;
Matches 1123;  Conservative 11;  Mismatches 11;  Indels 44;  Gaps 2;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
           :||||   ||||||||||||:||||||||||||||||||||||||||||||||||||||
Db   30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy  122 VILLNCVTLGMERPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   90 VQALPQVGNLGLLFMLLFFIYAAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLTLF 149

Qy  182 DTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
          |||||||||||||:||||||||||||||||||||||||||||||||||:||||||||||
Db  150 DTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy  242 MLGNVLLLCFFVFFIFGIVGVQVLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
          |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db  210 MLGNVLLLCFFVFFIFGIVGVQVLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy  302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  270 ICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy  362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy  422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy  482 RLAQVSRAIGVRAGLLSSPVARSGQEPQSPGSGCTRSHRRLSVHHLVHHIHHHYHLGN 541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  450 RLAQVSRRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHYHLGN 509

Qy  542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
          |||:|||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db  510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ 569

Qy  602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGGPPTLTSFNIPPGPF 661
          ||||:|||||||||||||||||||||||||||||||||||||:||||||||||:|||||
Db  570 APPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

Qy  662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
          ||||||||||||||||||||||||||||||||||||||||||:||||||||||:|||||
Db  630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Qy  722 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLLICDTFRKIVDSKYFGRG 781
          ||||||||||||||||||||||:-:::|||||||||||||||||||||||||||||||||
Db  690 SEAVYEFTQDAQHSDLRDPHS--RRQRSLGPDAEPSSVLAFWRLLICDTFRKIVDSKYFGRG 748

Qy  782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVTSLFALEMLLKLLVYGPFGYIKNPYN 808

Qy  842 IFDGVIVISWEIVGQQGGGLSVLRTFRIMRVLKLVRFLPALQRQLVVLMKIMDNVATF 901
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  809 IFDGVIVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 868

Qy  902 CMLLMLFIPFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  869 CMLLMLFIPFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 928

Qy  962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
          |||||||||||||||||||||||||||:||||||||||||:|||:|:|:||||||:|:
Db  929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDANKSESSEPDFFSPSLD 988

Qy 1022 GDGDRKKRLALVALGEHAELRKSLLPPLLIHTAATPMSHPKSSTGVGRALGSSGRRTSS 1081
          |||||||||||||||||||||||||||||||||||||||:||:|||||||||||||||||
Db  989 GDGDRKKCLALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSS 1048
```

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Qy 1617 ITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLIVAFAPRRFFQDRWN 1676
          ||:|:||:|:|||||||:||:|||||||:||||||||||||||:||||||:||||||||||
Db 1623 ITFFICVNVITMSMEHYNQPKSLDEALKYCNYVFTTIVFVFEAALKLVAFGFRRRFFKDRWN 1682

Qy 1677 QLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKNAVGMRALLHTV 1736
          ||||||||||||||||||||||:||:||||||||||||||||||||||||:||||||||||
Db 1683 QLDLAIVLLSIMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKNATGMRALLDTV 1742

Qy 1737 MQALPQVGNLGLLFMLLFFIFAAIGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLF 1796
          :|||||||||||||||||:||| |||||:||||| ||:|||||||||||||:|||||||
Db 1743 VQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLTLF 1802

Qy 1797 RVSTGDNWNGIMKDPSRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKH 1853
          ||||||||||||||:||| ::||:|||:|:|||:||||||||||||:||:||:||||||
Db 1803 RVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPVYFVTFVLVAQFVLNVVVAVLMKH 1862

Qy 1854 LEESNKEAKEAEELAELELEMKTILSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTA 1913
          ||||||||||:|||||||||||||:|::|:::||
Db 1863 LEESNKEAREDAEILDAEIELEMA-----------QGPGSARRVDADRP---------- 1899

Qy 1914 HIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--- 1970
          :||||::|||::|||||||||:::|||||||||:
Db 1900 ------------PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP 1943

Qy 1971 ------ERSLGHRGWGLPKAQSGSIILSVHSQPADTSCILQLPKDVH----------YLLQP 2015
          :|:||||||||||:: :|| ||||| ||||||||||::|||
Db 1944 HPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIPLAVSSPARSGEPLHALSP 2000

Qy 2016 HGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEV---SGPSC 2071
          ||:: :||::| |||||::
Db 2001 RGT----------ARSPSLSRLLCRQEAVHTDSLEGK-IDSPRDTLDPAEPGEKTPVR 2047

Qy 2072 PLTRSSSFWGGSSIQVQQRSGIQSKV--SKH------IRLPAPCPGLEPSWAKDPPETRS 2123
          ||::| ::: ||||||||||||
Db 2048 PVTQ------GGSLQSPPRSPRPASVRTRKHTFGQHCVSSRPAAPGGEEABASDP----- 2096

Qy 2124 SLELDTELSWISGDLLP-SSQEEFLFP------RDLKKCYSVETQSCRRRPGFWLDE 2173
          ::||:::::||| |:||| | :: ||| |||
Db 2097 ---ADEEVSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGFLDKPG-RADE 2152

Qy 2174 QRRHSIAVSCLDSGSQOPRLCPSPSSLGGQPLGGP--GSRPKKKLSPPSISIDPP-ESQGS 2230
          |: :||:|:: |||| || ::::| ||| ||||||||| :|::: | |
Db 2153 QWRPSAE---LGSGE------PGEAKAWG-PEAEPALGARRKKMSPPCISVEPPAEDEGS 2203

Qy 2231 -RPPCSPG--VCLRRRAPASDSKDPSVS-SPLDSTAASPSP------------KKDTLSL 2274
          ||||||| ||||||||:::: :||:| ::
Db 2204 ARPSAAEGGSTTLRRRTPSCEATPHRESLEPTEGSGAGGDPAAKGERWGQASCRAEHLTV 2263

Qy 2275 SGLSSDPTDM-----DP 2286
          :|: | :| |||
Db 2264 PSFAFRPLDLGVPSGDP 2280
```

RESULT 3

US-09-398-522-52

; Sequence 52, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene ecoding a T-type calcium channel

```
Qy   570  STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSP  629
          :   :  ::                         :      ::::    ::       :
Db   475  AKPGP------------------------HAK--EPRHYQLCPQHSPLDA--------TPHT--  502

Qy   630  PPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK  688
          ::                                                 :   ::
Db   503  --------LVQ----PIPATLAS----------------------DPASCPCCQHEDGRRPSGLGS  534

Qy   689  ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS  748
          ::                                                     :
Db   535  TDSQEGSGS-----GSSAGGEDEA-------DGDGA--RSSEDGASSELGKEEEEEQ--  579

Qy   749  LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTN  806
             :   ::       ::   ||||||||||:||||||||||||:|||||:||||||||||
Db   580  ----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN  635

Qy   807  ALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQOQGGLSVL  866
          :||| |||||:||||||:|||| |||||:|||||||||:|||:||||||||||  |||||
Db   636  ILEICNVVFTSMFALEMILKLLAAFGLFDYLRNPYNIFDSIVIISIWEIVGQADGGLSVL  695

Qy   867  RTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS  926
          ||||:|||||||||:|||:|||||||||||||||||||||||||||||||||||:|||:
Db   696  RTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSL  755

Qy   927  ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
           :  ||| |||||||||||||||:||||||||||||:|||||||||:||:|||:||||||
Db   756  RTDTGDTVPDRKNFDSLLWAIVFVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGN  815

Qy   986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSV----------DGDRKKRLALVAL 1035
          |||||||||||||||||||||| :::  :                :
Db   816  YVLFNLLVAILVEGFQAEGDANRSYSDEDQSSNIEEFDKLQEGLDSSGDPK-LCPIPM  873

Qy  1036  GEHAELRKSLLPPLIIHT---AATPMSHPKSSTGVGEALGSGSRRTSSSGSAEPGAAH 1091
           :  :  :::|| ::          : ::    :    :     :     :::
Db   874  TPNGHLDPSL--PLGGHLGPAGAGPA--PRLSLQPDPMLVALGSRKSSVMSL---GRMS  926

Qy  1092  HEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES 1150
           :  :    :: ::  ||| || :|||:  ::                :   :
Db   927  YDQRSLSSSRSSYYGPWGRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGA  980

Qy  1151  QDEEESSBE--DRASPAGSDH------------------RHRGSLEREAKSSFDLPDTLQVPG 1193
           ::   ::     :  : ::                   ||:
Db   981  RVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVG 1040

Qy  1194  LHRTASGRSS-ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDNDEGNLSKGERIQAW 1250
           |  :    :  ||: | ||| : :   :                 :  :
Db  1041  AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEEIDYTLCFRVRKM 1098

Qy  1251  VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCTTIAMERPK 1310
           :  :|  :   ||||:|:| |:|||:|:|| | ::|:||::|||:|:|||:|||:|||:
Db  1099  IDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIAHKLFDYVVLAFIFLNCIITIALERPQ 1158

Qy  1311  IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVI 1370
           :    ||||||:|||||||:|:|||||:||| ||:||||||||||||||||| ||::||||
Db  1159  IEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFVSII 1218

Qy  1371  DILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC 1430
           ||:||:|:   ||||::|||||||||||||||||||| ||||||||::||||||||:|:|
Db  1219  DIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278

Qy  1431  CAFFIIFGILGVQLFKGKFPVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSL 1490
           ||||||||||||||||||| :|  ||||||||:|||:|::||||:|||||||||||||||
Db  1279  CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL 1338

Qy  1491  FVLASKDGWVDIMYDGLDAVGDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVEN 1550
           |||||||||:|||:|||||| |||| :||||||||||||||||:||||||||||||||
Db  1339  FVLASKDGWVNIMYNGLDAVADQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVEN 1398

Qy  1551  FHKCRQHQEEEEARRREEKRLEKRRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
           ||||||||||  ||||||||| |:||        ::   |||: :  ||| ||:|||
Db  1399  FHKCRQHQEEAEARRREEKRLRLEKRR--------KAQRLPYYATYCHTRLLLIHSMCTS 1451
```

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Qy  1082  SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141
          ||||||||| |||| |||||||||||||||||||||||||||||||||||||||||||||
Db  1049  SGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1107

Qy  1142  LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
          |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db  1108  LLSGEGQESQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1167

Qy  1202  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNL 1241
           ||||||||||||||||||| ||  ||| |||| |:|||
Db  1168  GSASEHQDCNGKSASGRLARALRPDDPPLDGDGDDADDEGNL 1207
```

RESULT 4
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 2175
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-404-650-2

```
Query Match             45.0%;  Score 5409;  DB 3;  Length 2175;
Best Local Similarity   50.5%;  Pred. No. 0;
Matches  1225;  Conservative  236;  Mismatches  513;  Indels  450;  Gaps  64;

Qy    51  ASRSSTTCPGPGAAGAGSTEKDPG-SADSEAEGL----------PYPALAPVVFFYLS   97
          || ::  : : ||   |: :  :     :  ||          :| ||| :||||:
Db     5  ASPSSSSAAAP-AAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLR   63

Qy    98  QDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIF  157
          :  :| :||::||||||||:||||:||||||||||:: | |   ||:|||:|||||||
Db    64  QTTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMCLSDRCKILQVFDDFIF  123

Qy   158  AFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFPSAVRTVRVL  217
           ||| |||:||||||||||||||||||||||||||:|||:|||||:||:  :|:|||||||
Db   124  IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDDLQNINLSAIRTVRVL  183

Qy   218  RPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE  277
          ||| |||||||||||:  ||||||||||||||||||||||||||||||||||||||||
Db   184  RPLKAINRVPSMRIILVNLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLEE  243

Qy   278  NFSLPLSVDLEPYYCQTENEDESSPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL----- 332
          || : |:| ||||| :  ::  :|||||   ::|:  |:        :    : : :
Db   244  NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIIPPLKEQ--GRECCLSKDDV  300

Qy   333  -DYETYNSSSNTT--CVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV  389
            : :::  ::     |||||:| :|: : ||:|||||||||||||||:||||||||||
Db   301  YDFGAGRQDLNASGLCVNWNRYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV  360

Qy   390  DIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFL  449
          :||: ||||||||||||||||||||||||||||||||||||||||||| :||:|||:: |
Db   361  EIMYYVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYL  420

Qy   450  SNASTLASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ  509
          | :||:||:  ||.||||::|:|  ||||| :|    ::                ::
Db   421  S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR-----RALGLIYQALQS---------  462

Qy   510  PSGSCTRSHRRLSVSHHLVHHLVHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP 569
              :  ||:||                                            :
Db   463  --------RRQAL----------------------------GPE-------------APAP  474
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; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-2

Query Match          45.0%;   Score 5409;   DB 4;   Length 2175;
Best Local Similarity   50.5%;   Pred. No. 0;
Matches 1225;   Conservative 236;   Mismatches 236;   Indels 513;   Gaps 450;
```

```
Qy   51 ASRSSTTCPGPGAAGAGSTEKDPG--SADSEAEGL----------PYPALAPVFFYLS   97
         :  :    ||| ||  |     ||::    :   :            |::| :|||::|
Db    5 ASPPSSSAAAP-AAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLR   63

Qy   98 QDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF  157
         | : | :||: ||||||| ||||||||||||| ||:  || ::| |:||:||| ||||||
Db   64 QTTSPRNWCIKMVCNPWFECVSMLVILLNCVTLLGMYQPCDDMDCLSDRCKILQVFDDFIF  123

Qy  158 AFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL  217
         ::||:||| ||||||||||||||||||||||||||:||:|||||||: : :|:||||||
Db  124 IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVL  183

Qy  218 RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLICFFVFFIFGIVGVQLWAGLLRNRCLPE  277
         |||:|||||||||||| ||||||||||||||| ||||||||||:|||||||||||||  :
Db  184 RPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEE  243

Qy  278 NFSLPLSVDLBPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL-----  332
         ||::  .||:|||||  |::|:||| || :||||  | :   ||.|  |  |
Db  244 NFTIQGDVALPPYYQPBEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV  300

Qy  333 -DYETYNSSSNTT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV  389
          |   ::| ::    |||||:||:||| | ||| ||||||||||||| .||||||||||
Db  301 YDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWTVIFQVITLEGWV  360

Qy  390 DIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFL  449
         :||| |||||||||||||||||||||||||||||||||||||||||||. :|:||:|: |
Db  361 EIMYYVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYL  420

Qy  450 SNASTLASFSEPGSCYEELLKYLVIYIRKAARRLAQVSRAIGVRAGLLSSPVARSGQPEPQ  509
         |  :| || ||||:||| :  ||  | ||| ||                :  ||
Db  421 S--SSTVASYAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQALQS-            462

Qy  510 PSGGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP  569
         .  : ..|  ::                                         .  ||
Db  463 ------RRQAL----------------GPE------------------------APAP  474

Qy  570 STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSP  629
          :   ::     | .|||:                                    ||:
Db  475 -------HAK---EPRHYQLCPQHSPLDA----------------------TPHT-     502

Qy  630 PPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK  688
                  |:|                                   :.  |  |.|
Db  503 ---------LVQ----PIPATLAS----------------DPASCPCCQHEDGRRPSGLGS  534

Qy  689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVVEFTQDAQHSDLRDPHSRRRQRS  748
           || ..      |  ||  |    :. . |  :                  :::|::| :
Db  535 TDSGQBGSGS----GSSAGGEDEA---------DGDGA--RSSEDGASSELGKEEEEEQ-  579

Qy  749 LGPDAEPSSVLA--FWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTN  806
          | |||  .:    ||  |   |: :|||||||.||||:||||||.|||||:| ||||||
Db  580 ----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHOPEELTN   635

Qy  807 ALEISNIVFTSLFALEMLLKLLVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVL  866
          ||| | |||| ||||| :|| | | | |::||||||| :|| |:|||||||  ||||||
Db  636 ILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVL  695

Qy  867 RTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFAS  926
         |||||:|||||||| ||| ||||||||||||||||||||||||||||||||:||||| |
Db  696 RTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFSILGMHIFGCKFSL  755

Qy  927 ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
         ::| || :|||||||||||||||||||||||||| ||||||||| ||| ||:|||||||
Db  756 RTDTGTDVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGN  815
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Qy 1611 HYLDLFITGVIGLNVVMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRF 1670
         ||||:|||  | ||||.|::|||:||:  | |||||||:||:||::||:|||||| :|||
Db 1452 HYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLVAFGLRRF 1511

Qy 1671 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
         |:||||||||||||||:||||||||::| ||||||||||||||||||||||||||| |||
Db 1512 FKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMR 1571

Qy 1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLRHATFRNFGM 1790
         |||:||.|||||||||||||||||||:|||||||||:| || :|||| ||||||.|||
Db 1572 ALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEGMSRHATFENFGM 1631

Qy 1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1847
         |||||| |||||||||||||. |||  ::|::|     :|| |||||||||||||:|||:
Db 1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVV 1691

Qy 1848 AVLMKHLEESNKEAKEBARLEABLELEM-KTLSPQHSPLGSPFLWPG---------- 1894
         ||||||| :|||||:|: :::|| ||||| |  |:||  |: 
Db 1692 AVLMKHLDDSNKEAQEAEMDAELELEMAIGLGPGRPLPTGSPGA-PGRGPGGAGGGDT 1750

Qy 1895 --------VEG-VNSTDSPKPGAPHTAHIGAASG------------------ 1920
                 .:.   .| :  |||  |:| :|
Db 1751 EGGLCRRCYSPAQDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHHDKQEVQLAETEA 1807

Qy 1921 -------FSLEHPTMVP------------HPEEVPV-PLGPDLLTVRKSGVS 1952
                ||:. .   :            ||  ||  ||| || :. :|
Db 1808 FSLNSDRSSSILLGDDLSLEDDPTACPPGRKDSKGELDPPEPMRVGDLGECFFPLSSTAVS 1867

Qy 1953 RTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHY 2011
          :   ||  .  |  |.         ::|.   :: : ||   :  |:| || |  : ::
Db 1868 -PDPENFLCEMEEIPFNPV--RSW--LKHDSQAPPSPFSPDASSPLLPMPAEFFH      1918

Qy 2012 ------LLQPHGAPTWGAIPKLPPPG-----RSPLAQRPLRRQAAIRTDSLDVQGLGSRE 2060
               .  |:|   .  | ||.        |||: .  :| ||| | ||:  |  ::|
Db 1919 PAVSASQKGPBKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS----- 1972

Qy 2061 DLLSEVSGPSCPLTRSSSFWGSSIOVQQRGIQSKVSKHIRLPAPCPGLEPSWAKDPPE 2120
          :|   ||| || ::.|   ..: ..:: |    :.| |||.|.   .  |
Db 1973 ------PSSSAGSLQTTLEDSLTLSDSPRRAIGPPAPAPG----------------  2006

Qy 2121 TRSSLELDTELSWISGDLLPSSQBEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIA 2180
          |:|:|  |.|     |       :.|                     |  |:|:|: :
Db 2007 --------SLRGRGLFSLRGLRAHQRS                              2038

Qy 2181 VSCLDSGSGSQPRLCPSPSSL---------GGQPLGGPGSRPKKKLSPPSIS---IDPPESQG 2229
         .|  ::||..  :.| ||||:          || |.|| .  | :|    |    :|| .|
Db 2039 HS--SGGSTSPGCTHHDSMDPSDEBGRGAGGGAGSEHSETLSLSLTSLFCPPP----   2092

Qy 2230 SRPPCSPGVCLRR-----------------------------RAP----ASDSKDPSVSSPLLDSTA 2262
          .||      .:                             ||    ||||||| :..|| :.|
Db 2093 --PPPAPGLITPARKFSSTSSLAAPGRPHAAAALAHGLARSPSWAADRSKDPPGRAPLPMGL 2150

Qy 2263 ASPSPKKDTLSLSGLSGSDPTMDP 2286
          .|.      :| .||.|.   ||
Db 2151 GPLAPPPQPL------PGELEP 2166
```

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Qy   986 YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSV---------DGDGDRKKRLALVAL 1035
         |||||||||||||||||||||||.:.:::||    .::.:                 
Db   816 YVLFNLLVAILVEGFQAEGDANRSYSDEDQSSSNIEEFDKLQBGLDSSGDPK--LCPIPM  873

Qy  1036 GEHAELRKSLLPPLIIHT---AATPMSHPKSSTGVGEALGSGSRRTSSSGSAEPGAAH   1091
         ::.   ||||  |||::         ::  ||| .|| ::                    
Db   874 TPNGHLDPSL--PLGGHLGPAGAAGPA--PRLSLQPDPMLVALGSRKSSVMSL--GRMS   926

Qy  1092 HEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES 1150
         :. . ||| .|| . || . || ||||||.||    .|| |||          .|      
Db   927 YDQRSLSSSRSSYYGPWGRSAAWASRRSSWN------SLKHKPPSAEHESLLSAERGGGA  980

Qy  1151 QDEEESEE--DRASPAGSDH----------------RHRGSLEREAKSSFDLPDTLQVPG 1193
         :.    ::  |||  |.                   ||.|  ::                 
Db   981 RVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVG  1040

Qy  1194 LHRTASGRSS--ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDDNDEGNLSKGERIQAW 1250
          | | ||..   |||.|||||    |||| | |    .  :   ::       |::|    
Db  1041 AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEERIDYTLCFRVRKM 1098

Qy  1251 VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLIVIIFLNCITIAMERPK 1310
          .   | . | ||||||.:||.  ||| ||:||:  ||:||:|||.:.|||||||||:||  
Db  1099 IDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQ 1158

Qy  1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVI 1370
         ::  ||||||| ||||||||:|.||||:||| ||  |||||||||||||||| |||:|||  
Db  1159 IEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFVSII 1218

Qy  1371 DIIVSMVSDSGTKILGMRVLRLLRTLRPLRVISRAOGLKLVETLMSSLKPIGNIVVIC   1430
         |||||| | .| ||||:||||||||||||||||||.||||| ||:|||||||||||:||  
Db  1219 DIVVSLASAGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC  1278

Qy  1431 CAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSL 1490
         |||||||||||||||||||:.|  .|||||||:||.  |.|||.||||||||||||||||  
Db  1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL 1338

Qy  1491 FVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISPLLIVAFFVLNMFVGVVVEN 1550
         |||||||||::|||:|||||.||||| :||||||||||||.|||.:|||||||||||||||  
Db  1339 FVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVEN 1398

Qy  1551 FHKCRQHQEEEARRREEKRLRRLEKKRRSKEKQMAEAAQCKPYYSDYSRFLLVHHLCTS  1610
         ||||||||| ||||||||||||||||||      | |                 :| ||  
Db  1399 FHKCRQHQEAEARRREEKRLRRLEKKRR------KAQRLPYYATYCHTRLLIHSMCTS  1451

Qy  1611 HYLDLFITGVIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVFESVFKLVAFARRF  1670
         ||||:||| .| |||||||::|||.||  || |:|||:||.:|||| :|:|||||. |||  
Db  1452 HYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVFLEAVLKLVAFGLRRF 1511

Qy  1671 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIRIMRVLRIARVLKLLKMAVGMR  1730
         |:|||||||||||||| ||||||||   |||||||||||||||||||||||||: |.||  
Db  1512 FKDRWNQLDLAIVLLSVMGITLEEINAALPINPTIRIMRVLRIARVLKLLKNATGMR  1571

Qy  1731 ALLHTVMQALPQVGNIGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1790
         |||.||.||||||||||||||||||:|||||||||| ||| |.|||| | |||||.||||  
Db  1572 ALLDTVVQALPQVGNIGLLFMLLFFIYAALGVELFGKLVCNDENPCEGMSRHATFENFGM 1631

Qy  1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1847
         ||||||.|||||||||||||  |||  ||.  | .    ||:||||||||||||:||||:  
Db  1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVV 1691

Qy  1848 AVLMKHLEESNKEAKEAELEAEELEM-KTLSPQPHSPLGSPFLWPG----------    1894
         |||||||:.||||| | |: . || | .||||.|.|| ||| ||               
Db  1692 AVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGRLPTGSPGA-PGRGPGAGGGGDT  1750

Qy  1895 ----------VEG-VNSTDSPKGPAPHTTAHIGAASG----------            1920
                   :|.  .|| |||                                     
Db  1751 EGGLCRRCYSPAQDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHHDKQEVQLAETEA 1807

Qy  1921 ----------FSLEHPTMVP-----------HPEEVPV-PLGPDLLTVRKSGVS       1952
                   ||| |  .|             ||.|.|| ||| |:|| .:| |.|.     
Db  1808 FSLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGECFFPLSSTAVS  1867
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```
Qy  1953 RTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSSILVHSQPADTSCILQLPKDVHY 2011
          |  || |:  .| .:.|.|.|. .  ||  |  ::          ::    | ::||  
Db  1868 -----PDPENFLCEMEIFPNPV--RSW--LKHDSQAPPSFSPDASSPLLPMPAEFFH  1918

Qy  2012 ------LLQPHGAPTWGAIPKLPPPG----RSPLAQRPLRRQAAIRTDSLDVQGLGSRE 2060
               || ..|.  | | |||        |||.|.|  |     | |.||||||| :     
Db  1919 PAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLRQATGSDTSLDAS------- 1972

Qy  2061 DLLSEVSGPSCPLTRSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPE 2120
         |  |   | |  |  ||   ||   |   | ::|                           
Db  1973 --------PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAPG---------------    2006

Qy  2121 TRSSLELDTELSWISGDLLPSSQEEPLFPPDLKKCYSVETQSCRRRPGFWLDEQRRHSIA 2180
         .|  ||    |   .                                 |.| .|  |.    
Db  2007 ----------------------SLRGRGLFSLRGLRAHQRS                    2038

Qy  2181 VSCLDSGSQPRLCPSPSSL---------GGQPLGPGSRPKKKLSPPSIS--IDPPESQG  2229
          |  |.| . |  ||||.          |||||||||||   || ||:   ||||     
Db  2039 HS--SGGSTSPGCTHHDSMDPSDEEGRGGAGGGAGSEHSETLSSLSITSLFCPPP-----  2092

Qy  2230 SRPPCSPGVCLRR------------------RAP---ASDSKDPSVSSPLDSTA       2262
          |||.. |                       |||   |||||||| .|||              
Db  2093 --PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKDPPGRAPLPMGL 2150

Qy  2263 ASPSPKKDTLSLSLSSDPTDMDP                                     2286
          .|||   || ||| |  | . |                                      
Db  2151 GPLAPPPQPL---------PGELEP                                    2166
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RESULT 6
US-09-404-650-4
; Sequence 4, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-4

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Query Match             44.9%;  Score 5405.5;  DB 3;  Length 2188;
Best Local Similarity   50.3%;  Pred. No. 0;
Matches 1225;  Conservative 236;  Mismatches 514;  Indels 461;  Gaps 64;

Qy    51 ASRSSTTCPGPGAAGAGSTEKDPG-SADSEAEGL---------PYPALAPVVFFYLS   97
         ||| ||   || ||||.|.||:||  |||:|.||         ||:|:||:||||| |  
Db     5 ASPPSSSAAAP-AAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLR  63

Qy    98 QDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF 157
         |:: ||:||.: |||||||.||||||||||||||:.||:|: .| ||||:||||||||||  
Db    64 QTTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIF 123

Qy   158 AFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVL   217
          ||| ||| ||||||||||||||||||||||||||||| |||||||||.  .|:||||||  
Db   124 IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVAGMVEYSLDLQNINLSAIRTVRVL  183

Qy   218 RPLRAINRVESMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE 277
         ||| |||||.||||||.||||||||||||||||||||||||||:|||||||||||||| |  
Db   184 RPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEE 243

Qy   278 NFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVFTLRGRGGGGPPCSL----- 332
         ||:    ||.|||| .||:|:.||||| . .||:. |||.|                    
Db   244 NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300
```

```
Qy   333  -DYETYNSSSNT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWTAIFQVITLEGWV   389
Db   301  YDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV  360

Qy   390  DIMYFVMDAHSFYNFIYFLLIIVGSFFMINLCLVVIATQFSETKQRRSOLMREQRVRFL   449
Db   361  EIMYVVMDAHSFYNFIYFLLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYL   420

Qy   450  SNASTLASFSEPGSCYEEILKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ  509
Db   421  S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR------RALGLYQALQS---------   462

Qy   510  PSGGSCTRSHRRLSVIHHLVHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP   569
Db   463  --RRQAL----------GPE-------APAP                              474

Qy   570  STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVPTVHTSP   629
Db   475  AKPGP----------HAK--EPRHYQLCPQHSPLDA----------TPHT-         502

Qy   630  PPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK  688
Db   503  ------LVQ----PIPATLAS----------DPASCPCCQHEDGRRPSGLGS         534

Db   689  ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS  748
Qy   535  TDSSQEGSGS----GSSAGGEDEA-----DGDGA---RSSEDGASSELGKEEEEEEQ-   579

Qy   749  LGPDARPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIALLVNTLSMGIEYHEQPEELTN  806
Db   580  ----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN 635

Db   807  ALEISNIVFTSLFALEMLLKLLIVYGPFGYIKNPYNIFDGVIVIVISVWEIVGQOGGGLSVL 866
Qy   636  ILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVL  695

Qy   867  RTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS  926
Db   696  RTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSL  755

Qy   927  ERD-GDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
Db   756  RTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGN  815

Qy   986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSV----DGDGDRKKRLALVAL      1035
Db   816  YVLFNLLVAILVEGFQAEGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPM  873

Qy  1036  GEHAELRKSLLPPLIIHT----AATPMSHPKSSTGVGEALGSGSRRTSSSGSAEPGAAH 1091
Db   874  TPNGHILDPSL--PLGGHLGPAGAAGPA--PRLLSLQPDPMLVALGSRKSSVMSL--GRMS 926

Qy  1092  HEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSILLSGE-GQES 1150
Db   927  YDQRSLSSRSSSYYGPWCRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGA   980

Qy  1151  QDEEESSEE--DRASPAGSDH-----RHRGSLEREAKSSFDLPDTLQVPG         1193
Db   981  RVCEVAADEGPPRAAPLHTPHAHHIHGPHLAHRHHRHRTLSLDNRDSVDLAELVAVG    1040

Qy  1194  LHRTASGRSS--ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDDNDEGNLSKGERIQAW 1250
Db  1041  AHPRAAWRAAGPAPGHEDCNGRMPS---IAKDVFTKMGDRGDRGEDEEEIDYTLCFRVRKM 1098

Qy  1251  VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPK 1310
Db  1099  IDVYKPDWCEVREDWSVVLFSPENRFRVLCQTIIAHKLFDYVVLAFIFINCITIALERPQ 1158

Qy  1311  IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCHFGEQAYLRSSWNVLDGLLVLISVI 1370
Db  1159  IRAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFSSII 1218

Qy  1371  DIIVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC 1430
Db  1219  DIVVSLASAGGAKIIGVLVRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278

Qy  1431  CAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSL 1490
Db  1279  CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL 1338

Qy  1491  FVLASKDGWVDIMYDGLDAVGVDQQPIMNENPWMLLYFISFLLIVAFFVLNMFVGVVVEN 1550
Db  1339  FVLASKDGWVNIMYNGLDAVADVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVEN 1398

Qy  1551  FHKCRQHQEBEARRREEKIRLRLEKKRRSEKEKQWAEAQCKPYYSDYSRFRLLVHHLCTS 1610
Db  1399  FHKCRQHQEBEARRREEKIRLRRLEKKRR------KAQRLPYYATYCHTRLLIHSMCTS  1451

Qy  1611  HYLDLFITGVIGLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRF 1670
Db  1452  HYLDIPITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKIVAFGLRRF 1511

Qy  1671  FQDRWNQLDLAIVLLSIMGTLEEIEVNLSLPINPTIIRMRVLRIARVLRLKLKMAVGMR  1730
Db  1512  FKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRMRVLRIARVLRLKLKMATGMR 1571

Qy  1731  ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGM 1790
Db  1572  ALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEGMSRHATFENFGM 1631

Qy  1791  AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1847
Db  1632  AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVV 1691

Qy  1848  AVLMKHLEESNKEAKEAELEABLELEM-KTLSPQPHSPLGSP                  1889
Db  1692  AVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTSPGAPGRGPGPGAGGGGGDTE 1751

Qy  1890  ----------FLW------PGVEG-VNSTDSPKPGAPHTTAHIGAASG-----        1920
Db  1752  GGLCRRCYSPAQENLWLDSVSLIIKDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHH 1808

Qy  1921  ----------FSLEHPTMVP----------HPEEVPV-PLG                   1940
Db  1809  DKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLG 1868

Qy  1941  PDLLTVRKSGVSRTHSLPN-DSYMCRNGSTABRSLGHRGWGLPKAQGSSILSVHSQPADT 1999
Db  1869  ECFFPLSSTAVS------PDPENFLCEMEBIPFNPV--RSW--LKHDSSQAPPSPFSPDAS 1919

Qy  2000  SCIIQLPKDVHY------LLQPHGAPTWGAIPKLPPPG----RSPLAQRPLRRQAAIRT 2048
Db  1920  SPLLMPAEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSD  1979

Qy  2049  DSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWCGSSIVQQRGIQSKSHIRLPAPCP    2108
Db  1980  TSLDAS--------------PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAP       2018

Qy  2109  GLEPSWAKDPPETRSSLELDTELSWISGDLLPPSQEEPLFPRDLKKCYSVETQSCRRRPG 2168
Db  2019  G------------PRAGLSPAARRRL----SLRGRGL                       2039

Qy  2169  FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSL-----GGQPLGGPGSRPKKKLSPPSI  2220
Db  2040  FSLRGLRAHQRSHS--SGGSTSPGCTHHDSMDPSDEEGRGGAGGGAGSEHSETLSLSL  2097

Qy  2221  S---IDPPESQGSRPPCSPPGVCLRR----------RAP---ASDSK           2250
Db  2098  TSLFCPPP--------PPPAPGLITPARKFSSTSLLAAPGRPHAAALAHGLARSPSWAADRSK 2151

Qy  2251  DPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP                        2286
Db  2152  DPPGRAPLPMGLGPLAPPPQPL----------PGELEP                      2179
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RESULT 7

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US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
;  APPLICANT: Dietrich, Paul S.
;  APPLICANT: McGivern, Joseph G.
;  TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;  TITLE OF INVENTION:  AND USES
;  FILE REFERENCE: R0043B-REG sequence listing
;  CURRENT APPLICATION NUMBER: US/09/935,541
;  CURRENT FILING DATE: 2001-08-23
;  PRIOR APPLICATION NUMBER: 09/404,650
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;  LENGTH: 2188
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-935-541-4

Query Match           44.9%;  Score 5405.5;  DB 4;  Length 2188;
Best Local Similarity 50.3%;  Pred. No. 0;
Matches 1225;  Conservative 236;  Mismatches 514;  Indels 461;  Gaps   64;
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Qy   51 ASRSSTTCPGPGAAGAGSTEKDPG--SADSEAEGL------------PYPALAPVVFFYLS  97
           :|  ||| |:   ||||:|:  |||||:|            | :|||||||||||||
Db    5 ASPPSSSAAAP-AAEPGVTTEQFGPRSPSSPPGLEEPLDGADPHVPHDLAPIAFFCLR   63

Qy   98 QDSRPRSWCLRTVCNPWFERVSMIVILLNCVTLGMRFCPEDIACDSQRCRILQAFDDFIF  157
           |: |:  | | :|||| :|| ||:||:||||||:|  |  :| |   | |||:||||||
Db   64 QTTSPRNWCIKMVCNPWFECVSMIVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIF  123

Qy  158 AFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL  217
           :||:| |::|||||||||||||||||||||||||:| ||:||||||:|||:||:|||||
Db  124 IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVL  183

Qy  218 RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE  277
           ||||||||||||||||| :|||||||||||||||||||||||||||||:||||||||:
Db  184 RPLKAINRVPSMRILVLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLEE  243

Qy  278 NFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL----  332
          |:  |  ||::  |  |:  : :   |   ||| ||| ||| : |:||||||| ::
Db  244 NFTIQGDVALPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDV  300

Qy  333 -DYETYNSSNNTT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV  389
             |  |   |   |   | |||||||||||:| |||||||||||||  :|||||||||||
Db  301 YDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV  360

Qy  390 DIMYFVWDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFL  449
          :||| | |||||||||||||||||||||||||||||||||||||||| :|  | ||:||
Db  361 EIMYYVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYL  420

Qy  450 SNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ  509
          | :|   :|: | |::    |||||:|: :|||| |   |||||| :| |
Db  421 S-SSTVASYAEPGDCYEEIFQVCHILRKAKR------RAIGLYQALQS-----------  462

Qy  510 PSGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP  569
          |  |  |  |||:  |:||
Db  463 --------RRQAL-------------------------GPE----------APAP  474

Qy  570 STPTPSGSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSP  629
            |
Db  475 AKPGP--------HAK---EPRHYQLCPQHSPLDA----------------TPHT--  502

Qy  630 PPEILKDKALVEVAPSPGPPLTSFNIPPGPFSSMHKLLFTQSTGAC-HSSCKISSPCSK  688
          |
Db  503 -------LVQ----PIPATLAS--------DPASCPCQHEDGRRPSGLGS  534

Qy  689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS  748
             : |:     :|: |                 :|          |  ||
Db  535 TDSGQEGSGS---GSSAGGEDEA------DGDGA--RSSEDGASSELGKEEEEEEQ--  579

Qy  749 LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTN  806
          |  |        |||:|||||||||||||||||:|| |||||||||||||:||||||||
Db  580 ----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPEELTN  635

Qy  807 ALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVISWEIVGQGGGLSVL  866
          | ||||||| ||||||||||||||  || |||||||||||:|:| |||::|  |||| |||||:|
Db  636 ILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQDADGGLSVL  695

Qy  867 RTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKPAS  926
          |||:|||||||||||||||:|:|||||||||||||||||||||||||||||||||||||
Db  696 RTFRLLRVLKLVRFMPALRRQIVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFPSL  755

Qy  927 ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
          |:  ||||:|||||||||||||:|||||||||:|:|||||||||::||||:|||||||||
Db  756 RTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGN  815

Qy  986 YVLFNLLVAIIVEGFQAEGDATKSESEPDFFSPSV----------DGDGRKKRLALVAL  1035
          |||||||||||||||||||| : || :|:||  |              |  | :| ::
Db  816 YVLFNLLVAIIVEGFQAEGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPM  873

Qy 1036 GEHAELRKSLLPPLIIHT----AATPMSHPKSSSTGVGEALGSGRRTSSSGSAEPGAAH  1091
           |  |  ||| ||:|||     : ||  |||||| |   ||||:|||||:| |   | |
Db  874 TPNGHLDPSL--PLGGHLGPAGAAGPA--PRLSLQPDMLVALGSRKSSVMSL--GRMS  926

Qy 1092 HEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES  1150
          :  :         |||   :||   :   :||     :|||:|::
Db  927 YDQRSLSSSRSSYGPWGRSAAWASRRSSWN-------SLKHKPSAEHESLLSAERGGGA  980

Qy 1151 QDEEESSEE--DRASPAGSDH----------------------RHRGSLEREAKSSFDLPDTLQVPG  1193
           :||: ||  |   | |  |                      |  ||  | : |  ||||:  ||
Db  981 RVCEVAADEGPRRAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVG  1040

Qy 1194 LHRTASGRSS--ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDDNDEGNLSKGERIQAW  1250
            |  |         :|||   |:   | :|  |    :||  || | |:  ::|  :|
Db 1041 AHPRAAWRAAGPAPCHEDCNGRMPS--IAKDVFTKMGDRGRGEDEEEIYTLCFPVRKM  1098

Qy 1251 VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPK  1310
          :   |       ::   |:|| :|||   ||| ||||  |||| | | ||||||:|||:|
Db 1099 IDVYKPDWCEVREDWSVLFSPENRFRVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQ  1158

Qy 1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGQAYLRSSWNVLDGLLVLLISVI  1370
          |: |:  |||| |||||||  |||:|||||| |  |  |||||||||||| |:|||:|:
Db 1159 IEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGQAYLRSSWNVLDGFLVFVSII  1218

Qy 1371 DIIVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC  1430
          |:||| | |: ||||| | ||||||||||||||||| |||||||||||| |||||||||
Db 1219 DIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC  1278

Qy 1431 CAFFIIFGILGVQLFKGKFFVCCGGEDTRNITNKSDCARASYRWVRHKYNFDNLGQALMSL  1490
          |||||||||||||||||||| | ||:||||||||||| |||||||||||||||||||||||
Db 1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL  1338

Qy 1491 FVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVEN  1550
          |||||||||| :|| ||| ||| || |  |||||||||||||||| |||||||||||||
Db 1339 FVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVEN  1398

Qy 1551 FHKCRQHQEEEEARRREKRLRRLEKKRSKEKQMAEAQCKPYYSDYSRFLLVHHLCTS  1610
          |||||||||| ||||||||||||||||| ||| |
Db 1399 FHKCRQHQEAEARRREKRLRRLEKKRR----------KAQRLPYYAATYCHTRLLIHSMCTS  1451

Qy 1611 HYLDLFITGVIGLNVTMAMEHYQQPOILDEALKICNYIFTVIFPVFESVFKLVAFAFRRF  1670
          |||| | : ||||| || || | || |:|||| |||| |:|  | || |:||| | :|||
Db 1452 HYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLVAFGLRRF  1511

Qy 1671 FQDRWNQLDLAIVLLSIMGITLEEIVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR  1730
          |  |||||||||:|||| ||||||:||  |||| |||||||||||||||||||| :|||
Db 1512 FKDRWNQLDLAIVLLSVMGITLEEINAALPINPTIIRIMRVLRIARVLKLLKMATGMR  1571

Qy 1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGM  1790
          |||:||   |||||:|||| |||||  |||||||   :|:|||| ||| |  || | |||
Db 1572 ALLDTVVQALPQVGNIGLLFMLLFFYAALGVELFGKLVCNDENPCEGMSRHATFPNFGM  1631

Qy 1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI  1847
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Db          ||||||||||||||||||||:|:...:||||:||||||||||||||||
        63 TTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFI 122

Qy   159 FFAVEMVKRMVALGFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSPSAVRTVRVLR 218
         ||:||||:|||||:||||||||||||||||||:|||:|||:|||||||:||:||||||
Db   123 FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVWAGMVEYSLDLQNINLSAIRTVRVLR 182

Qy   219 PLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLPEN 278
         ||:|||||||||||:||||||||||||||||||||||||||||:|||||||||||||| 
Db   183 PLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNCFLPEEN 242

Qy   279 FSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL------ 332
         |:  ::|::|:|||:: ::::||||| :  :||  | : :||::  :|::|       
Db   243 FTIQGDVALFPYYQPEDDEMPFICSLTGDNGIMGCHEIPPLKEQ---GRECCLSKDDVY 299

Qy   333 DYETYNSSSNTT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD 390
         |  : :::::    ||:|  |  ||   :|||||||||||||||| : :||:||||||:
Db   300 DFGAGRQDLNASGLCVWNRYRVNVCRTGNANHPKGAINFDNIGYAGTIVFVFIFVITLEGWVE 359

Qy   391 IMYFVMDAHSYFNFIYFILLLIVGSFFMINICLVVIATQFSETKQRESQLMREQRVRFLS 450
         |||:||||||:|||||||||||||||||||||||||||||||||||::|:|||:|::|| 
Db   360 IMYYVMDAHSFYNFIYFILLLIVGSFFMINICLVVIATQFSETKQREHRLMEQRQRYLS 419

Qy   451 NASTLASFSEPGSCYEELLKYIVYIILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQP 510
         :  : :|::||  |||::|:|:| ::|||| ||                  ||::::::  
Db   420 -SSTVASYAEPGDCYEEIFQYVCHILRKAKR----------RALGLYQAL 458

Qy   511 SGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPS 570
            |  :|                 |:|                          ||:|
Db   459 ----------QNRRQA-----------------MGPGT--------------PAPA 473

Qy   571 TPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPP 630
                :|  || ||  :|       || :|     ||                 :|:
Db   474 KPGP----------HAK---EPSHCKLCPRHSPLD--------------PTPHT------- 500

Qy   631 PEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKAD 690
                  ||:                 |                           
Db   501 ----------LVQ----------PISAIL 509

Qy   691 SGACGPDSCPYC--------ARTGAGEPESADHVMPDSDEAVYEFTQDAQH 734
          ::  | ||  |        | :| ||| ||:             :::  
Db   510 --ASDPSSCPHCQHEAGRPSGLGSTDSGQEGSGSGSAE----AEANGDGL-QSSEDGVS 563

Qy   735 SDLRDPHSRRRQRSLGPDAEPSSVLA----------FWRLICDTFRKIVDSKYFGRGIMIAILVN 789
         ||                               |   |:|  :||||||||||:|||||:||||
Db   564 SD-------------------LGKEEEQEDGAARLCGDVWRETRKKLRGIVDSKYFNRGIMMAILVN 611

Qy   790 TLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVV 849
         |:|||||:||||| |||:|| ||||||:|||||:|||  :|||:|::||||||||:|:| 
Db   612 TVSMGIEHHEQPEELTNLEICNVVFTSMEALEMILKLAAFGLFDYLRNPYNIFDSIIVI 671

Qy   850 ISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFI 909
         ||:||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   672 ISIWEIVGQADGGLSVLRTFRLLRVLKLVRFMPALRRQLVLMKTMDNVATFCMLLMLFI 731

Qy   910 FIFSILGMHLFGCKPASERD-GDTLPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMAS 968
         ||||:|||||::|||||::|| |||:||||||||||||||||||||||||||||||||||
Db   732 FIFSLGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIVTVFQIITQEDWNVVLYNGMAS 791

Qy   969 TSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDG------- 1022
         |: ||:||::||||||||||||||||||||||||||||::| ||| :::          
Db   792 TTPWASLYFVALMTFGNYVLFNLLVAILVEGFQAEGDANRSCSDEDQSSSNLEEFDKLPE 851

Qy  1023 --DGDRKKRIALVALGEHAELRKSLLLPPLIIH--TAATPMSHPKSSSTGVGEALGSGSRR 1078
            | |:||:|||:  :: |:|:|:|       :|:  |  :                   
Db   852 GLDNSRDLKLCPIPMTPNGHLDPSL--PLGAHLGPAGTMGTAPRLSLQPDPVLVALDSRK 909

Qy  1079 TSSSGSABPGAAHHEMKCPPSARSSPHSPWSAASWTSRRSSRNSLGRAPSLKRRSPSGE 1138
         :|| | : |   :  :   || | | || |   |:|||||:            ::    
Db   910 SSVMSL---GRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWN----SLKHKPPSAE 960

Qy  1139 RRSLLSGEGQES--QDEEESSEE-DRASPAGSDH----------RHRGSLEREA 1179
         |:||                 ::  :   ::                      
Db  1139 DSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFA 158
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Db  1632 AFULTLFQVSTGDNWNGIMKDTLRDCTHDERSCLLSSLQFVSPLIYFVSFVLTAQFVLINVVV 1691
         ||:|  | ::|::    |:|::|  :  ::  ::|:|||  :|  :|:||::|::||:::||:|:
Qy  1848 AVLMKHLEESNKEAKBRALEAELELEM-KTLSPQPHSPLGSP------------- 1889
         |||||||::|||||  : |||:|||||  ||:|:|:||||              
Db  1692 AVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTGSPGAPGRGPGAGGGGDTE 1751

Qy  1890 -----------FLW--------PGVEG-VNSTDSPKPGAPHTTAHIGAASG------- 1920
                    ||           ::  :|::| |    : :    :: ::        
Db  1752 GGLCRRCYSPAQENIWLDSVSLIIKDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCKH 1808

Qy  1921 -------------FSLEHPTMVP------------HPEEVPV-PLG 1940
                      |:|::|::           :|:|:| :|| |
Db  1809 DKQEVQLABTEAFSINSDRSSILLGDDLSLEDPTACFPGRKDSKGELDPPEPMRVGDLG 1868

Qy  1941 PDLLTVRKSGVSRTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSGSLLSVHSQPADT 1999
         |  :  |:|  |  |                   | :                      
Db  1869 ECFFPLSSTAVS------PDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSPDAS 1919

Qy  2000 SCIIQLPKDVHY--------LLQPHGAPTWGAIPKLPPPG-----RSPLAQRPLRRQAAIRT 2048
          ::  :| :       :     |     | | : | |     :|| :      ::    |
Db  1920 SPLLPMPAEPFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSD 1979

Qy  2049 DSLDVQGLGSGREDLLSEVSGPSCPLTRSSSFWGGSSIQVQORSGIQSKVSKHIRLPAPCP 2108
          || |                 | |:|:     :||      | |   ::||:|||| |  
Db  1980 TSLDAS-------------PSSSAGSLGQTTLEDSLITLSDSPRRALGPPAPAP 2018

Qy  2109 GLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQBEPLFPRDLKKCYSVETQSCRRRPG 2168
                                 :::  |                              
Db  2019 G------------------------PRAGLSPAARRRL-----SLRGRGL 2039

Qy  2169 FWLDEQRRHSIAVSCLDSGSQOPRLCPSPSSL-----GGQPLGGPGSRPKKKLSPPSI 2220
         |  :   |:|    ::  | ::    :|| |:     ||  :     |:         
Db  2040 FSLRGLRAHQRSHS--SGGGSTSPGCTHHDSMDPSDEEGRGGAGGGGGAGSEHSETLSSLSL 2097

Qy  2221 S---IDPPESQGSRPPCSPGVCLRR-----------RAP--ASDSK 2250
         |   |                        |   :|||  |||:|
Db  2098 TSLFCPPP-----------PPPAPGLTPARKFSSTSSLAAPGRPHAAAALAHGLARSPSWAADRSK 2151

Qy  2251 DPSVSSPLDSTAASPSPKKDTLSLGLSSDPTDMDP 2286
         || | :|  :           |:|         :::
Db  2152 DPPGRAPLPMGLGPIAPPPQPL------PCGELEP 2179
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Query Match      44.4%;   Score 5345;  DB 3;  Length 1835;
Best Local Similarity 55.4%;  Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

Qy    43 PRSRDSPVASRSSTTCPGPGAAGAGSTEKDPGSADSEASG---LPYPALAPVVFFYLSQ 98
         | |:||  |   :|  |||       | :| |:     ||   ||:||||||||||:|:|
Db     8 PSSAAAPAPEPGITTEQPGP----RSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQ 62

Qy    99 DSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFA 158
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; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1835
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-935-541-5

Query Match           44.4%;   Score 5345;   DB 4;   Length 1835;
Best Local Similarity 55.4%;   Pred. No. 0;
Matches 1138;   Conservative 216;   Mismatches 375;   Indels 324;   Gaps 45;

Qy   43  PRSRDSPVASRSSTTCPGPGAAGAGSTEKDPGSADSEAEG----LPYPALAPVFFYLSQ  98
Db    8  PSSAAAPAPEPGITEQPGP----RSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQ  62

Qy   99  DSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIPA  158
Db   63  TTSPRNWCIKMVCNPWFBCVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFI  122

Qy  159  FFAVBMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLR  218
Db  123  FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLLDLQNINLSAIRTVRVLR  182

Qy  219  PLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPEN  278
Db  183  PLKAINRVPSMRLLVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEEN  242

Qy  279  FSLPLSVDLEPYYQTENEDESPPICSQPRENGMRSCRSVPTLRGEGGGGPPCSL------  332
Db  243  FTIQGDVALPPYYQPEEDDEMPFICSLTGDNGIMGCHEIPPLKEQ--GRECCLSKDDVY  299

Qy  333  DYETYNSSSNTI-CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD  390
Db  300  DFGAGRQDLNASGLCVNWNRYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVE  359

Qy  391  IMYFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLS  450
Db  360  IMYYVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS  419

Qy  451  NASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQP  510
Db  420  -SSTVASYAEPGDCYEEIFQVVCHILRKAKR------RALGLYQAL-------------  458

Qy  511  SGSCTRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPS  570
Db  459  ----------QNRRQA--MGPGT---------------------------PAPA  473

Qy  571  TPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPP  630
Db  474  KPGP--------HAK--EPSHCKLCPRHSPLD------------------PTPHT---  500

Qy  631  PEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKAD  690
Db  501  -------LVQ--------PISAIL----------------  509

Qy  691  SGACGPDSCPYC------------ARTGAGEPESADHVMPDSDSEAVYEFTQDAQH  734
Db  510  --ASDPSSCPHCQHEAGRRPSGLGSTDSGQEGSGSGSGSAE--AEANGDGL-QSSEDGVS  563

Qy  735  SDLRDPHSRRRQRSLGPDAEPSSVLA----FWRLLCDTFRKIVDSKYFGRGIMAILLVN  789
Db  564  SD------------LGKEEBQEDGAARLCGDVWRETRKKLRGIVDSKYFNRGIMAILVN  611

Qy  790  TLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVV  849
Db  612  TVSMGIEHHQPEELTNILEICNVVFTSMFALEMLLKLAAFGLFDYLRNPYNIFDSIIVI  671

Qy  850  ISVWEIVGQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFI  909

Db  961  HESLLSGEGGGSCVRACEGAREEAPTRTAPLHAPHAHHAHHGPHLAHRHRHRRTLSLDT  1020

Qy 1180  KSSFDLPDTLQVPGLHRTAS--GRSSASEHQDCNGKSASGRLARTLRTD-DPQLDGDDDN  1236
Db 1021  RDSVDLGEIVPVVGAHSRAAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDDRRDRGEDE  1078

Qy 1237  DEGNLSKGERIQAWVRSRLPACCRERDSWSAYIPPPQSRPFRLLCHRIITHKMFDHVVLVI  1296
Db 1079  EEIDYTLCFRVRKMIDVYKPDWCEVREDWSVYLFSPENKFRILCQTIIAHKLFDYVVLAF  1138

Qy 1297  IFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSS  1356
Db 1139  IFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSS  1198

Qy 1357  WNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETL  1416
Db 1199  WNVLDGFIVFVSIIDIVVSVASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETL  1258

Qy 1417  MSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRH  1476
Db 1259  ISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCVAANYRWVHH  1318

Qy 1477  KYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVA  1536
Db 1319  KYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVADGQPVTNHNPWMLLYFISFLLIVS  1378

Qy 1537  FFVLNMFVGVVVENFHKCRQHQEEEEARREEKRLREKKRRSKEKQMAEAQCKPYYSD  1596
Db 1379  FFVLNMFVGVVVENFHKCRQHQEAEEARRREEKRLRLEKKRR------KAQRLPYYAT  1431

Qy 1597  YSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVF  1656
Db 1432  YCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTVFVL  1491

Qy 1657  ESVFKLVAFARFRFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRI  1716
Db 1492  EAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEINAALPINPTIIRIMRVLRI  1551

Qy 1717  ARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPC  1776
Db 1552  ARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIFYAALGVELFGKLVCNDENPC  1611

Qy 1777  EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVS  1833
Db 1612  EGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVSPIYFVS  1671

Qy 1834  FVLTAQFVLVNVVIAVLMKHLEESNKEAKEAEALEAELELEMKTLSPQPHSPLGSPFLWP  1893
Db 1672  FVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAEIELEM----------------  1713

Qy 1894  GVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVP-LGPDLLTV----  1946
Db 1714  -AHGLGPCPGPCPG---------PCPCPCPCPCAGPRLPTSSPGAPG  1750

Qy 1947  RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQL  2005
Db 1751  RGSGGAGAG-DTESHLCRHCYSPAQETL----W----LDSVSLIIKDSLEGELTIIDNL  1801

Qy 2006  PKDV-HYLLQPHG  2017
Db 1802  SGSVFHHYASPDG  1814
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Db   1714 -AHGLGPCPGPCPG----------------------------------PCPCPCPCPCAGPRLPTSSPGAPG 1750

Qy   1947 RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQL 2005

Db   1751 RGSSGGAGAG-DTESHLCRHCYSPAQETL----W----LDSVSLIIKDSLEGELTIIDNL 1801

Qy   2006 PKDV-HYLLQPHG 2017

Db   1802 SGSVFHHYASPDG 1814

RESULT 10
US-09-268-163-4
; Sequence 4, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 4
;   LENGTH: 2343
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-268-163-4

Query Match   14.0%;   Score 1678; DB 3;   Length 2343;
Best Local Similarity 23.3%;   Pred. No. 4.5e-126;
Matches 625;   Conservative 354; Mismatches 828; Indels 872; Gaps   81;

Qy   59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----------------VFFYLSQDSRPRSWCLRT 109

Db   32 PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI   91

Qy   110 VCNPWFERVSMLVLLNCVTLGMFRPCEDIACDSQRCRILQAFDD--FIFAFFAVEVV 166

Db   92 TEWPPFEYMILATIIANCIVLAL----EQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI 147

Qy   167 KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDLQNVSFSAVRTVRVLRPLRA 222

Db   148 KIIALGFVFHKGGSYLRNGWNVMDFVVVLTGILATAGTDFDLR----TLRAVRVLRPLKL 202

Qy   223 INRVPSMRILVTLLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP 282

Db   203 VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-------P 255

Qy   283 LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPCSLDYETYNSSSN 342

Db   256 NSTDAEPV--------------------------------GDFPCGKEAPARLCEGD 280

Qy   343 TTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF 401

Db   281 TEC---REYWP-------GPNFGITNFDNLLFAILTVFQCITMEGWTDLLYNTNDAAGNT 330

Qy   402 YNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES----QLMREQRVRFLSNASTL 455

Db   331 WNWLYFIPLIIIGSFFMLNIVLGVLSGEFAKERERVENRRAFLKLRRQQIE-------- 382

Qy   456 ASFSEPGSCYEELLKYLYVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT 515

Db   383 ----------RNAEEKSPLDVLK 417

Qy   516 RSHRRLSVIHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS 575

Db   418 RAATKKKSRNDLIH---------AEEGEDRFAD--------- 440

Qy   576 GGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPFILK 635

Db   672 ISIWEIVGQADGLSVLRTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFI 731

Qy   910 FIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQLTTQEDWNKVLYNGMAS 968

Db   732 FIFSILGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIVTVFQLTTQEDWNVVLYNGMAS 791

Qy   969 TSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDG------ 1022

Db   792 TTPWASLYFVALMTFGNYVLFNLLVAILVEGFQAEGDANRSCSDBDQSSSNLEEFDKLPE 851

Qy   1023 --DGDRKKRLALVALGEHAELRKSLLPPLIIH--TAATPMSHPKSSSTGVGEALGSGSRR 1078

Db   852 GLDNSRDLKLJCPIPMTPNGHLDPSL--PLGAHLGPAGTMGTAPRLSLQPDPVLVALDSRK 909

Qy   1079 TSSSGSAEPGAAAHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGE 1138

Db   910 SSVMSL--GRMSYDQRSLSSSSRSSYYGPWGRSGTWASRRSSWN-----SLKHKPPSAE 960

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Db   961 HESLLSGEGGGSCVRACEGAREEAPTRTAPLHAPHAHHAHHGPHLAHRHRHRHRTLSLDT 1020

Qy   1180 KSGSFDLPDTLQVPGLHRTAS--GRSSASEHQDCNGKSASGRLARTLRTD-DPQLDGDDDN 1236

Db   1021 RDSVDLGELVPVGAHSRAAWRGAQOAPGHEDCNGRMPN--IAKDVFTKMDDRRDRGEDE 1078

Qy   1237 DEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRPRLLCHRIITHKMFDHVVLVI 1296

Db   1079 EEIDYTLCFRVRKMIDVYKPDWCEVREDWSVYLFSPENKFRILCQTIIAHKLFDYVVLAF 1138

Qy   1297 IFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKKVVALGWCFGEQAYLRSS 1356

Db   1139 IFLNCITIALERPQIEAGSTERIFLTVSNYIFTALFVGEWTLKVVSLGLYFGEQAYLRSS 1198

Qy   1357 WNVLDGLLVLLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETL 1416

Db   1199 WNVLDGFLVFVSIIDIVVSVASAGAKILGVIRVLRLLRTLRPLRVISRAPGLKLVVETL 1258

Qy   1417 MSSLKPIGNIVVICCAFFIFGILGVQLFKGKFFVCQGEDTRNITNKSDCABASYRWVRH 1476

Db   1259 ISSLKPIGNIVLICCAFFIFGILGVQLFKGKFYHCLGVDTRNITNRSDCVAANYRWVHH 1318

Qy   1477 KYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVA 1536

Db   1319 KYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVS 1378

Qy   1537 FFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSD 1596

Db   1379 FFVLNMFVGVVVENFHKCRQHQEAEARRREEKRLRRLEKKRR-------KAQRLPYYAT 1431

Qy   1597 YSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQLIDEALKICNVIFTVIFVE 1656

Db   1432 YCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNVMFTTVFVL 1491

Qy   1657 ESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRI 1716

Db   1492 EAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEINAALPINPTIIRIMRVLRI 1551

Qy   1717 ARVLGRHAFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVS 1776

Db   1552 ARVLKLLKMAIGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPC 1611

Qy   1777 EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVS 1833

Db   1612 EGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVSPLYFVS 1671

Qy   1834 FVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEALEMKTLLSPQHSPLGSPFLWP 1893

Db   1672 FVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAEIISLLEM--------- 1713

Qy   1894 GVEGVNSTDSPKPGCAPHTTAHIGAASGFSLEHPTMVPHPEEVVPQ-LGPDLLTV------ 1946

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Db  1326  CRGQYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE  1385

Qy  1514  QQPIMNHNPXMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRR  1573
Db  1386  QGPSPGYRMELSIFYVYVFVVPFFFVNIFVALIIITF----QEQGDKVMSE---CS  1435

Qy  1574  LEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVTMAME  1631
Db  1436  LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYPIMAMIALNTVVLMMK  1495

Qy  1632  HYQQPQILDEALKICNYIFTVIFVVESVFKLVAFAPRRFFQDRWNQLDAIVLLSLMGIT  1691
Db  1496  FYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL  1555

Qy  1692  LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNL  1746
Db  1556  -------FLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYV  1606

Qy  1747  GLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLLFRVSTGDNWNG  1806
Db  1607  CLLIAMLFFIYAIIGMQVFGNIALDDD----TSINRHNNPRTFLQALMLLFRSATGEAWHE  1663

Qy  1807  IMKD--PSRDCDQE--STCVNTVISPIYFVSFVLTAQFVLVNVVIAVLM  1851
Db  1664  IMLSCLSNQACDEQANATECGSDPAYFVYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS  1723

Qy  1852  --KHLEE-----------  1856
Db  1724  ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMN  1783

Qy  1857  SNKEAKEEAELEAEL------ELEMKTLS-  1879
Db  1784  MPISNEDMTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDL  1843

Qy  1880  -PQPHSP----LGSPF---LWPGVEGVNSTDSPKPGAPHTAHIGAASGFSLEHPTMVP  1930
Db  1844  LVPPHKPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLF---HPLKAT  1900

Qy  1931  HPEEVPVPL-GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI  1989
Db  1901  LEQTQPAVLRGARVFLRQKSST----SLSNGGAIQNQESGIKESV--SWGTQRTQDA-  1951

Qy  1990  LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD  2049
Db  1952  --PHEA----------RPPLERGHSTEIPVGRSGALAVD  1978

Qy  2050  --------SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSG  2092
Db  1979  VQMQSITRRGPDGEPQPGLESQG--RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG  2035

Qy  2093  IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS----------SLELDTELSWIS  2135
Db  2036  -----THLCSTTP--------DRPPSQASSHHHHHRCHRRRDRKQRSLEKGPSLS-AD  2080

Qy  2136  GDLLPSSQEEPLFP----------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDS  2186
Db  2081  MDGAPSSAVGPGLPPGEGPTGCRRERERRQERGRSQERRQPSSSSEKQRF---YSCDRF  2137

Qy  2187  GSQPRLCPSPS------------SLGGQPL-----------GGPGSRPKK  2213
Db  2138  GGREPKPKPSLSSHPTSPTAGOEPGPHPQGSGSVNGSPLLSTSGASTPGRGRRGQLPQT  2197

Qy  2214  KLSP-PSISIDPPES---------QGSRPPCSPG--------VCLRRRAPASD---  2248
Db  2198  PLTPRPSITYKTANSSPIHFAGAQTSLPAFSPGRLSRGLSEHNALLQRDPLSQPLAPGSR  2257

Qy  2249  -SKDPSVSSPLDSTRAASPPKKDTLSL---------SGLSS  2279
Db  2258  IGSDPYLGQRLDSEASVHALPEDTITFEEAVATNSGRSS  2296

RESULT 11
US-08-713-118-2
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Db   441  ---------  440

Qy   636  DKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG  695
Db   441  --------LCAVGSPFARAS-  452

Qy   696  PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDACHSDLRDPHSRRQRSLGPDAEP  755
Db   453  --------LKSGKTESSSYF---RRKEK-------  469

Qy   756  SSVLAFWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISNIVF  815
Db   470  -MFRFF-----IRRMVKAQSFYWVVLCVVALNTLCVAMVHYNQPRRLTTTLLYFAEFVF  521

Qy   816  TSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVG----QGGGLSVLRTFR  870
Db   522  LGLFLTEMSLKMVGLGPRSYFRSSFNCFDFGVIVGSVPEVVWAAIKPGSSFGISVLRALR  581

Qy   871  LMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDG  930
Db   582  LLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFVFALLGMQLFGGQFNFQDET  641

Qy   931  DTLPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGM------ASTSSWAALYFIALMTFGN  985
Db   642  PT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIVLTLFGN  697

Qy   986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSL  1045
Db   698  YTLLNVFLAIAVDNLANAQELTKDEEEMEEAA--------NQKLALQKAKEVAEV--SP  746

Qy  1046  LPPLIIHTAATPMSHPKSSSTGVGEA  1071
Db   747  MSAANISIAARQONSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLR  806

Qy  1072  --------LGSGSRRTSSSGSAEPGAA---------HH----EMKCP---  1097
Db   807  PDMKTHLDRPLVELGRDGARGPVGGKARPEAAEAPEGVDPRRHRHRDKDKTPAAGDQ  866

Qy  1098  --------PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL  1142
Db   867  DRAEAPKAESGEPGAREERPRPHRSHSKEAA--GPPEARSERGRGP-----GPEGGRRHH  919

Qy  1143  LSGEGQESQDEE----------ESSEEDRASPAGSDHRHRGSLE---REAKSSFDLLPDTL  1189
Db   920  RRGSPEEAAEREPRHRAHRHQDPSKECAGAKGERRARHRGGPRAGPREAESG-------  972

Qy  1190  QVPG-LHRTASGRSSASE-HQDCNGKSASGRLA---------RTLRTDDPQLDGDDDNDE  1238
Db   973  EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS  1032

Qy  1239  GNLSKGERIQAWVRSRLPACCRER---------DSW-----  1265
Db  1033  GTVTVGP------MHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPDPNTIVHIPVMLTG  1086

Qy  1266  ----------SAYIFPPQSRFRLLCHRI  1283
Db  1087  PLGRATVVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRPCHYI  1146

Qy  1284  ITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVAL  1343
Db  1147  VTMRYFEVVLVVIALSSIALAAEDF-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDL  1205

Qy  1344  GWCFGEQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTURPLRV  1402
Db  1206  GLLLHPGAYFRDLWNILDFIVVSGALVAFAFSSFVGGSKGDINTIKSLRVLRVLRPLKT  1265

Qy  1403  ISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGE-----D  1456
Db  1266  IKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERD  1325

Qy  1457  TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQAALMSLFVLASKGWVDIMYDGLLDAVGVD  1513
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; Sequence 2, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
;   APPLICANT:
;     Franco, Rodrigo
;   APPLICANT: Sun Chen, Ai Ru
;   APPLICANT: Suey, David J.
;   TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
;   TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;     STREET: Two Militia Drive
;     CITY: Lexington
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02173-4799
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/713,118
;     FILING DATE: 16-SEP-1996
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mata, Elizabeth W.
;     REGISTRATION NUMBER: 38,236
;     REFERENCE/DOCKET NUMBER: ACC96-01
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-861-6240
;     TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2337 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-713-118-2

Query Match     13.9%;
Best Local Similarity   23.4%;   Score 1677;   Pred. No. 5.4e-126;   DB 3;   Length 2337;
Matches 627;   Conservative 350;   Mismatches 829;   Indels 868;   Gaps 82;

         Qy     59  PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV------VFFYLSQDSRPRSWCLRT 109
         Db     32  PGPGGLPGQRVLYKQSIAQARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI 91

         Qy    110  VCNPWFERVSMLVILLNCVTLGMFRPCDIACDSQRCRILQAFDD---FIFAFFAVEMVV 166
         Db     92  TEWPPFEYMIATIIANCIVLAL---EQHLPDGDKIPMSERLDDTEPYFIGIFCFEAGI 147

         Qy    167  KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA 222
         Db    148  KIIALGPVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL 202

         Qy    223  INRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP 282
         Db    203  VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF------P 255

         Qy    283  LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPCSLDYETYNSSSN 342
         Db    256  NSTDAEPV------GDFPCGKEAPARLCEGD 280

         Qy    343  TTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVIILEGWVDIMYFVMD-AHSF 401
         Db    281  TEC---REYWP------GPNFGLTNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT 330

         Qy    402  YNPFYFILIIVGSFFMNLCLVVIATQPSETKQRES--QLMREQRVRFLSNASTL 455
         Db    331  WNWLYFIILIIGSFFMNLNLVLGVLSGEFAKERERVENRAFLKLRRQQQIE------ 382

         Qy    456  ASFSEPGSCYEELLKYLYLVYLRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT 515

         Db    383  ------RELNGYLEWIFKAEVMLABED------RNAEEKSPLDVLK 417

         Qy    516  RSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSPTPTPS 575
         Db    418  RAATKKSRNDLIH------AEEGEDRFAD------ 440

         Qy    576  GGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSBASGRTVGSGKVYPTVHTSPPEILK 635
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         Qy    636  DKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG 695
         Db    441  ------LCAVGSFFARAS 452

         Qy    696  PDSCPYCARTGAGEPESADHVMPDSDSEAVVEFTQDAQHSDLRDPHSRRRQRSLGPDAEP 755
         Db    453  ------LKSGKTESSSYF------RRKKK---- 469

         Qy    756  SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQEPELTNALEISNIVF 815
         Db    470  --MFRFF------IRRMVKAQSFYWVVLCVVALNTLCVAMVHYNQPRRLTTTLYFAEFVF 521

         Qy    816  TSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVCQ------QGGGLSVLRTFR 870
         Db    522  LGLFLTEMSLKMYGLGPRSYRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGISVLRALR 581

         Qy    871  LMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIPSILGMHLFPGCKFASERDG 930
         Db    582  LLRIFKVTKYWSSLRNLVVSSLRNLVVSLLNSMKSIISLLLLFLFIVVFALLGMLQFGGQFNFQDET 641

         Qy    931  DTLPDRQNFDSLLWAIVTVFQILTQEDWNKVLYNGM------ASTSSWAALYPIALMTFGN 985
         Db    642  PT----TNFDTFPAAILTVFQIITGEDWNAVMYHGIRESQGGVSKGMPSSFYFVLTLFGN 697

         Qy    986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSL 1045
         Db    698  YTLLNVFLAIAVDNLANAQELTKDEEMEEAA------NQKLALQKAKEVAEV--SP 746

         Qy   1046  LPPLIIHTAATPMSHPKSSSTGVGEA------ 1071
         Db    747  MSAANISIAARQQNSAKARSVHEQRASQLRLQNLRASCEALYSEMDPBERLRFATTRHRR 806

         Qy   1072  ------HH----EMKCP---- 1097
         Db    807  PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRDKDKTPAAGDQ 866

         Qy   1098  ------PSARSS--PHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSL 1142
         Db    867  DRAEAPRAESGEPGAREERRPRPRHSHKEAA--GPPEARSERGRGP--GPEGGRHH 919

         Qy   1143  LSGEGQESQDEE------ESSEEDRASPAGSDHRHRGSLE--REAKSSFDLPDTL 1189
         Db    920  RRGSPEEAAEREPRHRAHRHQDFSKECAGAGKERRARHRGGPRAGPREAESG---- 972

         Qy   1190  QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA----RTLRTDDPQLDGDDDNDE 1238
         Db    973  EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQQPREPHCDLETS 1032

         Qy   1239  GNLSKGERIQAWVRSRLPACCRER------DSW 1265
         Db   1033  GTVTVGP------METLFSTCLQKVEEQPEDADNQRNVTRMGSQQPPDPNTIVHIPVMLTG 1086

         Qy   1266  ------SAYIFPPQSRFRLLCHRI 1283
         Db   1087  PLGEATVVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146

         Qy   1147  VTMRYFEVVILVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDL 1205
         Db   1284  ITHKMPDHVVLIVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343

         Db   1344  GWCFGEQAYLRSSWNVLDGLLVLLISVIDIIVSMV-SDSGTKILGMLRVLRLLRTLRPLRV 1402
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Qy    2253  SVSSPLDSTAASPSPKKDTLSL------SGLSS  2279
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Db    2257  YLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS  2290
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RESULT 12

US-09-452-007-2

; Sequence 2, Application US/09452007
; Patent No. 6140495
; GENERAL INFORMATION:
;   APPLICANT: Franco, Rodrigo
;   APPLICANT: Sun Chen, Ai Ru
;   APPLICANT: Suey, David J.
;   TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
;   TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;   STREET: Two Militia Drive
;   CITY: Lexington
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02173-4799
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/452,007
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/713,118
;   FILING DATE: 16-SEP-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mata, Elizabeth W.
;   REFERENCE/DOCKET NUMBER: 38,236
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-861-6240
;   TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2337 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-452-007-2

  Query Match   13.9%; Score 1677; DB 3; Length 2337;
  Best Local Similarity   23.4%; Pred. No. 5.4e-126;
  Matches 627; Conservative 350; Mismatches 829; Indels 868; Gaps 82;

Qy   59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----------VFFYLSQDSRPRSWCLRT 109
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Db   32 PGPGGLQPGQRVLYKGSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKIYAKRI 91

Qy   110 VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV 166
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Db   92 TEWPPPEYMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI 147

Qy   167 KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDLQNVSFSSAVRTVRVLRPLRA 222
           |||||:: :||||| ||| |||| |||:| ||:| :| |: |||||:
Db   148 KIIALGFVFHKGSYLRNGWNVMDFVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL 202

Qy   223 INRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVCLWAGLLRNCFLPENFSLP 282
           :::||| :||::: |:|| || |||:| || | |||||||:|||| |:
Db   203 VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLELFYMGKFHKACF------P 255

Qy   283 LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSN 342
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Db   1206  GLLLHPGAYFRDLMNILD---FIVVSGALIVAFAFSGSKGKDINTIKSLRVLRVLRPLKT  1261
Qy   1403  ISRAQGLKLVVETIMSSLKPIGNIVVICCAFFIIFGILGVQLPFKGKFPVCQGE-----D  1456
Db   1262  IKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLPFKGKFFYCTDESKELERD  1321
Qy   1457  TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAGVD  1513
Db   1322  CRGQYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE  1381
Qy   1514  QQPIMNHNPWMLLYFISPLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRR  1573
Db   1382  QGPSPGYRMELSIFYVVFVVFVFPFFVNIFVALIIITF------QEQGDKVMSE---CS  1431
Qy   1574  LEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAME  1631
Db   1432  LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMK  1491
Qy   1632  HYQOPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDIAIVLLSIMGIT  1691
Db   1492  FYDAPYEYELMKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDPVTVLGSITDIL  1551
Qy   1692  LEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFM  1751
Db   1552  VTEIANNF---IN--LSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIA  1605
Qy   1752  LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD-  1810
Db   1606  MLFFIYAIIGMQVFGNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSC  1662
Qy   1811  -PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM-----------------K  1852
Db   1663  LSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSIIGPH  1722
Qy   1853  HLEE--------------------------------------------------------  1856
Db   1723  HLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISN  1782
Qy   1857  -----------------------------SNKEAKEAEALEAEL----ELEMKTLS--PQPH  1883
Db   1783  EDMTVHFTSTIMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDLLVPPH  1842
Qy   1884  SP----LGSPF--LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEV  1935
Db   1843  KPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLF--HPLKATLEQTQ  1899
Qy   1936  PVPL-GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGGSILSVHS  1994
Db   1900  PAVLRGARVPLRQKSST----SLSNGGAIQNOESGIKESV--SWGTQRTQDA-------  1945
Qy   1995  QPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD----  2049
Db   1946  -----------PHEA----RPPLERGHSTEIFVGRSGALAVDVQMQS  1977
Qy   2050  ---------SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKV  2097
Db   1978  ITRRGPDGEPQPGLESQG---RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG----  2029
Qy   2098  SKHIRLPAPCPGLEPSWAKDPPETRS-----------SLELDTBLSWTSGDLLP  2140
Db   2030  --THLCSTTP------DRPPPSQASSHHHHRCHRRRDRKQRSLEKGPSLS-ADMDGAP  2079
Qy   2141  SSQEEPLFP------RDLKKCYSVETQSCRRPGFWLDEQRRHSIAVSCLLDSGSQPR  2191
Db   2080  SSAVGPGLLPEGPGTGCRRBERRQERSRSQERRQPSSSSSEKQRF--YSCDRFGGREP  2136
Qy   2192  LCPSPS-----------SLGGQPL-----------GGPGSRPKKKLSP-  2217
Db   2137  PKPKPSLSSHPTSPTAGQEPGHPQGSGSVNGSPLLSTGASTPGRGGRRQLPQTPLTPR  2196
Qy   2218  PSISIDPPES-------QGSRPPCSPG---------VCLRRRAPASD---------SKDP  2252
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Db   281  TEC---REYWP-------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT  330
Qy   402  YNFIYFILLIVGSFFMNLCLVVIATQFSETKQRES-------QLMREQRVRFLSNASTL   455

Db   331  WNWLYFIPLIIIGSFFMNLNLVLGVLSGEFAKEERVENRRAFLKLRRQQQIE-------  382
Qy   456  ASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT  515

Db   383  ----------RELNGYLEWIFKAEEVMLAEED------RNAEEKSPLDVLK          417
Qy   516  RSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS    575

Db   418  RAATKKKSRNDLIH----------AEEGEDRFAD---                        440
Qy   576  GGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILK  635

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Qy   636  DKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGCACHSSCKISSPCSKADSGACG 695

Db   441  -----------------------LCAVGSPFARAS-----                     452
Qy   696  PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEP   755

Db   453  ----------LKSGKTESSSYF                                       469
Qy   756  SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF  815

Db   470  --MPRFF------IRRMVKAQSFYWVVLCVVALNTLCVAMVHYNQPRRLITTLIYFAEFVF 521
Qy   816  TSLFAIEMLLKLLVVGPFGYIKNPYNIFDGVIVISWREIVGQ-----QGGGLSVLRTFR   870

Db   522  LGLFLTEMSLKMYGLGPRSYFPRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGISVLRALR 581
Qy   871  LMRVLKLVRFLPALQRQLVVIMKTMDNVATPCMLMLFIFIPSILGMHLFGCKFASERDG   930

Db   582  LLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFIVVFALLGMQLFGGQFNFQDET  641
Qy   931  DTLPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGM----ASTSSWAALYFIALMTFGN   985

Db   642  PT-----TNFDTFPAAILTVFQLLTGEDWNAVMYHGIESQGGVSKGMFSSFYFIVLTLFGN 697
Qy   986  YVLFNLLIVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHARLRKSL 1045

Db   698  YTLLNVFLAIAVDNLANAQELTKDEEMEEAA------NQKLALQKAKEVAEV--SP      746
Qy   1046 LPPLIIHTAATPMSHPKSSSTGVGEA                                   1071

Db   747  MSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHRR  806
Qy   1072 --------LGSGSRRTSSSGSAEPGAA                                  1097

Db   807  PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRDKDKTPAAGDQ  866
Qy   1098 --------PSARSS---PHSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGERRSL       1142

Db   867  DRAEAPKAESGEPGAREERPRPHRSHSKEAA--GPPEARSERGRGP-----GPEGGRRHH  919
Qy   1143 LSGEGQRSQDEE-------ESSEEDRASPAGSDHRHRGSLE---REAKSSFDLPDTL     1189

Db   920  RRGSPEEAAEREPRRHRAHRHQDPSKECAGAKGERRARHRGGPRAGPREAESG-----    972
Qy   1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA---------RTLRTDDPQLDGDDDNDE 1238

Db   973  EEPARRHRARHKAQPAHEAAVEKETTEKEATEKEAIVEADKEKELRNIQPREPHCDLETS  1032
Qy   1239 GNLSKGERIQAWVRSRLPACCRER-----DSW------                       1265

Db   1033 GTVTVGP-----MHTLPSTCLQKVEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTG     1086
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Right column:

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Qy   1266 --------------------------------------------------SAYIFPPQSRFRLLCHRI 1283
Db   1087 PLGEATVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI  1146

Qy   1284 ITHKRMFDHVVLVIIFLNCTIAMERPKIDPHSABRIFLTLSNYIFTAVFLAEMTVKVVAL 1343
Db   1147 VTMRYFEVVILVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVTFPEMVIKMIDL  1205

Qy   1344 GWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRV  1402
Db   1206 GLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSGKGKDINTKSLRVLRVLRPLKT  1261

Qy   1403 ISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE-------D 1456
Db   1262 IKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERD  1321

Qy   1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD  1513
Db   1322 CRGQYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLLTFTVSTGEGWPMVLKHSVDATYEE  1381

Qy   1514 QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREKRLRR   1573
Db   1382 QGPSPGYRMELSIFYVVYFVVFPFFFVNIFVALIIITF------QEQGDKVMSE----CS  1431

Qy   1574 LEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAME  1631
Db   1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMK  1491

Qy   1632 HYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVILLSIMGIT 1691
Db   1492 FYDAPYEYELMKLCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL  1551

Qy   1692 LEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFM  1751
Db   1552 VTEIANNF---IN--LSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIA   1605

Qy   1752 LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD-  1810
Db   1606 MLFFIYAIIGMQVFGNIALDDD--TSINRHNFRTFLQALMLLFRSATGEAWHEIMLSC    1662

Qy   1811 -PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM------------K     1852
Db   1663 LSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPH  1722

Qy   1853 HLEE-----------                                              1856
Db   1723 HLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISN  1782

Qy   1857 SNKEAKEABLEAEL------ELEMKTLS--PQPH                           1883
Db   1783 EDMTVHFTSTLMALIRTALEIKLAPAGTKQHCQCDAELRKEISVVWANLPQKTLDLLVPPH 1842

Qy   1884 SP---LGSPF--LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEV     1935
Db   1843 KPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLF--HPLKATLEQTQ   1899

Qy   1936 PVPL-GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLEPKAQSGSILSVHS 1994
Db   1900 PAVLRGARVFLRQKSST----SLSNGGAIQNQESGIKESV---SWGTQRTQDA------   1945

Qy   1995 QPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD----   2049
Db   1946 --------PHEA------RPPLERGHSTEIPVGRSGALAVDVQMQS               1977

Qy   2050 ------SLDVQLGSREDLLSVSGPSCPLTRSSFWGGSSIQVQQRSGIQSKV          2097
Db   1978 ITRRGPDGBPQPGLESQG---RAASMPRLAAETQPVTDASPMKRSISTLAQPRPRG----  2029

Qy   2098 SKHIRLPAPCPGLEPSWAKDPPETRS------SLELDTELSWISGDLLP            2140
Db   2030 -THLCSTTP------DRPPPSQASSHHHHHRCHRRRDRKQRSLEKGPSLS-ADMDGAP    2079
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;     REFERENCE/DOCKET NUMBER:      6362-52517
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:    (619)238-0999
;       TELEFAX:      (619)238-0062
; INFORMATION FOR SEQ ID NO:     47:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:    2339 amino acids
;     TYPE:      amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:      linear
;   MOLECULE TYPE:   protein
;   FRAGMENT TYPE:   internal
; US-08-455-543A-47

Query Match         13.9%;     Score 1676;    DB 1;    Length 2339;
Best Local Similarity    23.4%;    Pred. No. 6.5e-126;
Matches  627;    Conservative 350;    Mismatches 826;    Indels 876;    Gaps  82;

Qy    59  PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV--------VFFYLSQDSRPSWCLRT 109
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Db    32  PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVRKYAKRI  91

Qy   110  VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFPD---FIFAFFAVEMVV 166
              ||:|||:||:::| |||:|:| |:::|| : ::| ::|     ||:|||:|||
Db    92  TEWPPFENMLATIIANCIVLAL--EQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI 147

Qy   167  KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDLQNVSFSAVRTVVIRPLRA 222
              |:|:|  |||:|  :|:.|:||:.:|:: |:|     :: |||  |  || ||:|
Db   148  KIIALGFVFHKGSYLRNGNVMDFVVVLTGILATAGTDFLR----TLRAVRVLRPLKL 202

Qy   223  INRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGQLWAGLLRNRCFLPENFSLP 282
              :|:|:||| |::|:|.|:   | :| || : | ||:||||:|.: : :::::|:|
Db   203  VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF------P 255

Qy   283  LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYFTYNSSSN 342
              |||                                       ||||||||||
Db   256  NSTDAEPV-----------------------------------GDFPCGKEAPARLCEGD 280

Qy   343  TTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF 401
              :|:|||:||::|:|||||:||||||||:||||||||:|||:|:||||||||||||  |||
Db   281  TEC--REYWP--------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT 330

Qy   402  YNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES-----QLMREQRVRFLSNASTL 455
              |||||||:|||||||||||||||||||||||||||:     ||||||||||||||||||
Db   331  WNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE------ 382

Qy   456  ASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT 515
              :|                                       ::
Db   383  ------RELNGYLEWIFKAEEVMLAEED------------------RNAEEKSPLDVLK 417

Qy   516  RSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS 575
              |:||||:
Db   418  RAATKKSRNDLIH--------------------------------AEEGEDRFAD---- 440

Qy   576  GGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPPEILK 635
Db   441  ---------------------------------------------------------- 440

Qy   636  DKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG 695
              |: |:                                   |||||:|||||
Db   441  --------------------------------------------LCAVGSPFARAS--- 452

Qy   696  PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEP 755
              ||: :
Db   453  LKSGKTESSSYF--------------------------------------RRKEK- 469

Qy   756  SSVLAPWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF 815
              :| |                                    |:|| :
Db   470  --MFRFF-------IRRMVKAQSFYWVLCVAMVHYNQPRRLTTTLYFAEFVF 521

Qy   816  TSLFALEMLLKLLVVGPFGVYKNPYNIFDGVIVISWEIVGQ-------QGGGLSVLRTFR 870
              |||||::|:|||||||||||||||||||||||||||:||:|       |||||:||||
Db   522  LGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIGVSVFEVVVAAIKPGSSFGISVLRALR 581
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Qy  2141  SQEEPLFP-----------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPR 2191
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Db  2080  SSAVGPGLPPGEGPTGCRRERERQERSRSQERRQPSSSSSEKQRF---YSCDRFGGREP 2136

Qy  2192  LCPSPS-----------SLGGQPL-----------GGPGSRPKKKLSP- 2217
              :::                                 :|:|
Db  2137  PKPKPSLSSHPTSPTAGQEPGPHPQGSGSVNGSPLLSTSGASTPGRGGRRQLPQTPLTPR 2196

Qy  2218  PSISIDPPES-----------QGSRPPCSPG-----------VCLRRRAPASD 2252
              |||                                     ||||||||
Db  2197  PSITYKTANSSPIHFAGAQTSLPAFSPGRLSRGLSEHNALLQRDPLSQPLAPGSRIGSDP 2256

Qy  2253  SVSSPLDSTAASPSPKKDTLSL-----------SGLSS 2279
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Db  2257  YLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS 2290
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RESULT 13
US-08-455-543A-47
; Sequence 47, Application US/08455543A
;; Patent No. 5792846
; GENERAL INFORMATION:
;   APPLICANT:  Harpold, Michael
;   APPLICANT:  Ellis, Steven
;   APPLICANT:  Williams, Mark
;   APPLICANT:  Feldman, Daniel
;   APPLICANT:  McCue, Ann
;   APPLICANT:  Brenner, Robert
;   TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;   TITLE OF INVENTION:  METHODS
;   NUMBER OF SEQUENCES:  57
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Brown, Martin, Haller & McClain
;     STREET:   1660 Union Street
;     CITY:     San Diego
;     STATE:    California
;     COUNTRY:  USA
;     ZIP:      92101-2926
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:   Diskette
;     COMPUTER:      IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:      FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/455,543A
;     FILING DATE:  May 31, 1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/223,305
;     FILING DATE:  April 4, 1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/868,354
;     FILING DATE:  April 10, 1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/745,206
;     FILING DATE:  15-AUG-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/620,250
;     FILING DATE:  30-NOV-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/482,384
;     FILING DATE:  20-FEB-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/603,751
;     FILING DATE:  04-APR-1989
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  WO PCT/US89/01408
;     FILING DATE:  04-APR-1989
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/176,899
;     FILING DATE:  04-APR-1988
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Seidman, Stephanie L.
;     REGISTRATION NUMBER:  33,779
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Qy   871 LMRVLKLVRFLPALQRQIVVLMKTMDNVATFCMLLMLFIFISILGMHLFGCKFASERDG 930
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Db   582 LLRIFKVTKYWSLRNLVVSLLNSMKSIISLLFLLFLFIVVFALLGMQLFGGQFNFQDET 641

Qy   931 DTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----ASTSSWAALYFIALMTFGN 985
             : :|:: ||:|| |:|| ||| | :|| :|: : ||| || ||::|
Db   642 PT----TNFDTFPAAILVFQILTGEDWNAVMYHGIESQGVSKGMFSSFYFIVLTLFGN 697

Qy   986 YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKRLALVALGEHAELRKSL 1045
             ||: | :||: ||::|::||: |:||
Db   698 YTLLNVFLAIAVDNLANAQELTKDEEEMEEAA-------NQKLALQKAKEVAEV--SP 746

Qy 1046 LPPLLIHTAATPMSHPKSSSTGVGEA-------------------------------- 1071
             |::
Db   747 MSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLR 806

Qy 1072 ------LGSGRRTSSSGSAEPGAA---------------HH----EMKCP-------- 1097
             :||:| |:
Db   807 PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRDKDKTPAAGDQ 866

Qy 1098 --PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL 1142
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Db   867 DRAEAPKAESGEPGAREEERPRHRSHSKEAA---GPPEARSERGRCP------GPEGGRRHH 919

Qy 1143 LSGEGQESQDEE-------------ESSEEDRASPAGSDHRHRGSLE---RFAKSSFDLPDTL 1189
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Db   920 RRGSPEEAAEREPRHRAHRHQDPSKECAGKGERRARHRGGPRAGPREABSG--------- 972

Qy 1190 QVPG-LHRTASGRSSASE--HQDCNGKSAGRLA------RTLRTDDPQLDGDDDNDE 1238
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Db   973 EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032

Qy 1239 GNLSKGERIQAWVRSRLPACCRER------------------DSW----------- 1265
             |||:|:||: | : :|
Db 1033 --MHTLPSTCLQKVEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTG 1086

Qy 1266 ----------------------SAYIFPPQSRFRLLCHRI 1283
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Db 1087 PLGEATVVPSGNVDLESQAEGKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146

Qy 1284 ITHKMFDHVVIVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343
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Qy 1344 GWCFGEGQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRV 1402
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Db 1206 GLLLHPGAYFRDLWNILD--------FIVVSGALVAFSGSKGKDINTIKSLRVLRVLRPLKT 1261

Qy 1403 ISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGLLGVQLFKGKFFVCQGE-----D 1456
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Db 1262 IKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERD 1321

Qy 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD 1513
             ||| :| :| | | ::| ||| ||||:|||:||||||| | || |:: :
Db 1322 CRGQYILDYEKEVEAQPRQWKKYDFHYDNVLWALLLFTVSTGEGWPMVLKHSVDATYEE 1381

Qy 1514 QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRR 1573
             ||| | | ||:| |::|: ||::| ||| |:   : | || ::::
Db 1382 QGPSPGYRMELSIFYVVYFVVPFFFVNIFVALIIITF-----QEQGDKVMSE-----CS 1431

Qy 1574 LEKKRRSKEKQMAEAAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1631
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Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491

Qy 1632 HYQQPQIIDEALKICNYIFTVIFVIFVFESVFKLVAFAFRRFFQDRWNQLDLIAIVLLSIMGIT 1691
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Db 1492 FYDAPYEVMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL 1551

Qy 1692 LERIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNL 1746
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Db 1552 VTEIAETNNFINLS-------FLRLFRAARLKLLRQGYTIRILLWTFVQSFKALPYV 1602

us-09-611-257a-24.rai

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    COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: DOS
        SOFTWARE: FastSEQ Version 1.5
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/223,305C
        FILING DATE: April 4, 1994
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/868,354
        FILING DATE: April 10, 1992
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/745,206
        FILING DATE: 15-AUG-1991
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/620,250
        FILING DATE: 30-NOV-1990
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/482,384
        FILING DATE: 20-FEB-1990
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/603,751
        FILING DATE: 04-APR-1989
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: WO PCT/US89/01408
        FILING DATE: 04-APR-1989
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/176,899
        FILING DATE: 04-APR-1988
    ATTORNEY/AGENT INFORMATION:
        NAME: Seidman, Stephanie L.
        REGISTRATION NUMBER: 33,779
        REFERENCE/DOCKET NUMBER: 52516 (P519739)
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (619)238-0999
        TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 47:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 2339 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: protein
    FRAGMENT TYPE: internal
US-08-223-305C-47:

Query Match       13.9%; Score 1676; DB 2;   Length 2339;
Best Local Similarity  23.4%; Pred. No. 6.5e-126;
Matches  627; Conservative  350; Mismatches  826; Indels  876; Gaps  82;
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Qy    59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----------VFFYLSQDSRPRSWCLRT 109
Db    32 PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI 91

Qy   110 VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV 166
Db    92 TEWPPFENMLLATTIANCIVLAL---EQHLPDGDKTPMSERLLDDTEPYFIGIFCFEAGI 147

Qy   167 KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDLQNVSFSAVRTVRVLRPLRA 222
Db   148 KIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR----TLRAVRVLRPLKL 202

Qy   223 INRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGQLWAGLLRNRCFLPENFSLP 282
Db   203 VSGIPSLQVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF----P 255

Qy   283 LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSN 342
Db   256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280

Qy   343 TTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF 401
Db   281 TEC--REWP------GPNFGTINFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT 330

Qy   402 YNFYFILLIIVGSFFMINLCLVVIATQFSETKQRES------QLMREQRVRFLSNASTL 455
Db   331 WNWLYIFIPLIIIGSFFMLNIVLGVLSGEFAKERERVENRRAFLKLRRQQQIE------ 382

Qy   456 ASFSEPGSCYEELLKYLVVYLRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT 515
Db   383 ----------RELNGYLEWIFKAEEVMLAEED------RNAEEKSPLDVLK 417

Qy   516 RSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS 575
Db   418 RAATKKSRNDLIH----------AEEGEDRFAD------ 440

Qy   576 GGPPRGAESVHSFYHADCHLEPVRCQAPPPRCFSEASGRTVGSGKVYPTVHTSPPPEILK 635
Db   441 --------- 440

Qy   636 DKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG 695
Db   441 ------LCAVGSPFARAS--------- 452

Qy   696 PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEP 755
Db   453 ----------LKSGKTESSSYF--------RRKEK------ 469

Qy   756 SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF 815
Db   470 --MRFF-------IRRMVKAQSFYWVLCVALNTLCVAMVHYNQPRRLTTTLYFAEFVF 521

Qy   816 TSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ----QGGGLSVLRTFR 870
Db   522 LGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGISVLRALR 581

Qy   871 LMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDG 930
Db   582 LLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFIVFALLGMQLFGGQFNFQDET 641

Qy   931 DTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----ASTSSWAALYFIALMTFGN 985
Db   642 PT----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFVLTLFGN 697

Qy   986 YVLFNLLVAILVEGFQABGDATKSESEPDFFSPVDGDGDRKKRLALVALGEHAELRKSL 1045
Db   698 YTLLNVFLAIAVDNLANAQELTKDEEEMEEAA--------NQKLALQKAKEVAEV-SP 746

Qy  1046 LPPLIHTAATPMSHPKSSSTCVGEA 1071
Db   747 MSAANISIAARQQNSAKARSVWEQRASOLRLQNLRASCEALYSEMDPEERLRFATTRHLR 806

Qy  1072 ---------LGSGSRRTSSSGSAEPGA----HH---EMKCP------ 1097
Db   807 PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHRHRDKDKTPAAGDQ 866

Qy  1098 ----------PSARSS---PHSPWSAASWTSRRSSRNSLGRAPSLKRRSPSGERRSL 1142
Db   867 DRAEAPKAESGEPGAREERPRHRSHSKEAA--GPPEARSERGRGP----GPEGGRRHH 919

Qy  1143 LSGEGQESQDEE---------ESSEEDRASPAGSDHRHRGSLE---REAKSSFDLPDTL 1189
Db   920 RRGSPEEAAEREPRHRAHRHQDPSKECAGAGKGERRARHRGGPRAGPREAESG---- 972

Qy  1190 QVPG-LHRTASGRSSASE-HQDCNGKSASGRLA------RTLRTDDPQLDGDDDNDB 1238
Db   973 EEPARRHPARHKAQPAHEAVEKETTEKEATEKEAETVEADKEKELRNHQPREPHCDLETS 1032

Qy  1239 GNLSKGERIQAWVRSRLPACCRER-------DSW------ 1265
Db  1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPDPNTIVIHIPVMLTG 1086

Qy  1266 ---------SAVIFPPQSRFLLCHRI 1283
Db  1087 PLGEATVPSGNVDLESQAEGKKEVEADDVMRSGPRIVPYSSMFCLSPTNLLRFCHYI 1146
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Qy 2187 GSQPRLCPSPS----------------------------SLGGQPL---------------GGPGSRPKK 2213
                 : : || ::
Db 2134 GGREPPKPKPSLSHPTSPTAGQEPGPHPQGSGVNGSPLLSTSGASTPGRGGRRQLPQT 2193

Qy 2214 KLSP-PSISIDPPES---------QGSRPPCSPG------VCLRRRAPASD----- 2248
                  :|:   :|: ||
Db 2194 PLTPRPSITYKTANSSPIHPAGAQTSLPAFSPGRLSRGLSEHNALLQRDPLSQPLAPGSR 2253

Qy 2249 -SKDPSVSSPLDSTAASPSPKKDTLSL-----SGLSS 2279
             ::||| : || ||::||
Db 2254 IGSDPYLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS 2292

RESULT 15
US-09-268-163-6
; Sequence 6, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 6
; LENGTH: 2339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-163-6

  Query Match   13.9%;   Score 1674; DB 3; Length 2339;
  Best Local Similarity 23.4%;   Pred. No. 9.4e-126;
  Matches   627;   Conservative 350;   Mismatches 826;   Indels 876;   Gaps 82;

Qy   59 PGPGAAGAGSTEKDPGSADSEABGLPYPALAPV--------------VFFYLSQDSRPRSWCLRT 109
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Db   32 PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVSEDNVVRKYAKRI 91

Qy   110 VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV 166
          || ::   ::   :
Db   92 TEWPPFEYMILATIIANCIVLAL----BQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI 147

Qy   167 KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA 222
          ||:| |:| ||
Db   148 KIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR----TLRAVRVLRPLKL 202

Qy   223 INRVPSMRILVTLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP 282
          :   :: |:: ::| :::
Db   203 VSGIPSLQVLKSIMKAMVPLLQIGILLFFAAILMFAIIGLEFYMGKFHKACF------P 255

Qy   283 LSVDLEPYYQCTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSN 342
                                                            ||
Db   256 NSTDAEPV--GDFPCGKEAPARLCEGD 280

Qy   343 TTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIPQVITLEGWVDIMYFVMD-AHSF 401
                                    :::| ||
Db   281 TEC---REYWP-------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT 330

Qy   402 YNFIYFILLIIVGSFFMINLCLVVIATQPSETKQRES--------QLMREQRVRFLSNASTL 455
                                     |::   ::::: |
Db   331 WNWLYFIPLIIIGSFFMNLVLGVLSGEFAKERERVENRAFLKLRRQQIE--------- 382

Qy   456 ASFSEPGSCYEELLKYLVYLLRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT 515
          ||| RNAEEKSPLDVLK 417
Db   383 ------------------------RELNGYLEWIFKAEEVMLAEED----

Qy   516 RSHRRLSVHHLVHHHHHHHHYHLLGNGTLRVPRASPEIQRDANGSRRILMLPPPSTPTPS 575
                                                            |||
Db   418 RAATKKSRNDLIH-----------------------------AEEGEDRFAD-------- 440

Qy 1284 ITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLABMTVKVVAL 1343
          ||| | ::::|
Db 1147 VTMRYFEVILVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDL 1205

Qy 1344 GWCFCEGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKIIGMLRVLRLLRTLRPLRV 1402
          | ::::   : | | ||||||||||||||
Db 1206 GLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSGKGKDINTIKSLRVLRVLRPLKT 1261

Qy 1403 ISRAQGLKLJVVETLMSSLKPIGNIVICCAFFIIFGLIGVQLPKGKFFVCQGE-----D 1456
          | ||||: ||||
Db 1262 IKRLPKLKAVFDCVVNSLKNVLNILLIVMLFMFIFAVIAVQLFKGKFFYCTDESKELERD 1321

Qy 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD 1513
                                 ::||:: : ::| | ::: ||: |:
Db 1322 CRGQYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381

Qy 1514 QQPIMNHNPWMLIYFISFLLIVAFPVLNMFVGVVVENFHKCRQHQEEEBARREKRLRR 1573
          | :: ||--CS 1431
Db 1382 QGPSPGYRMELSIFYVVYFVVFPFFVNIFVALIIITF------QEQGDKVMSE

Qy 1574 LEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVIHHLCTSHYLDLFITGVIGLNVVTMAME 1631
          ||| |: ||
Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491

Qy 1632 HYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDIAIVLLSIMGIT 1691
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Db 1492 FYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGITDIL 1551

Qy 1692 LEETE------VNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRAILHTVMQALPQVGNL 1746
                     || ::
Db 1552 VTEIAETNNFINLS-------FLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYV 1602

Qy 1747 GLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNG 1806
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Db 1603 CLLIAMLFFIYAIIGMQVFGNIALDDD---TSINRHNRFTFLQALMLLFRSATGEAWHE 1659

Qy 1807 IMKD--PSRDCDQE--STCVNTVISPIYFVSFVLTAQFVLVNVVIAVLM---------- 1851
          || |
Db 1660 IMLSCLSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMNLFVAVIMDNFEYLTRDSS 1719

Qy 1852 --KHLEE--- 1856
            |:
Db 1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMN 1779

Qy 1857 ------SNKEAKEAELEAEL----ELEMKTLS- 1879
                 || |||
Db 1780 MPISNEDMTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDL 1839

Qy 1880 -PQPHSP-----LGSPF----LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVP 1930
          || ::
Db 1840 LVPPEHKPDEMTVGKVVAALMIPDFYKQNKTTRDQMQQAPGGLSQMGPVSLF---HPLKAT 1896

Qy 1931 HPEEVPVPL-GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI 1989
          | :|
Db 1897 LEQTQPAVLRGARVFLRQKSST----SLSNGGAIQNQESGIKESV---SWGTQRTQDA-- 1947

Qy 1990 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRLRRQAAIRTD 2049
                               ||| ::
Db 1948 --------------------RPPLERGHSTEIPVGRSGALAVD 1974

Qy 2050 --------------------SLDVQGLGSREDLLSBVSGPSCPLTRSSSFWGGSSIQVQORSG 2092
                              |:
Db 1975 VOMQSITRRGPDGEPQPGLESQG--RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG 2031

Qy 2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS---------------SLELDTELSWIS 2135
          |||
Db 2032 ------THLCSTTP------DRPPPSQASSHHHHHRCHRRRDRKQRSLEKGPSLS-AD 2076

Qy 2136 GDLLPSSQEEPLFP----------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDS 2186
          |||| :::
Db 2077 MDGAPSSAVGPGLPPGEGPTGCRRERERRQERGRSQERRQPSSSSSSEKQRF--YSCDRF 2133

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Qy   576 GGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPPEILK  635
Db   441 ------------------------------------------------------------  440

Qy   636 DKALVEVAPSPGPPTLTSFNIPPGPFSSMEKLLETQSTGACHSSCKISSPCSKADSGACG  695
Db   441 ----------------------------------------LCAVGSPFARAS---  452

Qy   696 PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEP  755
Db   453 -------LKSGKTESSSYF-----------RRKEK------  469

Qy   756 SSVLAFWRLICDTFRKIYDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF  815
Db   470 --MFRFF---IRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLITTLYFAAEFVF  521

Qy   816 TSLFALEMLLKLLVYGPEGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGLSVLRTFR  870
Db   522 LGFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVWAAIKPGSSFGISVLRALR  581

Qy   871 LMRVLIKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDG  930
Db   582 LLRIFKVTKYWSSLRNLVVSLLNSMKSISISLLFLLFLFIVVFALLGMLFGGQFNFQDET  641

Qy   931 DTLPDRRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGM-----ASTSSWAALYFIALMTFGN  985
Db   642 PT----TNFDTFPAAILTVFQLLTGEDWNAVMYHGIESQGGVSKGMFSSFYFIVLTLFGN  697

Qy   986 YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDRKKRLALVALGEHAELRKSL  1045
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Qy  1046 LPPLIIHTAATPMSHPKSSSTGVGEA------------------------------  1071
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Qy  1072 -----LGSGSRRTSSSSGSSAEPGAA----------HH----EMKCP------  1097
Db   807 PDMKTHLDRPLVVELJRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRDKDKTPAAGDQ  866

Qy  1098 -----PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL  1142
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Qy  1143 LSGEQOESQDEE-----------ESSEEDRASPAGSDHRHRGSLE----REAKSSFDLPDTL  1189
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Qy  1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA------------RTLRTDDPQLDGDDDNDE  1238
Db   973 EEPARRHRARHKAQPAHEAVEKETTEKEAEIVEADKEKEKELRNHQPREPHCDLETS  1032

Qy  1239 GNLSKGERIQAWVRSRLPACCRER---------DSW------  1265
Db  1033 GTVTVGP--------MHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPDPNTIVHIPVMLTG  1086

Qy  1266 --------------------SAVIFPPQSRFRLLCHRI  1283
Db  1087 PLGEATVVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI  1146

Qy  1284 ITHKMFDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL  1343
Db  1147 VTMRYFEVVILVVILVVIALSSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDL  1205

Qy  1344 GWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMV-SDSGTKILGMLRVLRLIRTLRPLRV  1402
Db  1206 GLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRVLRPLKT  1261

Qy  1403 ISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILGVQLFKGKFFVCQGE------D  1456
Db  1262 IKLPKLAVPDCVVNSLKNVLNLLIVVMLFMFIFAVIAVQLFKGKFFYCTDESKELERD  1321


Qy  1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWDIMYDGLDAVGVD  1513
Db  1322 CRGQYLDYEKEPEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE  1381

Qy  1514 QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRR  1573
Db  1382 QGPSPGYRMELSIFYVVYFVVFPFFFVNIFVALIIITF---QEQGDKVMSE----CS  1431

Qy  1574 LEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAME  1631
Db  1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMTALNTVVLMKK  1491

Qy  1632 HYQQPQILDEALKICNYIFFVIFVIFVVESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGIT  1691
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Qy  1692 LEEIE---VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNL  1746
Db  1552 VTEIAETNNFINLS--------FLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYV  1602

Qy  1747 GLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNG  1806
Db  1603 CLLIAMLFFIYAIIGMQVFGNIALDDD----TSINRHNNPRTFLQALMLLFRSATGEAWHE  1659

Qy  1807 IMKD--PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM----------  1851
Db  1660 IMLSCLSNQACEDQANATBCGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS  1719

Qy  1852 ---KHLEE--------------------  1856
Db  1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMN  1779

Qy  1857 SNKEAKEEAELEAEL--------ELEMKTLS-  1879
Db  1780 MPISNEDMTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDL  1839

Qy  1880 -PQPHSP------LGSPF---LMPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVP  1930
Db  1840 LVPPHKPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLF--HPLKAT  1896

Qy  1931 HPEEVPVPL-GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI  1989
Db  1897 LEQTOPAVLRGARVFLRQKSST-----SLSNGGAIQNQESGIKESV---SWGTQRTQDA--  1947

Qy  1990 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD  2049
Db  1948 ----------------PHEA-------RPPLERGHSTEIPVCRSGALAVD  1974

Qy  2050 --------SLDVQGLGSREDLLSEVSGSCPLTRSSPFWGGGSIQVQQRSG  2092
Db  1975 VQMQSITRRGPDGEPQGLESQG--RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG  2031

Qy  2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS------SLELDTELSWIS  2135
Db  2032 ------THLCSTTP--------DRPPPSQASSHHHHHRCHRRRDRKQRSLEKGPSLS-AD  2076

Qy  2136 GDLLPSSQEEPLFP----------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDS  2186
Db  2077 MDGAPSSAVGPGLPPGEGPTCGRRERERRQPGRGSQERRQPSSSSSEKQRF--YSCDRF  2133

Qy  2187 GSQPRLCPSPS--------------SLGGQPL------GGPGSRPKK  2213
Db  2134 GGREPPKPXPSLSSHPTSPTAGQEPGHPQGSGSVNGSPLLSTSGASTPGRGRGRRQLPQT  2193

Qy  2214 KLSP-PSISIDPPES------------QGSRPPCSPG---------VCLRRRAPASD--  2248
Db  2194 PLTPRPSITYKTANSSPIHFAGAQTSLPAFSPGRLSRGLSEHNALLQRDPISQPLAPGSR  2253

Qy  2249 -SKDPSVSSPLDSTAASPSPKKDTLSL-------SGLSS  2279
Db  2254 IGSDPYLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS  2292
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us-09-611-257a-24.rai

Search completed: November 18, 2004, 13:35:56
Job time : 78.6868 secs

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    November 18, 2004, 13:32:41 ; Search time 180.328 Seconds
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                                   4491.206 Million cell updates/sec

Title:         US-09-611-257A-24
Perfect score: 12028
Sequence:      1 MLPHRVPRCVRTPLRGSAR.........KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters:     1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	11542.5	96.0	2425	10	US-09-383-894-4	Sequence 4, Appli
2	11532	95.9	2374	14	US-09-383-894-2	Sequence 2, Appli
3	10806.5	89.8	2243	16	US-10-408-765A-625	Sequence 625, App
4	10732.5	89.2	2377	17	US-10-757-262-16	Sequence 16, Appl
5	6222	51.7	2353	16	US-10-408-765A-1128	Sequence 1128, Ap
6	5409	45.0	2175	9	US-09-935-541-2	Sequence 2, Appli
7	5409	45.0	2175	14	US-10-425-800-2	Sequence 2, Appli
8	5405.5	44.9	2188	9	US-09-935-541-4	Sequence 4, Appli
9	5405.5	44.9	2188	14	US-10-425-800-4	Sequence 4, Appli
10	5345	44.4	1835	9	US-09-935-541-5	Sequence 5, Appli
11	5345	44.4	1835	14	US-10-425-800-5	Sequence 5, Appli
12	3950	32.8	1853	9	US-09-030-482B-19	Sequence 19, Appl
13	3553	29.5	1657	14	US-10-369-493-6836	Sequence 6836, Ap
14	1680.5	14.0	2264	15	US-10-627-370-2	Sequence 2, Appli
15	1678	14.0	2327	17	US-10-736-883-38	Sequence 38, Appl
16	1678	14.0	2343	13	US-10-033-026-4	Sequence 4, Appli
17	1676	13.9	2339	15	US-10-375-253-12	Sequence 12, Appl
18	1674	13.9	2339	15	US-10-033-026-6	Sequence 6, Appli
19	1674	13.9	2339	17	US-10-736-883-32	Sequence 32, Appl
20	1673	13.9	2331	17	US-10-736-883-44	Sequence 44, Appl
21	1662.5	13.8	2288	17	US-10-736-883-40	Sequence 40, Appl
22	1661	13.8	2333	17	US-10-736-883-28	Sequence 28, Appl
23	1647.5	13.7	2313	16	US-10-322-696-178	Sequence 178, App
24	1642.5	13.7	2237	15	US-10-375-253-14	Sequence 14, Appl
25	1642.5	13.7	2336	13	US-10-033-026-10	Sequence 10, Appl
26	1642.5	13.7	2336	13	US-10-736-883-30	Sequence 30, Appl
27	1640.5	13.6	2237	13	US-10-033-026-8	Sequence 8, Appli
28	1640.5	13.6	2237	17	US-10-736-883-34	Sequence 34, Appl
29	1638	13.6	2251	15	US-10-375-253-38	Sequence 38, Appl
30	1637.5	13.6	2270	16	US-10-322-696-84	Sequence 84, Appl
31	1636	13.6	2251	16	US-10-322-696-176	Sequence 176, App
32	1635.5	13.6	2270	16	US-09-457-571-10	Sequence 18, Appl
33	1634.5	13.6	1984	10	US-10-029-413A-18	Sequence 20, Appl
34	1631	13.6	2181	13	US-10-029-413A-20	Sequence 50, Appl
35	1631	13.6	2181	14	US-10-205-823-50	Sequence 29, Appl
36	1631	13.6	2181	14	US-10-411-010-29	Sequence 54, Appl
37	1631	13.6	2181	14	US-10-322-696-54	Sequence 42, Appli
38	1631	13.6	2181	17	US-10-736-883-42	Sequence 4, Appli
39	1631	13.6	2339	17	US-10-029-413A-4	Sequence 22, Appl
40	1630.5	13.6	2166	13	US-10-029-413A-22	Sequence 12, Appl
41	1628	13.5	1873	13	US-09-457-571-12	Sequence 16, Appli
42	1625.5	13.5	1989	10	US-09-457-571-16	Sequence 2, Appli
43	1617.5	13.4	1969	10	US-10-375-253-2	Sequence 367, App
44	1617	13.4	2161	15	US-10-375-253-2	
45	1614.5	13.4	1977	10	US-09-919-039-367	

ALIGNMENTS

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RESULT 1
US-09-383-894-4
; Sequence 4, Application US/0383894
; Publication No. US2003012S269A1
; GENERAL INFORMATION:
;   APPLICANT: Li, Ming
;   TITLE OF INVENTION: T-Type Calcium Channel
;   FILE REFERENCE: 004.00191
;   CURRENT APPLICATION NUMBER: US/09/383,894
;   CURRENT FILING DATE: 1999-08-26
;   EARLIER APPLICATION NUMBER: US 60/098,004
;   EARLIER FILING DATE: 1998-08-26
;   EARLIER APPLICATION NUMBER: US 60/117,399
;   EARLIER FILING DATE: 1999-01-27
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2425
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-383-894-4

Query Match             96.0%;  Score 11542.5;  DB 10;  Length 2425;
Best Local Similarity   95.4%;  Pred. No. 0;
Matches 2219;  Conservative  3;  Mismatches  54;  Indels  51;  Gaps   4;

Qy    3 PHRVPRCVRTPLRGSARPSSDPGPRLARGWTRRRMERAPRSRDSPVASRS----------  54
        ||||||||||||||||||||||||||   ||||||| :       ||||
Db   21 PTGVPRLREDTSSEGLRSPLFGPPGAPAG--------QRMDEEEDGAGAEESGQPRSFTQ  72

Qy   55 -STTCPGPGAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPPSWCLRTVCNP 113
         :||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   73 LNDLSGAGRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNP 132

Qy  114 WFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGI 173
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   133  WFERVSMIVILLNCVTIGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGI   192
Qy   174  FGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILV   233
Db   193  FGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILV   252
Qy   234  TLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQT   293
Db   253  TLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQT   312
Qy   294  ENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYT   353
Db   313  ENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYT   372
Qy   354  NCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIV   413
Db   373  NCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIV   432
Qy   414  GSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLV   473
Db   433  GSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLV   492
Qy   474  YILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHH   533
Db   493  YILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHH   552
Qy   534  HHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADC   593
Db   553  HHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADC   612
Qy   594  HLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTS    653
Db   613  HLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTS    672
Qy   654  FNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESA   713
Db   673  FNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESA   732
Qy   714  DHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDITFRKIV  773
Db   733  DHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDITFRKIV  792
Qy   774  DSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVYGPF  833
Db   793  DSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVYGPF  852
Qy   834  GYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMK   893
Db   853  GYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMK   912
Qy   894  TMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIL   953
Db   913  TMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIL   972
Qy   954  TQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIIVEGFQAE----------  1003
Db   973  TQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIIVEGFQAEEIGKREDASG  1032
Qy  1004  --------GDATKSESEPDFFSPSVDGDGDRKRLAIVALGEHAELRKSLLPPLI        1050
Db  1033  QLSCIQLPVNSQQGDATKSESEPDFFSPSVDGDGDRKRLAIVALGEHAELRKSLLPPLI    1092
Qy  1051  IHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSA  1110
Db  1093  IHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKSPPSARSSPHSPWSA  1152
Qy  1111  ASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEDRASPAGSDHR   1170
Db  1153  ASSWTSRRSSRNSIGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEDRASPAGSDHR   1212
Qy  1171  HRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQL  1230
Db  1213  HRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQL  1272


Qy  1231  DGDDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFD  1290
Db  1273  DGDDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFD  1332
Qy  1291  HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQ  1350
Db  1333  HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQ  1392
Qy  1351  AYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLK  1410
Db  1393  AYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLK  1452
Qy  1411  LVVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKFVCQGEDTRNTNKSDCAEAS    1470
Db  1453  LVVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKFVCQGEDTRNTNKSDCAEAS    1512
Qy  1471  YRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFIS  1530
Db  1513  YRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFIS  1572
Qy  1531  FLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKKR-----------  1579
Db  1573  FLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKKRRNLMLDDVIASG  1632
Qy  1580  SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIL  1639
Db  1633  SSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIL  1692
Qy  1640  DEALKICNYIFTVIFVFESVPKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNL  1699
Db  1693  DEALKICNYIFTVIFVFESVPKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNA  1752
Qy  1700  SLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAA  1759
Db  1753  SLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAA  1812
Qy  1760  LGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWNGIMKDSRDCDQES   1819
Db  1813  LGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQES  1872
Qy  1820  TCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAAELEAELLEMKTLS   1879
Db  1873  TCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAAELEAELLEMKTLS   1932
Qy  1880  PQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTAHIGAASGFSLEHPTMVPHPEEVPVPL   1939
Db  1933  PQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTAHIGAASGFSLEHPTMVPHPEEVPVPL   1992
Qy  1940  GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT  1999
Db  1993  GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT  2052
Qy  2000  SCIIQLPKDVHYLLQPHGAPTWGAIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSR   2059
Db  2053  SCIIQLPKDVHYLLQPHGAPTWGAIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSR   2112
Qy  2060  EDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP  2119
Db  2113  EDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP  2172
Qy  2120  ETRSSLELDTELSWISGDLLPSSQEEPLFPRDLLKKCYSVETQSCRRRPGWLDEQRRHSI  2179
Db  2173  ETRSSLELDTELSWISGDLLPSSQEEPLSPRDLLKKCYSVETQSCRRRPGWLDEQRRHSI  2232
Qy  2180  AVSCLDSGSQPRLCPSPSSLGGQPLGGPGGSRPKKKKLSPPSISIDPPESQGSRPPCSPGVC  2239
Db  2233  AVSCLDSGSQPRLCPSPSSLGGQPLGGPGGSRPKKKKLSPPSISIDPPESQGSRPPCSPGVC  2292
Qy  2240  LRRRAPASDSKDPSVSSSPLDSTAASSPKKDTLSLSGLSSDPTDMDP                2286
Db  2293  LRRRAPASDSKDPSVSSSPLDSTAASSPKKDTLSLSGLSSDPTDMDP                2339
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RESULT 2
US-09-383-894-2
; Sequence 2, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
;   APPLICANT: Li, Ming
;   TITLE OF INVENTION: T-Type Calcium Channel
;   FILE REFERENCE: 004.00191
;   CURRENT APPLICATION NUMBER: US/09/383,894
;   CURRENT FILING DATE: 1999-08-26
;   EARLIER APPLICATION NUMBER: US 60/098,004
;   EARLIER FILING DATE: 1998-08-26
;   EARLIER APPLICATION NUMBER: US 60/117,399
;   EARLIER FILING DATE: 1999-01-27
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2374
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-383-894-2

Query Match   95.9%; Score 11532; DB 10; Length 2374;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2206; Conservative 1; Mismatches 18; Indels 34; Gaps 2;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
                ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML   89

Qy   122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKVVALGIFGKKCYLG 181
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKVVALGIFGKKCYLG 149

Qy   182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLP 241
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLP 209

Qy   242 MLIGNVLLCFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   210 MLIGNVLLCFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy   302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy   362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy   422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy   482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 541
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 509

Qy   542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy   602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy   662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy   722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy   782 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   750 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy   842 IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLKIVRFLPALQRQLVVLMKTMDNVATF 901
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   810 IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLKIVRFLPALQRQLVVLMKTMDNVATF 869

Qy   902 CMLMLFIFFISILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870 CMLMLFIFFISILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy   962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVALLVEGFQAE------------------1003
                ||||||||||||||||||||||||||||||||||||||||||
Db   930 LYNGMASTSSWAALYFIALMTFGNVLFNLLVAILVEGFQAEEIGKREDASGQLSCIQLP 989

Qy   1004 ----GDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1058
                      || |||| |||||||||||||||||||||||||||||||||||||||||||||
Db   990 VNSQGGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1049

Qy   1059 SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRR 1118
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 SLPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKSPPSARSSPHSPWSAASSWTSRR 1109

Qy   1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLERE 1178
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLERE 1169

Qy   1179 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDE 1238
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDE 1229

Qy   1239 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1298
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1289

Qy   1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEGQAYLRSSWN 1358
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 LNCITIAMERPKIDPHSAERIFLTLSNVIFTAVFLAEMTVKVVALGWCFGEGQAYLRSSWN 1349

Qy   1359 VLDGLLVLISVIDILVSMVSDSGTKILGMRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1418
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 VLDGLLVLISVIDILVSMVSDSGTKILGMRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1409

Qy   1419 SLKPIGNIVICCAFFIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASYRWVRHKY 1478
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 SLKPIGNIVICCAFFIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASYRWVRHKY 1469

Qy   1479 NFDNLGQALMSLFVLASKDGWVDIMYDLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1538
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 NFDNLGQALMSLFVLASKDGWVDIMYDLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1529

Qy   1539 VLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKQR---------SKEKQMAE 1587
                ||||||||||||||||||||||||||||||||||||||||| :|
Db   1530 VLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRRNLMLDDVIASGSSASAASE 1589

Qy   1588 AQCKPYYSDYISRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN 1647
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 AQCKPYYSDYISRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN 1649

Qy   1648 YIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTI 1707
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 YIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTI 1709

Qy   1708 IRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD 1767
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 IRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD 1769

Qy   1768 LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDFDPSRDCDQESTCYNTVIS 1827
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVIS 1829

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Db   150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDTLP  209

Qy   242  MLGNVLLLCFFVFFlFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  301
          |||||||||||||||||||||||||||||||||||||||||||||| :||||||||||||
Db   210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF  269

Qy   302  ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYTNCSAGEHN  361
          ||||||||||||||||||||| ||||||| ||||:|||||||||||||||||||||||||
Db   270  ICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYEAYNSSSNTTCVNWNQYTNCSAGEHN  329

Qy   362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINL  421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINL  389

Qy   422  CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYELLKYIVIYILRKAAR  481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   390  CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYELLKYIVIYILRKAAR  449

Qy   482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN  541
          ||||||||:|||.||||||.|.||.| ||.||:|||||||||||||||||||||||||
Db   450  RLAQVSRAAGVRVGLLSSPAPLGGGETQPSSCSRHRRLSVHHLVHHHHHHYHLGN  509

Qy   542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ  601
          ||||.|||||||||||||||||||||||||||.|.|.||||||||||||||||||||||
Db   510  GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ  569

Qy   602  APPPRCPSEASGRTVSGGKVYPTVHTSPPPEILKDKALVEVAPSPGGPPTLTSFNIPPGPF  661
          |||||.||||||||.||||||||||||||||| | :||||||.|.|||||||| ||||||
Db   570  APPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY  629

Qy   662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721
          |||||||||||||||.|||||||||.|||||||||||||||||.||||||.||..:||||
Db   630  SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD  689

Qy   722  SEAVYFFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  781
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   690  SEAVYFFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  748

Qy   782  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPPGYIKNPYN  841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   749  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN  808

Qy   842  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  868

Qy   902  CMLMLFIFISILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVFQILTQEDWNKV  961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869  CMLMLFIFISILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVFQILTQEDWNKV  928

Qy   962  LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  1021
          |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||:|
Db   929  LYNGMASTSSWAALYFIALMTFGNYLVFNLLVAILVEGFQAEGDANKSESEPDFFSPSLD  988

Qy   1022  GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEBALGSGSRRTSS  1081
           ||||||| |||.|||| |||||||||||||:||||||:||:|:|||.||.|| |:||||||
Db   989  GDGDRKKCLALVSLGEHPELRKSLLPPLIIHTRATPMSLPKSTSTGLGEAlGPASRRTSS  1048

Qy   1082  SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS  1141
           |||||||| |||.||||||||||||||||||||||||||||||||||||||||||||||
Db   1049  SGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS  1107

Qy   1142  LLSGEGQESQDEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR  1201
           ||||||||||||||||||.||||||||||||||||||||||||||||||||||||||||
Db   1108  LLSGEGQESQDEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR  1167

Qy   1202  SSASEHQDCNGKSASGRLARTLRTDPDQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE  1261
           .|||.|||||||||||||||:||:|:|.||||||:|:|||||||:.||.|:||||||.|
Db   1168  GSASHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLE  1227

Qy   1262  RDSWSAYIFPPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228  RDSWSAYIFPPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1287
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Qy   1828  PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAELEAELELEMKTLSPQPHSPLG  1887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830  PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAELEAELELEMKTLSPQPHSPLG  1889

Qy   1888  SPPLWPGVEGVNSTDSPKPGAPHTTAHIGAAAGFSLEHPTMVPHPEEVPVPLGPDLLTVR  1947
           |||||||||||||.|||||||||||||||||.||||||||||||||||||||||||||||
Db   1890  SPPLWPGVEGVNSPDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVR  1949

Qy   1948  KSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSOPADTSCILQLPK  2007
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1950  KSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPK  2009

Qy   2008  DVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVS  2067
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010  DVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVS  2069

Qy   2068  GPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLEL  2127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070  GPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLEL  2129

Qy   2128  DTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSG  2187
           |||||||||||||||||||| |||||||.|||||||||||||.|||||||||||||||||
Db   2130  DTELSWISGDLLPSSQEEPLSPRDLKKCYYSVETQSCRRRPGSWLDEQRRHSIAVSCLDSG  2189

Qy   2188  SQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPPESQGSRRPPCSPGVCLRRRAPAS  2247
           ||||||||||||||||||||||||||||||||||||||||.||||| ||||||||||||||
Db   2190  SQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPPFSQGSRPPCSPGVCLRRRAPAS  2249

Qy   2248  DSKDPSVSSPLDSTAASPSPKKDTLSLSGLLSSDPTDMDP  2286
           ||||||||||||||||||||||||||||||||||||||||
Db   2250  DSKDPSVSSPLDSTAASPSPKKDTLSLSGLLSSDPTDMDP  2288
```

RESULT 3
US-10-408-765A-625

Query Match   89.8%; Score 10806.5; DB 16; Length 2243;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;

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Qy   62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRRTVCNPWFERVSML  121
         |.| | |:|||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   30  GRPGPGSAEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRRTVCNPWFERISML  89

Qy   122  VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90  VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  149

Qy   182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDTLP  241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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us-09-611-257a-24.rapb

US-10-757-262-16

Query Match   89.2%;   Score 10732.5;   DB 17;   Length 2377;
Best Local Similarity   88.3%;   Pred. No. 0;
Matches 2078;   Conservative   33;   Mismatches 109;   Indels 133;   Gaps   7;

Qy   62   GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
           |||||||||||||||||||||||||||||||||||||| |||:||||||||||||| :|||
Db   30   GRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy   122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90   VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy   182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLAINRVPSMRIIVTLLLDTLP 241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLAINRVPSMRIIVTLLLDTLP 209

Qy   242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269

Qy   302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
           ||||||||||||||||||| ||||||||||||:||||||||||||||||||||||||||||
Db   270 ICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy   362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

RESULT 4
US-10-757-262-16
; Sequence 16, Application US/10757262

Qy   1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1288 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1347

Qy   1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLG 1441
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1348 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLG 1407

Qy   1442 VQLFKGKPFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 VQLFKGKPFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1467

Qy   1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1527

Qy   1562 EARRREKRLRRLEKKRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1621
            |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1528 EARRREKRLRRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1580

Qy   1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVLFVFESVFKLVAFAFRRFFQDRWNQLDLA 1681
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 GLNVVTMAMEHYQQPQILDEALKICNYIFTVLFVFESVFKLVAFGFRRFFQDRWNQLDLA 1640

Qy   1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 IVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALP 1700

Qy   1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1760

Qy   1802 DNWNGIMKDPSRDCDQESTCVNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 DNWNGIMKDTLRDCDQESTCVNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1820

Qy   1862 KEEAEALEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAAASGF 1921
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 KEEAEALEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHF 1880

Qy   1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
            |||||||||||||||:|| |||||||||||||||||||||||::||||||||||||
Db   1881 SLEHPTMQPHPTELP--GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGL 1937

Qy   1982 PKAQSGSSLSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
            ||||:||||:|||||||||||||||||||||||||:||||||||||||||||||||||||
Db   1938 PKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLR 1997

Qy   2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQRSGIQSKVSKHI 2101
            |||||||||||||||||||||||||||||||||||||||||||: ||| |||| |||:||
Db   1998 RQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHM 2057

Qy   2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVET 2160
            | ||| || || : :|||||:||||| ||||||||||| ||:||||:|||||||||:||
Db   2058 TPPAPCPGPENWGKGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEA 2117

Qy   2161 QSCRRRPGFWLDEQRRHSIAVSCLDSGSQQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSI 2220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 QSCRRRPTSWLDEQRRHSIAVSCLDSGSQQPHLGGTDPSNLGGQPLGGPGSRPKKKLSPPSI 2177

Qy   2221 SIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSD 2280
            :|||||||:||| |:|||||||||| |:|||||| :|| |:::|||||||||:|||||||
Db   2178 TIDPPESQGPRTPPSGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSD 2237

Qy   2281 PTDMDP 2286
            | ||:|
Db   2238 PADLDP 2243

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Qy  1479 NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1538
Db  1468 NFDNLGQALMSLFVLA.SKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1527

Qy  1539 VLNMFVGVVVENFHKCRQHQEEEARRREKRLRLEKKKR------------SKEKQMAE    1587
Db  1528 VLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRNLMLDDVIASGSSASASE    1587

Qy  1588 AQCKPYYSDYSRFLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN 1647
Db  1588 AQCKPYYSDYSRFLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN 1647

Qy  1648 YIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDIAIVLLSIMGITLEEIEVNLSLPINPTI 1707
Db  1648 YIFTVIFVFLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTI 1707

Qy  1708 IRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD 1767
Db  1708 IRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD 1767

Qy  1768 LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVIS 1827
Db  1768 LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVIS 1827

Qy  1828 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAELEAELEAELEMKTILSPQPHSPLG 1887
Db  1828 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAEAELEAELEAELEMKTILSPQPHSPLG 1887

Qy  1888 SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPT----------           1927
Db  1888 SPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTDRQLFDTISLLIQGSLEWEL 1947

Qy  1928 --------------------------------------------------           1927
Db  1948 KLMDELAGPGGQPSAFPSAPSLGGSDPQIPLAEMEALSLTSEIVSEPSCSLALTDDSLPD 2007

Qy  1928 --------MVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL      1974
Db  2008 DMHTLLLSALESNMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPL 2064

Qy  1975 GHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSP 2034
Db  2065 GHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSP 2124

Qy  2035 LAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQ 2094
Db  2125 LAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHGRSH 2184

Qy  2095 SKVSKIHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLK 2153
Db  2185 SKISKHWTPPAPCPGPENWGKGPPETRSSLELDTELSWISGDLLPPGGGQEBPPSPRDLK  2244

Qy  2154 KCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSGQPRLCPSPSSLGGPLGPGSRPKK  2213
Db  2245 KCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSGQPHLGTDPSNLGGQPLGGPGSRPKK 2304

Qy  2214 KLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLS 2273
Db  2305 KLSPPSITIDPPESQGPRTPPSPGICLRRRAPASDSDSKDPLASGPPDSMAASPSPKKDVLS 2364

Qy  2274 LSGLSSDFTDMDP 2286
Db  2365 LSGLSSDPADLDP 2377
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Qy   422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEBLLKYLVVILRKAAR 481
Db   390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEBLLKYLVVILRKAAR 449

Qy   482 RLAQVSRAIGVRAGLLSSPVARSGQBPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN   541
Db   450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVHHLVHHHHHHHHYHLGN   509

Qy   542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPGAEBVHSFYHADCHLEPVRCQ  601
Db   510 GTLRAPRASPE-IQDRDANGSRRLMLPPPSTPALSGAPFGGAESVHSFYHADCHLEPVRCQ 569

Qy   602 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSENIPPGPF  661
Db   570 APPPRSPSEASGRTVGSGKVYPTVHTSPPPET.LKEKALVEVAASSGPPTLTSLNIPPGPY 629

Qy   662 SSMIKLLETQSTGACHSSCCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
Db   630 SSMIKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD  689

Qy   722 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  781
Db   690 SEAVYEFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  748

Qy   782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN  841
Db   749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN  808

Qy   842 IFDGVIVVLSVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
Db   809 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 868

Qy   902 CMLMLMFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
Db   869 CMLMLMFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 928

Qy   962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGPQAE---------          1003
Db   929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEEISKREDASGQLSCIQLP  988

Qy  1004 -----GDATKSESEDPFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1058
Db   989 VDSQGGDANKSESEDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPM  1048

Qy  1059 SHPKSSSTGVGEALGSGSRRTSSSGAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRR  1118
Db  1049 SLPKSTSTGLGEALGPASRRTSSSGAEPGAA-HEMKSPFSARSSPHSPWSAASSWTSRR  1107

Qy  1119 SSRNSLGRAPSLKRRSPSGERRSLLGEGQBSSQDEEESSEEDRASPAGSDHRHRGSLERE 1178
Db  1108 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEERASPAGSDHRHRGSLERE 1167

Qy  1179 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLGDDDNDE  1238
Db  1168 AKSSFDLPDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPPLGDGDPADDE 1227

Qy  1239 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1298
Db  1228 GNLSKGERVRAWIRARLLPACCLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1287

Qy  1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1358
Db  1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347

Qy  1359 VLDGLLVLISVIDILVSMWSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1418
Db  1348 VLDGLLVLISVIDILVSMWSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1407

Qy  1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKY 1478
Db  1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKY 1467
```

```
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1128

Query Match    51.7%;   Score 6222;   DB 16;   Length 2353;
Best Local Similarity 56.7%;   Pred. No. 0;
Matches 1370;  Conservative 208;  Mismatches 529;  Indels 310;  Gaps 62;
```

```
Qy    25 PPGPRLARGWTRRRMERAPRSRDSP--VASRSSTTCPGPGAAGAGSTEKDPGSADSEAEG     82
         ||||                          :  :    |   ::  :   | :
Db    19 PPGPAALVG------ASPESPGAPGRAEERGAELGVSPSESPAAERGAELGA--DEEQR     69

Qy    83 LPYPALAPVVFFYLSQDSRPRSWCLRITVCNPWFERVSMLVILLNCVTLGMFRPCEDIACD    142
         :|||||| ::||  |  ||||||||:  |||||| ||||||:::|||||||||||||:  |
Db    70 VPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVECG    129

Qy   143 SQCRRIIQAFDDFIFAFFAVEMVKKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLD    202
         | |   | ||:||||||||||||: |||||:||:|||||||||||||||||:|||:||||
Db   130 SERCNLEAFDAFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVAGMMEYSLD    189

Qy   203 LQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGV    262
          ::||:|| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 GHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGV    249

Qy   263 QLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENEDESPPICSQPRENGMRSCRSVPTLR    321
         ||||||||||||  ::    :    |:|||||  ||::|||| |  :||| :|  |
Db   250 QLWAGLLRNRCFLDSAFVRNNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHIP---    306

Qy   322 GEGGGGGPPCSLDYETYN------SSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGY    374
         |   : |   :  :||      :   ::| |:||||||||| ||:|||:::|||||||||||
Db   307 GRRELRMPCTLGWEAYTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGY    366

Qy   375 AWIAIFQVITLEGWDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETK    434
         ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db   367 AWIAIFQVITLEGWDIMYVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETK    426

Qy   435 QRESOLMREORVRFLSNASTLASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAIGVRA    494
         ||||||||| :| |||:|||||||||||||||||||| |  | ||  ||::|     |
Db   427 QRESOLMREQRARHLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLIYARWQSRW    486

Qy   495 GLLSSPVARSGQEPQPSGSCTRSHRR-------LSVHHLV-HHHHHHHHYHLGNGTLRV    546
          :   |  :| | | ::         |||||| |||||||:|||||||||||   || :
Db   487 RKKVDPSAVQGQGP-------GHRQRRAGRHTASVHHLVYHHHHHHHHYHFSHGSPRR    538

Qy   547 PRASPEIQDRDANGSRRLML--PPPSTPTPSGGPPRGAESVHSPYHADCHLE--PVRCQA    602
         |   |  :      || :|    ||| : | | ||||  |:| |||||||:|  | : |
Db   539 PGPEPGACD-----TRLVRAGAPPSPPSPGRGPP-DAEESVHSIYHADCHIEGPQERARV    591

Qy   603 PPPRCPSEASGR-TVGSGKV-YPTV-------HTSPPPEILKDKAIVEVAPSP---    646
          :      |:   | | | : ||::          | | | ::       |
Db   592 AHAAATAAASLRLATGLGTMNYPTLPLPSGVSGGKGSTSPGPK------GKWAGGPPGTG    644

Qy   647 --GPPTLTSFNIPPGPFSSMHKLLETQSTGAC--HSS----CKISSPCSKADSGACGPD    697
            | | |:      :|  :      |  |  |   | :     | | |  ||:| | |
Db   645 GHGPLSLNS----PDPYEKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP--PAGTLTCELK    698

Qy   698 SCPYCART-GAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDP-----------    740
         |||||:    | |||| |::: | |  :|||||||: : || |
Db   699 SCPYCTRALEDPEGELSGSESGDSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGS    758
```

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Qy   741 HSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ    800
           ||  |: || :|  |   |  | :| : | ||||||||:||||:|:||||||||:|||||
Db   759 PQRRAQQRAAP-GEPGWMGRLWVTFSGKLRRIVDSKYFSRGIMMALLVNTLSMGVEYHEQ    817

Qy   801 PEELTNALEISNIVFTSLFALEMLLKLLVLVGPFGYIKNPYNIFDGVIVISVWEIVGQQG    860
         |||||||||||||||||:|||||||||||  || |||:||||||||:|||||||||||| :
Db   818 PEELTNALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIIVISVWEIVGQAD    877

Qy   861 GGLSVLRTFRIMRVLKLVREFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLF    920
         |||||||||::||||||||| |||| ||::|: |||||||||| |||||||| |||||||||
Db   878 GGLSVLRTFRLLRVLKLVRFLPALRRRQLVLVKTMDNVATFCTLLMLFIF SILGMHLF    937

Qy   921 GCKFASERD-GDTLPDRKNFDSLLWAIVIVVFQILTQEDWNKVLYNGMASTSSWAALYFIA    979
         ||||:  :  |||:||||||||||||||||||||||||||||:||||||||||||||||:|
Db   938 GCKFSLKTDTGDTVPDRKNFDSLLWAIVIVVFQILTQEDWNVVLYNGMASTSSWAALYFVA    997

Qy   980 LMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALAVAL----   1035
         |||||||||||||||||||||||||||:||:: |      ::        |   : :
Db   998 LMTFGNYVLFNLLVAILVEGFQAEGDANRSDTDEDKTSVHFEEDFHKLRELQTTELKMCS   1057

Qy  1036 ------GEHAELRKSLLPLLIHTAATPMSHPKSSS-TGVGEALGSGSRRTSSSSGAEPGA   1089
                :  ||  : |||::| ||||||| ||||   |  | |  : ||| |||||: |
Db  1058 LAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGGSSSGDPPLG-   1116

Qy  1090 AHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE   1149
            :   |||   | |  |  :| || ||||||:|||||||||||   : || |||||||:
Db  1117 --DQKPASLRSSPCAPWGPSGAWSSRRSSWSSLGRAPSLKRRGQCCERESLLSGEGKG   1173

Qy  1150 SQDEEESSEEDRASPA--GSDHRHRGSLEREAKSSFDLPDTL--QVPGLH----R   1196
         |  ::     | : |    ||  :   :    | || :      ||  :
Db  1174 STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDGQVVALPSDFFLR   1231

Qy  1197 TASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLP   1256
          :|  ::  ||    :    ||| :      |    |                W
Db  1232 IDSHREDAAELDDDSEDSCCLRLHKVLEPYKPQ--------W--------   1265

Qy  1257 ACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSA   1316
            | | :::|||| | ||:|||  |::  ||||||||||: ||||:||| |||:|||| |
Db  1266 --CRSREAWALYLFSPQNRFRVSCQKVITHKMFDHVLVIFIFLNCVTIALERPDIDPGST   1323

Qy  1317 ERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVLDIVSM   1376
         ||:||::||||||| | |||:|||||||  | |:||| |||||:|||||||:|:|||| |
Db  1324 ERVFLSVSNYIFTAIFVAEMMVKVVALGLLSGEHAYLQSSWNLLDGLLVLVSLVDIVVAM   1383

Qy  1377 VSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVETLMSSLKPIGNIVLICCAFFII   1436
           : | ||||:|||||||||||||||||||| ||||||||:|||:|||||||||||||||
Db  1384 ASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVETLISSLRPIGNIVLICCAFFII   1443

Qy  1437 FGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASK   1496
         ||||||||||||| ||:| |||||: |: | ||:| ||: |:|||||||||||||||:||
Db  1444 FGILGVQLFKGKFYYCEGPDTRNISTKAQCRAAHYRWRVRRKYNFDNLGQALMSLFVLSSK   1503

Qy  1497 DGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQ   1556
         |||:||||||||||||||||: ||||||||||||||||||:||||||||||||||||||||
Db  1504 DGWVNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQ   1563

Qy  1557 HQEEEEARRREKRLREKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLF   1616
         |||  |||||||||||||||   ::  :   ||| :  | |  |    :::|||||||||
Db  1564 HQEAEEARRREKRLREKKRRLRLRERRRSTFPS-PEAQRRPYYADYSPTRRSIHSLCTSHYLDLF   1622

Qy  1617 ITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWN   1676
         || :| ||||||:|||| || :|||||| |||:||:||||| : ||||| ||||||:|||
Db  1623 ITFIICVNVVTMSMEHYNQPKSLDEALKYCNYVFTIVFVFEAALKLVAFGFRRFFKDRWN   1682

Qy  1677 QLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTV   1736
         |||||||||:||  ||||||: : :||||||||||||||||||||||||||| |||| ||
Db  1683 QLDLAIVLLSLMGTILEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTV   1742

Qy  1737 MQALPVQGNIGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLF   1796
          |||||||| |||||||||:|||||||||| |||:: |||||| ||||||:|||||||||
Db  1743 VQALPVQGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLTLF   1802

Qy  1797 RVSTGDNWNGIMKDPSRDC---DQESTCYNTVISPIYFVSFVLTAQFVLVNVIAVLMKH   1853
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Db  1803  RVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPVFVTFVLVNVVVAVLMKH   1862

Qy  1854  LEESNKEPAKEAEIEAELEELEMKTLSPQHSPLGSPFIMPGVEGVNSTDSPKPGAPHTTA  1913
Db  1863  LEESNKEAREDAEELDAEIELEMA---------QGPGSARRVDADRP---------     1899

Qy  1914  HIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--   1970
Db  1900  --------PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP         1943

Qy  1971  ------ERRSLGHRGWGLPKAQGSILSVHSQPADTSCIIQLPKDVH---------YLLQP  2015
Db  1944  HPRPLQEVEMETYGAGTP--LGSVASVHSPPABSCASLQIPLAVSSPARSGEPLHALSP   2000

Qy  2016  HGAPTWGAIPKLPPPGRSPLAQPRLRRQAAIRTDSLDVQGLGSREDLLSEV----SGPSC  2071
Db  2001  RGT----------ARPSLSRLLCRQEAVHIDSLEGK--IDSPRDTLDPABPGEKTPVR   2047

Qy  2072  PLTRSSSFWGGSSIQVQQRSGIQSKV--SKH------IRLPAPCPGLEPSWAKDPPEITRS 2123
Db  2048  PVTQ------GGSLQSPPRSPRPASVRTKHTFGQHCVSSRPAAPGGEEABASDP------  2096

Qy  2124  SLELDTELSWISGDLLP-SSQEEPLFP----------RDLKKCYSVETQSCRRRPGFWLDE 2173
Db  2097  --ADEEVSHITTSSACPWQPTABPHGPEASPVAGGERDLRRLYSVDAQGFLDKPG-RADE  2152

Qy  2174  QRRHSIAVSCLDSGSGQPRLCPSPSSLGGQPLGGP--GSRPKKKLSPPSISIDPP-ESQGS 2230
Db  2153  ----LGSGE------PGEAKAWG--PEAEPALGARRKKKKMSPPCISVEPPAEDEGS     2203

Qy  2231  -RPPCSPG--VCLRRRAPA------SDSKDPSVSSPLDSTAAS--------PSPKKDTLSL  2274
Db  2204  ARPSAAEGGSTTLRRRTPSCEATPHRDSLEPTEGSGAGDPAAKGERWGQASCRAEHLTV   2263

Qy  2275  SGLSSDPTDM-----DP  2286
Db  2264  PSFAFPFLDLGVPSGDP  2280
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Qy  158  AFPAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDDLQNVSFSAVRTVRVL  217
Db  124  IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDDLQNINLSAIRTVRVL   183

Qy  218  RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFPGIVGVQLWAGLLRNRCFLPE  277
Db  184  RPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFPGIIGVQLWAGLLRNRCFLEE   243

Qy  278  NFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL------  332
Db  244  NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDV    300

Qy  333  -DYETYNSSSNTT--CVNMNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV   389
Db  301  YDFGAGRQDLNASGLCVNMNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV   360

Qy  390  DIMYFVMDAHSFYNFIYFIILIIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVRFL   449
Db  361  EIMYVVMDAHSFYNFIYFIILIIVGSFFMNLCLVVIATQFSETKQREHRLMLEQRQRYL   420

Qy  450  SNASTLIASFSEPGSCYEELLKYLVVTLLRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ 509
Db  421  S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR-------RAIGLYQALQS-----------  462

Qy  510  PSGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP   569
Db  463  ------RRQAL----------------------------------------GPE------  474

Qy  570  STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSP   629
Db  475  AKPGP-----------------------HAK---EPRHYQLCPQHSPLDA--------    502

Qy  630  PPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMKKLLETQSTGAC-HSSCKISSPCSK  688
Db  503  --------------LVQ---PIPATLAS------------------DPASCPCCHEDGRRPSGLGS 534

Qy  689  ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYFTQDAQHSDLRDPHSRRRQRS   748
Db  535  TDSGQEGSGS-------GSSAGGEDEA--------DGDGA-RSSEDGASSELGKEEEEEQ-  579

Qy  749  LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTN  806
Db  580  ---ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN   635

Qy  807  ALEISNIVFTSLFALEMLLKLLVYGPGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVL   866
Db  636  ILEICNVVFTSMFALEMLLKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGLSVL   695

Qy  867  RTFRLMRVLKLVRPLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS  926
Db  696  RTFRLLRVLKLVRFMPALRRQLVVLMKIMDNVATFCMLLMLFIFSILGMHIFGCKFSL   755

Qy  927  ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
Db  756  RTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGN  815

Qy  986  YVLFNLLVAILVEGFQAEGDATKSESEPDPFFSPSV----------DGDGDRKKRLALAVAL 1035
Db  816  YVLFNLLVAILVEGFQAEGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPM  873

Qy  1036 GEHAELRKSLLPLLIHT-----AATPMSHPKSSSTGVEALGSGSRRTSSSGSAEPGAAH  1091
Db  874  TPNGHLDFSL--PLGGHLGPAGAGPA--PRLSLQPDPMLVALGSRKSSVMSL--GRMS   926

Qy  1092 HEMKCPPSARSSPHSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES  1150
Db  927  YDQRSLSSSRSSYYCPWGRSAAWASRRSSWN-----SLKHKPSAEHESLLSARGGGA    980

Qy  1151 QDEEESSEE--DRASPAGSDH-----------------RHRGSLEREAKSSPDLPDTIQVPG 1193
Db  981  RVCEVAADEGPPRRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVG 1040
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Query Match         45.0%;  Score 5409;  DB 9;  Length 2175;
Best Local Similarity  50.5%;  Pred. No. 0;
Matches 1225;  Conservative 236;  Mismatches 513;  Indels 450;  Gaps 64;

Qy  51  ASRSSTTCPGPGAAGAGSTEKDPG--SADSEAEGL----------PYPALAPVFFVLS  97
Db   5  ASPPSSSAAAP-AAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHDLAPIAFFCLR  63

Qy  98  QDSRPRSWCLRTYCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF  157
Db  64  QTTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIF  123
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Qy 1194 LHRTASGRSS--ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDNDEGNLSKGERIQAW 1250
        ||  ::   :  :|| ||| ||: |  | : || |  | : ::||: :||| |  : ::|
Db 1041 AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVF'TKMGDRGDRGEDEEEIDYTLCFRVRKM 1098

Qy 1251 VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPK 1310
        :||  ||  |||  |||  |:| :|||:| |  ::|| ||| :: ||||| :|||||||
Db 1099 IDVYKPDWCEVREDWSVVLFSPENRFRVLCQTTIAHKLFDYVVLAFIFLNCITTIALERPQ 1158

Qy 1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVI 1370
        |    :||||||:|||||||:|:|||||:||:||  |||||||||||||||||| :|: :||
Db 1159 IEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFIVFFVSII 1218

Qy 1371 DLLVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC 1430
        |::||: |:.|.|||| |||||||||||||||||||:.||||||||:||||||||||:||
Db 1219 DIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278

Qy 1431 CAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSL 1490
        |||||||||||||||||||:.|.|.|||||||:|||.|| ||||:|||||||||||||||
Db 1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL 1338

Qy 1491 FVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAPFVLNMFVGVVEN 1550
        |||||||||::|||:||||| |||||: |||||||||||||||||:|||||||||||||
Db 1339 FVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVEN 1398

Qy 1551 FHKCRQHQEEEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
        |||||||||:||||:||||||||||||||      |||:|||| :|  ||:|:|:.|||
Db 1399 FHKCRQHQEAEARRRREEKRLRRLEKKRR------KAQRLPYYATYCHTRLLIHSMCTS 1451

Qy 1611 HYIDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRF 1670
        ||:|:|||.:|.||||||::|||:||: | |:|||||:||||||||:::|||||||:|||
Db 1452 HYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKIVAFGLRRF 1511

Qy 1671 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
        |:|||||||||||||:||||||||||:|:|.|||||||||||||||||||||||||||||
Db 1512 FKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMR 1571

Qy 1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGGLECDETHPCEGLGRHATFRNFGM 1790
        ||| ||:|||||||||||||||||||:|||||||||.| |:::||||||||||||||||||
Db 1572 ALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEGMSRHATFENFGM 1631

Qy 1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1847
        ||||||:||||||||||||| |:|| |::|:|   ||  |||:|||||||||||||:|||
Db 1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVV 1691

Qy 1848 AVLMKHLEESNKEAKEAEELEAELELEM-KTLSPQPHSPLGSPFLWPG--------- 1894
        |||||||:.|||||:|||::|| ||||| ||:..|.||| | ||:| |
Db 1692 AVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGRPLPTGSPGA-PGRGPGGAGGGGDT 1750

Qy 1895 --------VEG-VNSTDSPKPGAPHTTAHIGAASG----------- 1920
                 | | ::|.|||||||.|| : :.:
Db 1751 EGGLCRRCYSPAQDSLEGELTIIDNLSGSIFH--HYSSPAGCKKCHHDKQEVQLAETEA 1807

Qy 1921 ------------FSLEHPTMVP------------HPEEVPV-PLGPDLLTVRKSGVS 1952
                     ||:.     |             ||::|||.||| ||| |:||.||
Db 1808 FSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPEPMRVGDLGECFFPLSSTAVS 1867

Qy 1953 RTHSLPN-DSYMCRNGSTABRSLGHRGWGLPKAQGSSILSVHSQPADTSCILQLPKDVHY 2011
          . || |    :|   | . :     :|| | | ::  :|||  | |  | | |  :|
Db 1868 ----PDPENFLCEMEEIPPNPV--RSW--LKHDSSQAPPSPFSPDASSPLLPMPAEFFH 1918

Qy 2012 -----LLQPHGAPTWGAIPKLPPG-----RSPLAQRPLRRQAAIRTDSLDVQGLGSRE 2060
             ::|  | . ||| | ||||||     |||.|:|  |:||||||| |||
Db 1919 PAVSASQKGPKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS------ 1972

Qy 2061 DLLSEVSGFSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCGLBPSWAKDPPE 2120
                    . :|| |                 :| ||  |:| ||
Db 1973 ------PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAG--------- 2006

Qy 2121 TRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIA 2180
           .:  | ::      ||| :  |  | |:|
Db 2007 --------PRAGLSPAARRL-----SLRGRGLFSLRGLRAHQRS 2038

Qy 2181 VSCLDSGSQPRLCPSPSSL--------GGQPLGGPGSRPKKKLSPPSIS--IDPPESQG 2229
         ||  ||||| |||||| |         ||||.|||||||||| |||||
Db 2181 VSCLDSGSQPRLCPSPSSL--------GGQPLGGPGSRPKKKLSPPSIS--IDPPESQG 2229
```

```
Db 2039 HS--SGGSTSPGCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSLSLTSLFCPPP--- 2092
        :|   | :|| |        :                           ||| |||||
Qy 2230 SRPPCSPGVCLRR--                RAP---ASDSKDPSVSSPLDSTA 2262

Db 2093 --PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKDPPGRAPLPMGL 2150
          ||| ||||| | |:::|||||  ||        : | ||||||:|||| |||| | |
Qy 2263 ASPSPKKDTLSLSGLSSDPTDMDP 2286

Db 2151 GPLAPPPQPL--------PGELEP 2166
        ||| |||:|         ||:|
Qy 2151 GPLAPPPQPL--------PGELEP 2166
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RESULT 7
US-10-425-800-2
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; Sequence 2, Application US/10425800
; Publication No. US2003018086A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-800-2

Query Match          45.0%;  Score 5409;  DB 14;  Length 2175;
Best Local Similarity  50.5%;  Pred. No. 0;
Matches 1225;  Conservative 236;  Mismatches 513;  Indels 450;  Gaps 64;

Qy 51 ASRSSTCTCPGPGAAGAGSTEKDPG--SADSEAEGL-----------PYPALAPVVFFYLS 97
       || |: :  |   ||:|.||::|||  || | | ||            |||||| : ||.|
Db 5  ASPPSSSAAAP-AAEPGVTTEQPGPRSPPSSSPPGLEEPLDGADPHVPHPDLAPIAFFCLR 63

Qy 98 QDSRPRSWCLRRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAPFDFIF 157
       : : | ||| : ||||||| .|||||||||||||||: || |: | |:.|| || || ||
Db 64 QTTSPRNWCIKMVCNPWFBCVSMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIF 123

Qy 158 AFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL 217
        .||| ||| :|||||||||||||||||||||||||::|||:||||||:::  ||||||||
Db 124 IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVL 183

Qy 218 RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE 277
        ||| ||||||||||||.|||||||||||||||||||||||||||||||||||||||||:
Db 184 RPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLEE 243

Qy 278 NFSLPLSVDLEPYYQTENEDESPPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL----- 332
        || .  .| ||||| ::||: ||||||| .|:||: || .  | :|  |
Db 244 NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300

Qy 333 -DYETYNSSSNTT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV 389
         | :   .::    ||||| |||.||: |:||||||||||||||||| ||||||||||||
Db 301 YDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV 360

Qy 390 DIMYFVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVRFL 449
        :||| |||||||||||||||||||||||||||||||||||.||||||. ||:|||  |
Db 361 EIMYYVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQPSETKQREHRLMLEQQRYL 420

Qy 450 SNASTLASFSEPGSCYEEBLLKYLVVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ 509
        |  :  ||: |||.||||   :|:|| ||||   ||  : | ||||  |
Db 421 S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR---RALGLIYQALQS-------------- 462

Qy 510 PSGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP 569
                  :                |
Db 463 ------------------GPE----------------------------------APAP 474
```

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Qy   570 STPTPSGGPPRGAESVRSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSP 629
                                     : :      |||||
Db   475 AKPGP------------------HAK---EPRHYQLCPQHSPLDA-------------TPHT-- 502

Qy   630 PPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK 688
         ||||                  :||
Db   503 -------LVQ----PIPATLAS-------------------DPASCPCCQHEDGRRPSGLGS 534

Qy   689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSSEAVVEFTQDAQHSDLRDPHSRRRQRS 748
         ||||                         :: :   |:
Db   535 TDSGQEGSGS-----GSSAGGEDRA------DGDGA---RSSEDGASSELGKEEEEEEQ-- 579

Qy   749 LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHRQPEELTN 806
            ||            ||  |||||||||  ||||||||||  ||||||| ||||||:|
Db   580 ---ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELIN 635

Qy   807 ALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVL 866
          || ||||| |||||| ||| |  |||||||||||||| ||| | |||||||   ||||||
Db   636 ILEICNVVFTSMFALEMILKLAAFGLFDYIRNPYNIFDSIIVIISIWEIVGQADGGLSVL 695

Qy   867 RTFRLMRVLKLVRFLPALORQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS 926
         ||| | ||||||||  ||| ||||||||||||||||||||||||||||||||| |||| :
Db   696 RTFLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSL 755

Qy   927 ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN 985
             ||| ||||||||||||||||||||||||| ||||||||||  ||:||||:|||||||
Db   756 RTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGN 815

Qy   986 YVLFNLLVAIIVEGFQAEGDATKSESEPDFFSPSV-----DGDGDRKKRLALAVAL 1035
         ||||||||||||||||||||| |:| :      ::       ||:
Db   816 YVLFNLLVAIIVEGFQAEGDANRSYSDEDQSSNIEEFDKLQEGLDSSGDPK--LCPIPM 873

Qy  1036 GEHAELRKSLLPPLLIHT----AATPMSHPKSSSTGVGEALGSGRRTSSSGSAAEPGAAH 1091
              :| :                 |           |  ||: |:
Db   874 TPNGHLDPSL--PLGGHLGPAGAAGPA--PRLSLQPDMLVALGSRKSSYVMSL---GRMS 926

Qy  1092 HEMKCPPSARSSPHSPWSAAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES 1150
             : ||: |||   ||||| | :: ||||||::|   | ||:        ||||  | ||
Db   927 YDQRSLSSSRSSYYGPWGRSAAWASRRSSWN-------SLKHKPSAEHESLLSAERGGGA 980

Qy  1151 QDEEBSSEE--DRASPAGSDH---------RHRGSLEREAKSSFDLPDTLQVPG 1193
                : :                       ||  ::
Db   981 RVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHHRRTLSLDNRDSVDLAELVPAVG 1040

Qy  1194 LHRTASGRSS--ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDNDEGNLSKGERIQAW 1250
                |   |   | ||| | ||:|   |   ::  |   :   |::
Db  1041 AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEEIDYTLCFRVRKM 1098

Qy  1251 VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPK 1310
            ::  || |  | |:|:||| :|||:|||| : |:||:||:||| |:|||||||||||||
Db  1099 IDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIIAHKLFDYVVLAFFLNCITIALERPQ 1158

Qy  1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKKVVALGWCFGEQAYLRSSWNVLDGLLVLISVI 1370
          |   |:|||||| |||||||:|:|||| |||| ||   ||||||||||||||||||:| |:
Db  1159 IEAGSTERIFLTVSNYIFTAIFVGEMTLKKVVSLGLIYFGEQAYLRSSWNVLDGFLVFSII 1218

Qy  1371 DILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIC 1430
          || ||:||| | |||| ||||||||||||||||||| |||||||||: ||||||||||||
Db  1219 DIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLLISSLKPIGNIVLIC 1278

Qy  1431 CAFFIIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSL 1490
          |||||||||||||||||||  | |||||||| ||| | :||||||:||||||||||||||
Db  1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRRVRHHKYNFDNLGQALMSL 1338

Qy  1491 FVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVEN 1550
          |||||||||| |||:|||||  |||| :||||||||||||||||| |||||||||||||||
Db  1339 FVLASKDGWVNIMYNGLDAVADVDQQPVTNHNPWMLLYPISFLLIVSFFVLNMFVGVVVEN 1398

Qy  1551 FHKCRQHQEEEEARREEKRLRRLEKKRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
          |||||||||  ||||||||||||||||       ||   | ||:|  ||| :|:| ||
Db  1399 FHKCRQHQEAEEAARREEKRLRRLEKKRR------KAQRLPYYATYCHTRLLIHSMCTS 1451

Qy  1611 HYLDLFITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLIVAFAFRRF 1670
          |||| ||| : |||||||: |||:||  :  ||| ||| || :||:|| || ||||  ::
Db  1452 HYLDIFITIFICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLKMAVGMR 1511

Qy  1671 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
          |:|||||||||||||| ||||||||:|  :||||||||||||||||||||||||||| ||
Db  1512 FKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMR 1571

Qy  1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1790
          ||| || ||||||||||||||||||| ||||||||| | :|  ||||  ||||:|.|||
Db  1572 ALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEGMSRHATFENFGM 1631

Qy  1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVI 1847
          |||||| |||||||||||||  |||  ::|:| :     ||:||||||||||||| |||
Db  1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLLNVVV 1691

Qy  1848 AVLMKHLEESNKEAKEEAEAELEAELELEM-KTLSPQHSPLGSPFLWPG--------- 1894
          ||||  |::||||| ::||  | | |||||    | ||||||||  |
Db  1692 AVLMKGHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTGSPGA-PGRGPGAGGGGDT 1750

Qy  1895 -----------------------------VEG-VNSTDSKPGAPHTTAHIGAASG----- 1920
                                       :|  :: :| |||    || :|
Db  1751 EGGLCRRCYSPAQDSLEGELTIIDNLSGSIFH--HYSSPAGCKKCHHDKQEVQLAETEA 1807

Qy  1921 ------FSLEHPTMVP------------------HPEEVPV-PLGPDLLTVRKSGVS 1952
                |||: |                      || | |  ||| ||||| |:| |
Db  1808 FSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGECFPPLSSTAVS 1867

Qy  1953 RTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHY 2011
                  |  |                     ||
Db  1868 ------PDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSDASSPLLMPAEFFH 1918

Qy  2012 ------LLQPHGAPTWGAIPKLPPPG---RSPLAQRPLRRRQAAIRTDSLDVQGLGSRE 2060
              : | :|  :  ||    ||    |||  |  :  ::  :   :: ||:| |
Db  1919 PAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS------- 1972

Qy  2061 DLLSEVSGPSCPLTRSSFWGGSIQSKVSKHIRLPAPCPGLEPSWAKDPPE 2120
            |  | :|                    : | |::    | |
Db  1973 ------PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAPG--------- 2006

Qy  2121 TRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIA 2180
            ||:  |   |                          |:| ||||
Db  2007 --------------------------------SLRGRGLFSLRGLRAHQRS 2038

Qy  2181 VSCLDSGSQPRLCPSPSSL----------GGQPLGGPGSRPKKKLSPPSIS---IDPPESQG 2229
                |||             |  |        :|  | |: |
Db  2039 HS--SGGSTSPGCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSLSLTSLFCPPP---- 2092

Qy  2230 SRPPCSPGVCLRR----------------------RAP--ASDSKDPSVSSPLDSTA 2262
            ||    | ||:                      |    ||:|||| |::   |
Db  2093 --PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKDPPGRAPLPMGL 2150

Qy  2263 ASPSPKKDTLSLSGLSSDPTDMDP 2286
             ||    |  ||| ::||
Db  2151 GPLAPPQPL---------PGELEP 2166
```

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; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4

Query Match      44.9%;    Score 5405.5;    DB 9;    Length 2188;
Best Local Similarity 50.3%;    Pred. No. 0;
Matches 1225;    Conservative 236;    Mismatches 514;    Indels 461;    Gaps 64;

Qy    51 ASRSSTTCPGPGAAGAGSTEKDPG--SADSEAEGL---------PYPALAPVVFFYLS  97
Db     5 ASPPSSAAAP-AAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLR  63

Qy    98 QDSRPRSWCLRTVCNPWFERVSMIVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF 157
Db    64 QTTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIF 123

Qy   158 AFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL  217
Db   124 IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFVMAGMVEYSLDLQNINLSAIRTVRVL  183

Qy   218 RPLRAINRVPSMRILVTLLLDDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE 277
Db   184 RPLKAINRVPSMRILVNLLLDDTLPMLGNVLLLCFFVFFIFGIIGYAWIVIFQVITLEGWV 243

Qy   278 NFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL----- 332
Db   244 NFTIQGDVALPYYQPEDDEMPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDV     300

Qy   333 -DYETYNSSSNTT--CVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV  389
Db   301 YDFGAGRQDLNASGLCVNWNRYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV  360

Qy   390 DIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFL 449
Db   361 EIMYYVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYL 420

Qy   450 SNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ 509
Db   421 S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR-----RAIGLYQALQS------        462

Qy   510 PSGSCTRSRHRLSVHHLVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP 569
Db   463 ------RRQAL--------------------------------GPE-----------APAP 474

Qy   570 STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCFSEASGRTVGSGKVYPTVHTSP 629
Db   475 AKPGP-----------HAK---EPRHYQLCPQHSPLDA-------------TPHT-     502

Qy   630 PPEILIKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK 688
Db   503 -----LVQ----PIPATLAS-----------------DPASCPCCQHEDGRRPSGLGS    534

Qy   689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS 748
Db   535 TDSGQEGSGS-----GSSAGGEDEA------DGDGA---RSSEDGASSELGKEEEEEQ-- 579

Qy   749 LGPDAEPSSVLA--FWRLICDTFPRKIVDSKYFGRGIMAILVNTLSMGIEYHQQPEELTN 806
Db   580 ---ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHQQPEELTN  635

Qy   807 ALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVLSIWEIVGQQGGGLSVL 866
Db   636 ILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVL 695

Qy   867 RTFRLMRVLKLVRFLPALQORLVVLMKIMDNVATFCMLLMLFIFIFSIIGMHLFGCKFAS 926
Db   696 RTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFSL 755

Qy   927 ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKLVLYNGMASTSSWAALYFIALMTFGN 985
Db   756 RTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVLVLYNGMASTSPWASLYFVALMTFGN 815

Qy   986 YVLFNLLVAILLVEGFQAEGDATKSESSEPDFFSPSV---------DGDGDRKKRLAIVAL 1035
Db   816 YVLFNLLVAILVEGFQAEGDANRSYSDEDQSSNIEFDKLQEGLDSSGDPK--LCPIPM    873

Qy  1036 GEHAELRKSLLPLLIIHT---AATPMSHPKSSSTGVGEALGSGRRTSSSGSAFPGAAH   1091
Db   874 TPNGHLDPSL--PLGGHLGPAGAAGPA--PRLSLQPDPMLVALGSRKSSVMSL--GRMS   926

Qy  1092 HEMKCCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES 1150
Db   927 YDQRSLSSSRSSYYGPWGRSAAWASRRSSWN-------SLKHKPPSAEHESLLSAERGGGA 980

Qy  1151 QDEEESEE--DRASPAGSDH---------------------RHRGSLEREAKSSFDLPDTLQVPG 1193
Db   981 RVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVG  1040

Qy  1194 LHRTASGRSS--ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDNDEGNLSKGERIQAW  1250
Db  1041 AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGEDEEEIDYTLCFRVRKM    1098

Qy  1251 VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMPDHVLVIIFLNCITIAMERPK  1310
Db  1099 IDVVKPDWCEVREDMSVYLFSPENRFRVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQ 1158

Qy  1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVI 1370
Db  1159 IEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFIVFVSII 1218

Qy  1371 DIIVSMVDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC  1430
Db  1219 DIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278

Qy  1431 CAFFIIFGILGVQLFKGKFVVCCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSL 1490
Db  1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL 1338

Qy  1491 FVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVEN 1550
Db  1339 FVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVEN 1398

Qy  1551 FHKCRQHQEEEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFLLVHHLCTS   1610
Db  1399 FHKCRQHQEAEARRREKRLRRLEKKRR------KAQRLPYYATYCHTRLLIHSMCTS    1451

Qy  1611 HYLDLFITGVIGLNVTMAMEHYQQPOILDEALKICNYIFTVIFVFBSVFKLVAFAPRRF  1670
Db  1452 HYLDIFITFICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLVAFGLRRF  1511

Qy  1671 FQDRWNQLDLAIVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR  1730
Db  1512 FKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKLKNATGMR 1571

Qy  1731 ALLHTVMQALPQVGNIGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1790
Db  1572 ALLDTVVQALPQVGNIGLLFMLLFFLYAALGVELFGKLVCNDENPCEGMSRHATFENFGM 1631

Qy  1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLIAQFVLVNVVI 1847
Db  1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVV 1691

Qy  1848 AVLMKHLEESNKEAKEEAELEAELELEM-KTLSPQHSPLGSP---------------   1889
Db  1692 AVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTGSPGAPGRGPGGAGGGDTE 1751

Qy  1890 ------------------FLW---------PGVEG-VNSTDSPKPGAPHTAHIGAASG------- 1920
Db  1752 GGLCRRCYSPAQENLWLDSVSLIIKDSLEGELTIIDNLSGSIFH--HYSSPAGCKKCHH 1808

Qy  1921 ----------------------------FSLEHPTMVP---------------------- 1921
Db  1809 DKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLG 1868
```

```
Db   244  NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV  300
          : :             ||||||||| ||||||||||| :::       ::|||||||
Qy   333  -DYETYNSSSNTT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV   389
           :              ||||| :| :  ||:|:|||||||||||||||| |||||||||||
Db   301  YDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV   360

Qy   390  DIMYFVMDAHSFYNFIYFILLIIVGSFEMINLCLVVIATQFSETKQRESQLMREQRVRFL   449
          :||:||||||||||||||||||||||||:|:||||||||||||||||||::::|||:||:
Db   361  EIMYYVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQREHRIMLEQRQRYL    420

Qy   450  SNASTLASFSEPGSCYEELLKYLVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQ   509
           :|:| ||:|||| ||||: ||:|::||| :|                 :|| :|||::
Db   421  S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR------RALGLYQALQS            462

Qy   510  PSGSCTRSHRRLSVIHHLVHHHHHHHHYHIGNGTLRVPRASPEIQDRDANGSRRLMLPPP  569
                                    ::               ::              :::
Db   463  ------RRQAL-----------------------------------------GPE----  474

Qy   570  STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSP  629
                                       || |                        ||||
Db   475  AKPGP--------------HAK--EPRHYQLCPQHSPLDA-----------TPHT----  502

Qy   630  PPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK  688
                                     :                    : ||:||:    :||
Db   503  -----------LVQ--PIPATLAS-------DPASCPCCQHEDGRRPSGLGS         534

Qy   689  ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS  748
           ||| |  : :              ::            :  :|    :::
Db   535  TDSGQEGSGS----GSSAGGEDEA----------DGDGA----RSSEDGASSELGKEEEEEQ--  579

Qy   749  LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFPGRGIMIAILVNTLSMGIEYHEQPEELTN  806
          :|  |        |  |:|  ||||||||||: |||||:|||||||:||||:||||||||||
Db   580  ----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN   635

Qy   807  ALEISNIVFTSLFALEMLKLLVGPGYIKNPYNIFDGVIVVISWEIVGQOGGGLSVL      866
          :||:||:|||:||||||:||  ::|| | :|||||:::|||||||||||| |:|||||
Db   636  ILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIVVIISWEIVGQADGGLSVL   695

Qy   867  RTFRLMRVLKLVRFLPALQRQLVLVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKPAS   926
          |||||:||||||||:|||:|||| ||||||||||||||||||||||||||||||||  |
Db   696  RTFRLRLVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFSL    755

Qy   927  ERD-GDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGN  985
             :|||:|||||||||||||||:|||::|||||:|||||||||| ||:||| |||||||
Db   756  RTDTGDTVPDRKNFDSLLWAIVVFQIITQEDWNVLYNGMASTSPWASLYFVALMTFGN    815

Qy   986  YVLFNLLVAILVEGFQAEGDAYKSESEPDFFSPSV----------DGDGDRKRLALVAL  1035
          ||||||||||||||||||||| :||:|  |  |||            |  |:|  | ::
Db   816  YVLFNLLVAILVEGFQAEGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPM  873

Qy  1036  GEHAELRKSLLPPLIIHT---AATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAH  1091
          |           |::         | ||:  ||  ||    | :||:||  |:  |::
Db   874  TPNGHLDPSL--PLGGHLGPAGAGPA--PRLSLQPDPMLVALGSRKSSVMSL--GRMS    926

Qy  1092  HEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGEERRSLLSGE-GQES  1150
                 ::|:||:||:||||:  |  ||||||||  |        || ||:   |||:| |::
Db   927  YDQRSLSSSRSSYYGPWGRSAAWASRRSSWN------SLKHKPFSAEHESLLSAERGGGA   980

Qy  1151  QDEEESSE--DRASPAGSDH------RHRGSLEREAKSSFDLPDTLQVPG           1193
          : ::  ::      | :               | :|  :    || ::|
Db   981  RVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAEIVPAVG  1040

Qy  1194  LHRTASGRSS--ASEHQDCNGKSASGRLAARTLRTD-DPQLDGDDNDEGNLSKGERIQAW  1250
           |  |  |     || |||| :  :|| || || || : :      | |:  :||||: |
Db  1041  AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEIDYTLCPRVRKM   1098

Qy  1251  VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPK  1310
          :   : |  :| ||:|:|:| |::||| ||: ||:||:|| |||  ||||||||:|||:
Db  1099  IDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQ  1158

Qy  1311  IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVI  1370
          |:  : ||||:|:||||||| ||.||| ||||:|  ||||||||||||||||| ||::||
Db  1159  IEAGSTERIFITVSNYIFTAIFLGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFVSII  1218


Qy  1941  PDLLTVRKSGVSRTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT  1999
              | :                 : :               :
Db  1869  ECFFPLSSTAVS-----PDPENFLCEMEIPFNPV--RSW-LKHDSSQAPPSPFSPDAS    1919

Qy  2000  SCILQLPKDVHY-----LLQPHGAPTWGAIPKLPPPG---RSPLAQRPLRRQAAIRT    2048
           :|| |                 |                ||| | ||:||:  | ::
Db  1920  SPILPMPAEFFHPAVSASQKGPBKGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSD   1979

Qy  2049  DSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQRSGIQSKVSKHIRLPAPCP  2108
           ||| |                 |||
Db  1980  TSLDAS----------------PSSSAGSLQTTLEDSLTISDSPRRALGPPAPAP     2018

Qy  2109  GLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPG  2168
          |                 ||:                                ::|| |:
Db  2019  G--------------PRAGLSPAARRRL-----SLRGRGL                    2039

Qy  2169  FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSL------GGQPLGPGSRPKKKLSPPSI    2220
          | | | |:|        ::|     |||||       ||    |    : ::||:::
Db  2040  FSLRGLRAHQRSHS--SGGSTSPGCTHHDSMDPSDEEGRGGAGGGAGSEHSETLSSLSL   2097

Qy  2221  S---IDPPESQGSRPPCSPGVCLRR------------RAP--ASDSK             2250
                : ||   :  |  |:                   ||   : ||
Db  2098  TSLFCPPP------PPPADGLITPARKFSSTSSLLAAPGRPHAAALAHGLARSPSWAADRSK  2151

Qy  2251  DPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP                        2286
          || : |       || ::             |: :|
Db  2152  DPPGRAPLPMGLGPLAPPPQPL-------PGELEP                         2179
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RESULT 9
US-10-425-800-4
; Sequence 4, Application US/10425800
; Publication No. US20030180086A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-800-4

Query Match   44.9%; Score 5405.5; DB 14; Length 2188;
Best Local Similarity   50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

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Qy    51  ASRSSTTCPGPGAAGAGSTEKDPG--SADSEAEGL----------PYPALAPVFFYLS    97
          || ::   | ||  ||      ||    ||  | ||          || |||  :|| |:
Db     1  ASPPSSSAAAP-AAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLR   63

Qy    98  QDSRPRSWCLRTVCNPWFERVSMLVILLNCVTIGMFRPCEDIACDSQRCRILQAFDDFIF  157
          | :  |:|| : |||||||  |||||||||||| || : |   :  : | |||| ||||||
Db    64  QTTSPRNWCIKMVCNPWFECVSMLVILLNCVTILGMYQCDDMCLSDRCKILQVFDDFIF   123

Qy   158  AFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL  217
          :||| |||:||||||||||||||||||||||||||:|||:|||||||| : ||:|||||||
Db   124  IFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVL  183

Qy   218  RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCCFVVFFIFGIVGVQLWAGLLRNRCFLPE  277
          |||:||||||||||:|| |||||||||||||||| ||||||||| ||||||||||||||  
Db   184  RPLKAINRVPSMRIILVNLLLDTLPMLGNVLLLCCPFVVFFIFGIIGVQLWAGLLRNRCFLEE  243

Qy   278  NFSLPLSVDLEPYYQTENEDESPICSQPRENGMRSCRSVPTLRGEGGGGPPCSL-----  332
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RESULT 10
US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
;   APPLICANT:
;   APPLICANT: Dietrich, Paul S.
;   APPLICANT: McGivern, Joseph G.
;   TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;   TITLE OF INVENTION: AND USES
;   FILE REFERENCE: R0043B-REG sequence listing
;   CURRENT APPLICATION NUMBER: US/09/935,541
;   CURRENT FILING DATE: 2001-08-23
;   PRIOR APPLICATION NUMBER: 09/404,650
;   PRIOR FILING DATE: 1999-09-23
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1835
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-935-541-5

Query Match             44.4%;   Score 5345;  DB 9;  Length 1835;
Best Local Similarity   55.4%;   Pred. No. 0;
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

Qy          43 PRSRDSPVASRSSTTCPGPGAAGAGSTEKDPGSADSEAEG---LPYPALAPVVFFYLSQ 98
               : |||:| |||||| |:||  :||    ||||| :  ||: | |       |:   ||
Db           8 PSSAAAPAPEPGITEQPGP------RSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQ 62

Qy          99 DSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFA 158
               :  ||:| |:| ||||:| :|:|:|||||||||| |     | ||||:| ||| ||:||
Db          63 TTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFI 122

Qy         159 FFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLR 218
               || | |||||||||||||||||||||||||||||:||:|||:||||:|::|:||||||||
Db         123 FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLR 182

Qy         219 PLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPEN 278
               ||:|||||||||||| |||||||||||||||||||||||||:||||||||||||||:||:
Db         183 PLKAINRVPSMRILVNLLLDTLPMLGNVLLCFFVFFIFGIIGVQLWAGLLRNRCFLEEN 242

Qy         279 FSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL--- 332
               |:|    :|||||: :  |: ||||  |||:|:| |||:|| ||: |||| ||:
Db         243 FTIQGDVALPYYQPEEDDEMPFICSLTGDNGIMGCHEIPPLKEQ--GRECCLSKDDVY 299

Qy         333 DYETYNSSSNNT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD 390
               |: ::| : :::: |: ||  ||:|:| ||::|||:|||||||| ||:|||:|||||||
Db         300 DFGAGRQDLNASGLCVNWNRYRYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVE 359

Qy         391 IMYFVMDAHSFYNFIYFIFLLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLS 450
               ||| ||||||||||||||||||||||||||||||||||||||| |||||||||||| |||
Db         360 IMYYVMDAHSFYNFIYFILFLLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS 419

Qy         451 NASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQP 510
               :|: || ||| |||:| :||| |:||||     : |||     |: ::|
Db         420 -SSTVASYAEPGDCYEEIFQVCHILRKAKR---------RAIGLYQAL 458

Qy         511 SGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPS 570
               :|: ||||
Db         459 ------QNRRQA---------------------------------------MGPGT 473

Qy         571 TPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPP 630
               ||  | :||                              ||  :|:||
Db         474 KPGP---HAK--EPSHCKLCPRHSPLD------------------------PTPHT-- 500

Qy         631 PEILKDKALVEVAPSPGPPTLTSNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKAD 690
               :  |:
Db         501 -----------LVQ----PISAIL--------------------------- 509

Qy         691 ARTGAGEPESADHVMPDSDSEAVYEFTQDAQH 734
               : |||| |   :   : ::: | :
Db         691 SGACGPDSCPYC 509
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Qy        1371 DILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC 1430
               |||:|| |: | ||||||||||||||||||||||||||:|||||||||||||||||:|||
Db        1219 DIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278

Qy        1431 CAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSL 1490
               ||||||||||||||||||||||||||||||||| ||||||||:|:|||||||||||||||
Db        1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSL 1338

Qy        1491 FVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVEN 1550
               ||||||||||:||:|||:|||:|||||:|||||||||||||||||||||||||||||||:
Db        1339 FVLASKDGWVNIMYNGLDAVADQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVEN 1398

Qy        1551 FHKCRQHQEEEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
               ||||||||||:||||||||||:||||||    |:    ||:||:|||||:|||||:||||
Db        1399 FHKCRQHQEAEARRREEKRLRRLEKKRR------KAQRLPYYATYCHTRLLIHSMCTS 1451

Qy        1611 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNVIFTVLFVFESVFKLVAFAFRRF 1670
               ||||:||||:| ||||||:|||||||||:|||:|||||:|||| |||||:|||| |  |
Db        1452 HYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLVAFGLRRF 1511

Qy        1671 FQDRWNQLDLAIVLLSMGILSTMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
               | |||||||||:||||||||:||||| ||||:||  ||||||||||||||||||:||||:|| ||
Db        1512 FKDRWNQLDLAIVLLSVMGITLEEIENAALPINPTIIRIMRVLRIARVLKLLKMATGMR 1571

Qy        1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECEDTHPCEGLGRHATFRNFGM 1790
               ||| ||||||||||||||||||||||||||||||||  :||  | |:|| ||| |  |||
Db        1572 ALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCESMSRHATFENFGM 1631

Qy        1791 AFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLNVVI 1847
               |||||| |||||||||||||| :|| | |||  |  ||||||||||||:|||||||||
Db        1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPIYFVSFVLTAQFVLNVVV 1691

Qy        1848 AVLMKHLEESNKEAKEAEEAELEAELEM-KTLSPQPHSPLGSP--------- 1889
               |||||||::|||||||:|:||||:|||| |:|  | ||||||
Db        1692 AVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTGSPGAPGRGPGAGGGGDTE 1751

Qy        1890 ---------FLW-------PGVEG-VNSTDSPKPGAPHTTAHIGAASG--- 1920
                        |||        || :| :  :      ||    ||  | :
Db        1752 GGLCRRCYSPAQENLWLDSVSLIIKDSLEGELTIIDNLSGSIFH--HYSSPAGCKKCHH 1808

Qy        1921 -------------FSLEHPTMVP----------HPEEVPV--PLG 1940
                            ||||| |:|             ||||||   ||
Db        1809 DKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLG 1868

Qy        1941 PDLLTVRKSGVSRTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSGSIISVHSQPADT 1999
               | |:    :  : :  :||  |: | | :|      | : ::|:  :  :  |
Db        1869 ECFPFLSSTAVS------PDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSPDAS 1919

Qy        2000 SCIIQLPKDVHY----LLQPHGAPTWGAIPKLPPPG----RSPLAQRPLRRQAAIRT 2048
                |:  |  | :       || ||  |||||  |:||||     |  |   |  |:|
Db        1920 SPLLPMPAEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSD 1979

Qy        2049 DSLDVQGLGSREDLLSEVSGPSCPLTRSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCP 2108
                       | :   | :| : |  | ::  :  || :  |  : |  :| | : ||
Db        1980 TSLDAS---------------------PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAP 2018

Qy        2109 GLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRPG 2168
               |              :         |   |     |   |  |     |
Db        2019 G-------------------------------------PRAGLSPAARRL----SLRGRGL 2039

Qy        2169 FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSL--------GGQPLGGPGSRPKKKLSPPSI 2220
                 : :     : |:          |  | ||        ||  : |:   | : || :|
Db        2040 FSLRGLRAHQRSHS--SGGSTSPGCTHHDSMPDSDEEGRGGAGGGGAGSEHSETLSSLSL 2097

Qy        2221 S---IDPPESQGSRPPCSPGVCLRR----------------RAP----ASDSK 2250
               :    |||||  | ||  ||  |              |     |
Db        2098 TSLFCPPP---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSK 2151

Qy        2251 DPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2286
               :: :: | |: || |  | | | ||:|| |
Db        2152 DPGRAPLPMGLGPLAPPQPL----PGELEP 2179
```

```
Db   1777 EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVS 1833
          ||||||||:||||.|||.||||||||||||||||.||||| :||::|||:  :|.:|:||
Qy   1612 EGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVSPLYFVS 1671

Qy   1834 FVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWP 1893
          |||||||||||||.||||||||:|||||||:|||||||||||||||
Db   1672 FVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDABIELEM----------------- 1713

Qy   1894 GVEGVNSTDSPKPGAPHTAHIGAASGFSLEHPTMVPHPEEVPVP-LGPDLLTV------ 1946
          :                                            PCPCPCPCAGPRLPTSSPGAPG
Db   1714 -AHGLGPCPGPCPG------------------------------PCPCPCPCAGPRLPTSSPGAPG 1750

Qy   1947 RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQL 2005
          ::|||
Db   1751 RGSGGAGAG-DTESHLCRHCYSPAQETL----W----LDSVSLIIKDSLEGELTIIDNL 1801

Qy   2006 PKDV-HYLLQPHG 2017
          :|:
Db   1802 SGSVFHHYASPDG 1814
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RESULT 11
US-10-425-800-5
; Sequence 5, Application US/10425800
; Publication No. US2003018086A1
; GENERAL INFORMATION:
;   APPLICANT: Dietrich, Paul S.
;   APPLICANT: McGivern, Joseph G.
;   TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;   TITLE OF INVENTION: AND USES
;   FILE REFERENCE: R0043B-REG sequence listing
;   CURRENT APPLICATION NUMBER: US/10/425,800
;   CURRENT FILING DATE: 2003-04-29
;   PRIOR APPLICATION NUMBER: US/09/404,650
;   PRIOR FILING DATE: 1999-09-23
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1835
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-425-800-5

  Query Match   44.4%; Score 5345; DB 14; Length 1835;
  Best Local Similarity   55.4%; Pred. No. 0;
  Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

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Qy     43 PRSRDSPVASRSSTTCPGPGAAGAGSTEKDPGSADSEAEG----LPYPALAPVVFFYLSQ 98
                                                           :
Db      8 PSSAAAPAPEPGITEQPGP------RSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQ 62

Qy     99 DSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCPEDIACDSQRCRILQAFDDFIFA 158
          |||.||||:|||||||||.:|||:|||||||||||.:||||||||||:||.|:||||||
Db     63 TTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFI 122

Qy    159 FFAVEMVKVVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVRTVRVLR 218
          ||| ||||.||||||||||||||||||||||.|||||||||||||:||:|||:.||||||
Db    123 FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLLDLQNINLSAIRTVRVLR 182

Qy    219 PLRAINRVPSMRIIVTLLDTLPMLGNVLLLCFPVFFIFGIVGVQLWAGLLRNRCFLPEN 278
          ||:||||||||||.||:||||:||||||||||||||:|||||||||||||||||||||
Db    183 PLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFPVFFIFGIVGVQLWAGLLRNRCFLEEN 242

Qy    279 FSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL------ 332
          |::| |:|:||||||: .|: |  ::||:|||:||  :||| : |      |
Db    243 FTIQGDVALLPYYQYPEEDDMPFICSLTGDNGIMGCHEIPPLKEQ--GRECCLSKDDVVY 299

Qy    333 DYETYNSSSNTT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD 390
          |:|:||.|:|||   :||::|: ||.:|||||||||||||||||||||||||||||||
Db    300 DFGAGRQDLNASGLCVNWNRYYNVCRTGNAPHKGAINFDNIGYAGIVIFQVITLEGWVE 359

Qy    391 IMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLS 450
          |:|||||.|||.||:| ||||||| ||||.:| | |:|| | |:::|||:|||||||:||
Db    360 ARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFPIFAALGVELFGKLVCNDENPC 1611
```

Db   360 IMYYVMDAHSFYNFIYFINLYFTILLIIVGSFFMLNLCLVVIATQFSETKQREHRLMLEQRQRYLS 419
          |||||:|||||||||||||||||||||||||||||||||||||||||||||:||||||| ||:||

Qy   451 NASTLASFSEPGSCYEELLKYLVLVILRKAARRLLAQVSRAIGVRAGLLSSPVARSGQEPQP 510
          |:||:::|:||:::|||| :||:|
Db   420 -SSTVASYAEPGDCYEEIFQYVCHLRKAKR------RALGLYQAL-------------- 458

Qy   511 SGGCTRSHRRLSVHHLVHHLVHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRIMLPPPS 570
          ||||||||| |||:||:|
Db   459 ------QNRRQA------------------MGPGT-----------------PAPA 473

Qy   571 TPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPP 630
          ||:|||||| ||||| |:||||
Db   474 KPGP-----------HAK--EPSHCKLCPRHSPLD--------------PTPHT--- 500

Qy   631 PEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKKLLETQSTGACHSSCKISSPCSKAD 690
          ||:||| ||
Db   501 ------------LVQ------------------PISAIL----------------- 509

Qy   691 SGACGPDSCPYC-----------ARTGAGEPESADHVMPDSDSEAVYEFTQDAQH 734
                                 || || :| :: :||:||
Db   510 --ASDPSSCPHCCQHEAGRRPSGLGSTDSGQEGSGGSGSAE---AEANGDGL--QSSEDGVS 563

Qy   735 SDLRDPHSRRRQRSLGPDAEPSSVLA------FWRLICDTFRKIVDSKYFGRGIMIAILVN 789
          ||| |||||:|||||||||||:||:|:|||||||
Db   564 SD-----------LGKEEEQEDGAARLCGDVWRETRKKLRGIVDSKYFNRGIMAILVN 611

Qy   790 TLSMGIEYHBQPEELTNALEISNIVFTSLFALEMLIKLLVYGPFGYIKNPYNIFDGVIVV 849
          |||||||||:||||||||:||:::||||||||:|||:||||||:|||||||||||| |||
Db   612 TVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVI 671

Qy   850 ISVWEIVGQQGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFI 909
          ||:|||| |:|||||||:||||||||:||||:||| |||||||||||||||||||||||
Db   672 ISIWEIVGQADGGLSVLRTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFI 731

Qy   910 FIFSIIGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMAS 968
          |||||||||||||||| ||: |:|||||||||||||||||||||||||||||||||||
Db   732 FIFSIIGMHIFGCKFSLRTDTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVLYNGMAS 791

Qy   969 TSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDG------- 1022
          |:| |||||||||||||||||:|||||||||||| |:::||:||||
Db   792 TTPWASLYFVALMTFGNYVALMTFGNYVLFNLLVAILVEGFQAEGDANRSCSDEDQSSSNLEEPDKLPE 851

Qy   1023 --DGDRKKRLALVALGEHAELRKSLLPPLIIH--TAATPMSHPKSSSTGVCEALGSGSRR 1078
                                                : |:
Db   852 GLDNSRDLKLCPIPWTPNGHLDPSL--PLGAHLGPAGTMGTAPRLSLQPDPVLVALDSRK 909

Qy   1079 TSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAAASWTSRSSRNSLGRAPSLKRRSPSGE 1138
                      :: ::| ||| : ||: :|
Db   910 SSVMSLJ---GRMSYDQRSLSSSRSSYYGPWGRSGTWASRSSWN-----SLKHKPPSAE 960

Qy   1139 RRSLLSGEGQES--QDEESSEE--DRASPAGSDH-----------------RHRGSLEREA 1179
          |:| ::||:| ||:|:|||
Db   961 HESLLSGEGGSCVRACEGAREEAPRTAPLHAPHAHHAHHGPHLAHRHRHRRTLSLDT 1020

Qy   1180 KSSFDLPDTLQVPGLHRTAS--GRSSASEHQDCNGKSASGRLAARTLRTD-DPQLDGDDDN 1236
                      |:: | ||||:|:
Db   1021 RDSVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDDRRDRGEDE 1078

Qy   1237 DEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRPRLLCHRIITHKMPDHVVLVI 1296
          :| |:|||| ||:||||:|:| :| |:|||||:
Db   1079 EEIDYTLCFRVRKMIDVYKPDWCEVREDWSVYLFSPENKFRILCQTIIAHKLFDYVVLAF 1138

Qy   1297 IFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSS 1356
          ||||||||:|||:|||||||||||:||:|||||:|||||||||||:||||||||||||||
Db   1139 IFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSS 1198

Qy   1357 WNVLDGLLVLISVDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETL 1416
          |||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||||
Db   1199 WNVLDGFLVFVSIIDIVSVASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETL 1258

Qy   1417 MSSLKPIGNIVVLCCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNKSDCAEASYRWVRH 1476
          |||||||||||||||||||||||||||||||||||||||||||||:||||||:||||||

Db   1259 ISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCVAANYRWVHH 1318
          ||||||||||:|||||||||||||||||||||||||||||||||||:|||::|||||:||

Qy   1477 KYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVA 1536
          |||||||||||||||||||||||||||||||:||:|:|||::|||||||||||:||||||
Db   1319 KYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVADQQPVTNHNPWMLLYFISFLLIVS 1378

Qy   1537 FFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRSKEKQMAEAQCKPYYSD 1596
          |||||||||||||||||||||||:||||||||||||||:||||| ||
Db   1379 FFVLNMFVGVVVENFHKCRQHQEAEARRREEKRLRRLEKKRR----------KAQRLPYYAT 1431

Qy   1597 YSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVF 1656
          | |:|| || :|:|| ||: |||| |: |||:||||||||||:||:|:|||
Db   1432 YCPTRLLIHSMCTSHYLDIPITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVL 1491

Qy   1657 ESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRMRVLRI 1716
          |:|||||| ||:||:|||||||||||||:| |:|||:||:: |||:|||:|||||||||
Db   1492 EAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRMRVLRI 1551

Qy   1717 ARVLKLLKMAVGMRALLHVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPC 1776
          |||||||:| ||||||| ||:|||||||||||:|||||||| |||||||||| ||:|||
Db   1552 ARVLKLLKNATGMRALLLDTVVQALPQVGNLGLLFMLLFIYAALGVELFGKLVCNDENPC 1611

Qy   1777 EGLGRHAITRNFGMAFLITLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVS 1833
          | ::||||||||||| || ||||||||||:|||||||| : || |||
Db   1612 EGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVSPLYFVS 1671

Qy   1834 FVILTAQFVLVNVVIAVLMKGHLEESNKEAKEAELEAELELEMKTLSPQPHSPLGSPFLWP 1893
          |||||||||:|:|| ||||| |:||:|||:||:| ||||:||
Db   1672 FVILTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAEIFLEM----------------- 1713

Qy   1894 GVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVP-LGPDLLTV------ 1946
                                                       | ||:|
Db   1714 -AHGLGPCPGPCPG----------------------PCPCPCPCAGPRLPTISSPPAPG 1750

Qy   1947 RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHRGWGLPKAQSGSLLSVHSQPADTSCILQL 2005
          |:| | |:| |||:| ||:|:| |
Db   1751 RGSGGAGAG--DTESHLCRHCYSPAQETL----W-----LDSVSLIIKDSLEGELTIIDNL 1801

Qy   2006 PKDV-HYLLQPHG 2017
          |:|| :||
Db   1802 SGSVFHHYASPDG 1814

RESULT 12
US-09-030-482B-19
; Sequence 19, Application US/09030482B
; Patent No. US2002000972A1
; GENERAL INFORMATION:
; APPLICANT: Snutch, Terry
; APPLICANT: NeuroMed Technologies, Inc.
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS
; FILE REFERENCE: 38109-20007.00
; CURRENT APPLICATION NUMBER: US/09/030,482B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 60/039,204
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: PRT
; ORGANISM: Human
US-09-030-482B-19

Query Match   32.8%; Score 3950; DB 9; Length 1853;
Best Local Similarity   46.9%; Pred. No. 3e-252;
Matches 905; Conservative 167; Mismatches 353; Indels 506; Gaps 45;

Qy   59 PGPG------AAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTV 110
          |||| ||:||| ::|:: | | |::: :|
Db   75 PGTGMHTGTFQEGAEPGSSQHPEAQATTYAGCTPAPTGDPTCCFVLD----------LV 123

Mon Nov 22 06:47:52 2004   us-09-611-257a-24.rapb

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Qy   111  CNPWFERVSMLVILLNCVTLGMERPCEDIACDSQRCRILQAFPDFIFAFFAVEMVKMVA  170
          ||||||||||||||||::|:|||||| ::|||::|||||||||||:||||||||||||
Db   124  CT-WFECVSMLVILLNCVTLGMYQPCDDMDCLSDRCKLLQVFDDFIFIFFAMEMVLKMVA  182

Qy   171  LGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDIQNVSFSAVRTVRVLRPLRAINRVPSMR  230
          ||||||||||||||||||||||||| ::|||::|||::|||||||||||||||||||||
Db   183  LGIFGKKCYLGDTWNRLDFFIVMAG---------NINLSAIRTVRVLRPLKAINRVPSMR  233

Qy   231  ILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVLWAGLLRNRCFLPENFSLPLSVDLEPY  290
          |||||| |||||||||||||||||||||||||||||||||||||||||||||::|||
Db   234  ILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPPY  293

Qy   291  YQTENEDESPFICSQPRENGMRSCRSVPFLRGEGGGPPCSL------DYETYNSSSNNT  344
          :|::|::|:||||| ||:|||||:|||||::::||     :
Db   294  YQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ----GRECCLSKDDVYDFGAGRQDLNAS  350

Qy   345  --CVNWNQYTNCSAGEHNPFKGAINFDNIGYAMIAIFQVITLLEGWVDIMYFVMDAHSFY  402
            :|||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   351  GLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAMIVIFQVITLLEGWVEIMYYVMDAHSFY  410

Qy   403  NFIYFPILLI------------------------------------------------  412
          ||||||||||
Db   411  NFIYFPILLIISELIHLVMPDCSFSTAQSPKCCQGDSLPGVAAESLLLRDSSSSVITDEAAA  470

Qy   413  -------------------------------------------------------------  412
Db   471  MENLLAGTSKGDESYLLRLAAGSQVHSQAQOMLGRGLGPESLETGEEPHSWSPRATRRWDP  530

Qy   413  ---------------------VGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLA  456
                               ::|||||||||||||||||||:|:||||:|| ::|| :
Db   531  QCQPGQPLPHFMQAQVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVA  589

Qy   457  SFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTR  516
                                  :||:|||:|| ||   :|
Db   590  SYAEPGDCYEIFQYVCHILRKAKR------RALGLYQALQSRRQALGPEAPAPA-----  638

Qy   517  SHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSG  576
Db   590  ...

Qy   577  GPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKD  636
          :||                     ::|::|
Db   639  --------------------------------------------KPGPHAKEPRH  649

Qy   637  KALVEVAP----SPGPPLTSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSKADS  691
Db   650  YPLTVWESILGRQAEBCTL---RAAAHP--------------------SSGASHPGVGSEEAPELCPQ  694

Qy   692  GACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGP  751
          :|          :|      |::|
Db   695  HSPLDATPHTLVQPIPATLAS------------DPASCPCCQHEDGRRPSGLGSTDS  739

Qy   752  DAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPE------  802
                     ::|||     |::|||:|||||||||||||||||||:::|:|
Db   740  GQEGSGS----GSSAGEDEA------DGDGA--RSSEDGASSELGKEEEEEQ-------  781

Qy   803  ------ELTNALE----------ISNIV----------------------------  814
                :|||:|            :|:||
Db   782  -ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMWALLVNTVSMGIEHHEQASAAQPGRA  840

Qy   815  FTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGGISLVLRTFRLMRV  874
          |||||||||||:||||||| ||||||||||||| |||::|||||||||| ||||||||||
Db   841  CGRGQNPDLCMTLKAPCLCHNVPSPGGQVLSHPVTPPHTAPWRMETGKQGHGCEEGPSQGR  900

Qy   875  LKLVRFLPALQRQLVVLMKTMDNVATPCMLLMLFIFIFSILGMVHLFGCKFPASERD-GDTL  933
          ||||||||||||||:|||||||||||| :||||:||||| |:||| ||||||||:
Db   901  SSDMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIIISIWEIVGQADGGLSVLRTFRLLRV  960

Qy   934  PDRKNFDSLLWAIVTVFQOLITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  993
          |||||||||||||||||||||||||||:|||||||||::|||:|||||||||:|:||:||
Db   961  LKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFTFSILGMHIFGCKFSLRTDTGDTV  1020

Qy   994  AILVFGFQAE-----------------------------------------------  1005
Db  1021  PDRKNFDSLLWAIVTVFQOLITQEDWNVVLYNGMASTSSWASLYFVALMTFGNYVLFNLLV  1080
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Db  1081  AILVEGFQAEVTVVLAEEAPPQGLRKTGRCRGGLDGGGLQFKLLAGNLSLKEGVADEVGD  1140
          ||||||||
Qy  1006  ATKSESEPDFFSPSV---------------------DGDGDRKKRLALVALGEHAELRKSLLPPLLIHT--  1053
          |:|:|||:::|::|
Db  1141  ANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPMTPNGHLDPSL--PLGGHLGP  1196

Qy  1054  --AATP--------------------------EALGSGGRRTSSSGSA-----  1085
            |:|:                         :||:|::||:::|:
Db  1197  AGAAGPAPRLSLQPDPMLVALGSRKSSVMSLGRMSYDQRSLVGGLRATAGVQAAFGHLVP  1256

Qy  1086  EP-----GAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERR  1140
          |:      ||:|:
Db  1257  QPWVCLWGADPNGNSFQSSSRSSYYGPWGKSAAWASRRSSWN---------  1310

Qy  1141  SLLSGE-GQESQDEESSEE--DRASPAGSDH-----------------------  1182
          :|:|:: |::::|:|::|   ||:|||:|:
Db  1311  SLLSAERGGGARVCEVAADEGPRAAPLHTPHAHHVHHGPHLAKRHHRHHRRTLSLDNRDS  1370

Qy  1183  FDLPDTLQVPGLHRTASGRSS--ASEHQDCNGKSASGRLARTIRT--DDPQLDGDDDND-  1237
          :|::|:| |::::|||:|:::  ||||::|:|:|||: |||||:|   :::|:| ::::
Db  1371  VDLAELVPAVGAHPRAAWRAAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGRGEDEEEI  1428

Qy  1238  --------------------------LLC-------------------------  1280
                                    |||
Db  1429  DYVSGGGAEGDLTLCFRVRKMIDVYKPDWCEVREDWSVYLFSPENRLRDLGWVSLECQGK  1488

Qy  1281  -------------------HRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSN  1325
                             ||||||||||::|:|:|||||||:|||:|:|||||:|:|||::|
Db  1489  VGDLVVWYGQRRQRQTIIAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSN  1548

Qy  1326  YIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKIL  1385
          |||||:|:||||:||||||||||||||||||||||||:|:|||||||:|||:|||:|||||
Db  1549  YIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVVSIIDIVVSLASAGGAKIL  1608

Qy  1386  GMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVOLF  1445
          |::||||||||||||||||||:|||||||||:|||||||||||:||:||||||||||||||
Db  1609  GVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLICCAFFIIFGILGVOLF  1668

Qy  1446  KGKFFVCQGEDTRNITNKSDCAEEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYD  1505
          |||||||||||||||:|||||||:||:||||||||||||||||||||||||||||:|||:
Db  1669  KGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYN  1728

Qy  1506  GLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHOEEEARR  1565
          |||||:|||||:|:||||||||||:|||||||::|:|||||||||||||||:||||:||
Db  1729  GLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEEARR  1788

Qy  1566  REEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRILLVHHLCTSHYLDLFITGVIGLNV  1625
          |||||||||||||||                    :|||||||:||::|||:||:|:||||
Db  1789  REEKRLRRLEKKRR------------------------KAQRLPYYATYCHTRLLIHSMCTSHYLDIFITFIICLNV  1841

Qy  1626  VTMAMEHYQQP  1636
          ||:|:||:||||
Db  1842  VTMSLEHYNQP  1852
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RESULT 13
US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

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; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6836
; LENGTH: 1657
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6836

Query Match       29.5%;  Score 3553;  DB 14;  Length 1657;
Best Local Similarity   42.2%;  Pred. No. 5.3e-226;
Matches   800;  Conservative 234;  Mismatches 436;  Indels 426;  Gaps  42;

Qy     66 AGSTEKDPG----------SADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCN 112
             ::   |||          :::::: ||||
Db     88 ASSSEASPRWEGRQIEWGNEEQIEESE-LPYPGFAEPALRCFYQARPPRKWALQMVMS 146

Qy    113 PWFERVSMLVILLNCVTLGMFRPCED-IACDSQRCRILQAFDDFIFAFFAVEMVKMVAL 171
             ||::|:::|||| ||:||| ||||| :|:: :|||||:::|| |:: ||||:::||||
Db    147 PWFDRITMAVIMNCVTLGMYRPCEDGPDCDTYRCQILDIIDNCIFVYFAFEMVIKIMAL 206

Qy    172 GIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQ---NVSFSAVRTVRVLRPLRAINRVPS 228
             ||| || :|||||||||||||| ||||:||:|  :: ||||||||||||||:||||:||
Db    207 GFYGPAAYMSDTWNRLDFFIVMAGIAEFVLHEYLGGNLTAIRTVRVLRPLRAVNRIPS 266

Qy    229 MRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCF--LPENFS------L 281
             ||||: :|||||||||||||||||||||||||||||||:|| |    |||||      |
Db    267 MRILVNLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCVINLPKTISENQSAL 326

Qy    282 PLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGSGGPPCSLDYETYNSSS 341
             |  :: ||||   :  |: :| :: |      :   |||| |  |||:|||||||||:
Db    327 FNNVKLTRFYIPE-DTSLEYICSQPDANGLHTCSNLPYTVD---GVKCNLTLDEYDKVT 382

Qy    342 NTTCVNWNQYYTNCSAG---------EHNPFKGAINFDNIGYAWIAIFQVIT 384
             |:|| || |   |||             | || :|| :|| |  | ||:|
Db    383 NDSCINWNIYNECQVNIYPSLMTIAISCFIKVMQRNPFQGSVSFDNIGFAWVAIFLVIS 442

Qy    385 LEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQ 444
             ||||:|||||: ||| |:|||||  ||||||||||||||||||| || ::|||:||
Db    443 LEGWTDIMYYYQDAHSFWNWIYFVLLIVIGAFFMINLCLVVIATQFAETKRRETERMLQE 502

Qy    445 RVRFLSNASTLASFSEPG----------SCYEELLKYIVYILRKAARRLAQVSRAIGVRAG 495
             | |:|:  :  | |             |||    ||::|  |   | : ::  :|  |
Db    503 RKMLNRDSISCTGSEIGGASSKEEGDTVYAAFVRFIGHTFRRTKRAAKKKYTAY----- 557

Qy    496 LLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQD 555
             |||  ||| ::| :  |||::| :|                 :|| ||
Db    558 ----MEERABRKSSERQQRRKSKL---------------------DDMATLSRIEEKAED 592

Qy    556 RDANGSRRLMLPPPSTPTPSGGPPRGAEBSVHSFYHADCHLEPVRCCAPPPRCPSEASGRT 615
             |                             :|:  :    : |:
Db    593 EE----------------DETTITRENGDDQIEQN--------------------- 611

Qy    616 VGSGKVYPTVTHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGA 675
             |    :|  |:  | | || |
Db    612 -GDGVRIKRVKIEEEPKI-------------------------------------- 628

Qy    676 CHSSCKISSPCSKADSGACGPDSCPYCARTQGAGEPESADHVMPDSDSEAVYEFTQDAQHS 735
             |: ::   |: ::|     |              ::| |::
Db    629 ----------------KIGNGNSNGPHYKHSSSDEES---DEDGEED 656

Qy    736 DLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTPRKIVDSKYFGRGIMIAILVNTLSMGI 795
             |:|   :::|  | :|   | : ::   |   :|:||: |  |  :|:||||||||:|||
Db    657 QVYDGEEAKKK-----STPSKL-WW- FREKIQKFVICDHFTRGILVAILVNTLSMGV 706

Qy    796 EYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGVIKNPYNIFDGVIVISVWEI 855
             ||| |||||  ||  |:|||:||| ||||||||| | || || ||||  |||:| |:|
Db    707 EYHQQPEILTVILEYSNLFFTALFALEMLLKIIASGLFGYLADGNLFDGGIVALSVLEL 766

Qy    856 VGQQOGGLSSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIL 915
             |:| |||||||||:||| :|:|||||| |:|||||:|| ||||  |  |||| |||||||
Db    767 FQEGKGGLSVLRTFRLLRILKLVRFMPALRYQLVVMLRTMDNVTVFFGLLVLFIFIFSIL 826

Qy    916 GMHLFGCKFASERD--GDTLP--DRKNFDSLIWAIVTVFQIILTQEDWNKVLYNGMASTS 970
             |: ||||        |  | :||| ||::|| |||:|||||||||||||:||:|| ::
Db    827 GMNLFGCKFCKVEEKPLGGLAKKCERKNFDTLLWALITVFQILTQEDWNMVLFNGMAQTN 886
```

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Qy    971 SWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRL 1030
             |:|||||:|::||||:|||||||||||||||:|  : :: :|  |      | : |:
Db    887 PWAALYFVALMTFGNYVLFNLLVAILVEGFQESKEEEKRQLEEDARKQAVEEDERKREL 946

Qy   1031 ALVALGEHAELRKSLLPLLIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAA 1090
             || |
Db    947 ELII---------------------------------------------AKTTSPAFNNGVA 963

Qy   1091 HHEMKC--PPSARSSPHSPWSAASWTSRRSSRNSLGRAPSLKRRSPSG----ERRSLL 1143
             | |:   :::   :  |:::::
Db    964 PAECTCQRPSSPEESP-SPRLLSANY---------------HPSPERKHSANLDAIIDKRLVL 1010

Qy   1144 SGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSS 1203
             |
Db   1011 ------------------RNSAPFDR-SPV-SEGRDDSRLNRRA--SLVLPVANGVP-- 1045

Qy   1204 ASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNEGNLSKGERTQAWVRSRL-PACCRER 1262
             |
Db   1046 -YRRQRVHSWKASQELKQALAEEKRNEAKQN---------------TFVRKLLKKTCLHNR 1091

Qy   1263 DSWSAYIFPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLT 1322
             |: :|| | ||| ||||||||:|| || ||||:|| |||||||||  | :||||||||
Db   1092 TEFSLFLMGPKNPLRIKCLQTTQKKWFDYTVLFFIGINCITILAMERPSIPPDSFERQFLH 1151

Qy   1323 LSNVIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGT 1382
             |   |||   |
Db   1152 ISGYIFTVIFTGEMMMK-------------------------------------------- 1168

Qy   1383 KILGMLRVLRLLRTLRPLRVISRAQGLKLVVETIMSSLKPIGNIVICCAFFIIFGILGV 1442
             |   |  |: |  |||||:|||| ||||||  :::|:|||||||:| ||||||||||||
Db   1169 --------------VSHRIPTLKPIGNIVLCCTFFIIFGILGV 1198

Qy   1443 QLFKGKFFVCQGEDTRNITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWV 1500
             |||||||| | |  ||:||||:||  || : : |:|||||:||||||||||||||||||
Db   1199 QLFKGMYHCIGPEVGNVTTKADCIE-DYRNKKVNHRYNFDNLGQALMSLFVLSSKDGWV 1257

Qy   1501 DIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE 1560
             || | ||| |||:|| | |  |:::| |:||||:| ||:|||| ||||||||||| | |
Db   1258 SIMYQGIDAVGVDVQPIENYNEWRMIYFISFLLLVGFFVLNMFVGVVVENFHKCKEALEK 1317

Qy   1561 EEARRREEKRLRRLEKKKRRSKEKQMARAQCK---------PYYSDYSRF 1600
             | |:||| |||:||||::|||||||   |  |         |:|:: |
Db   1318 EMREKEKEKRLKR-KLKRQKFEESMAGKRKKNRIVWAGSAIKSIFSVERNYPYHDYGHT 1376

Qy   1601 RLLVHHLCTSHYIDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVLFVFESVF 1660
             | | ||||  :| :  |||||||:|| || :||: |: ||| | :| ||| | :||||||
Db   1377 RLFLHGIVTSKYFDLAIAAVIGINVISMAMEFYMMPMGLKYVLKALNYFFTAVFTLEAAM 1436

Qy   1661 KLVAFAFRRFPQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVL 1720
             |: | |:|| :|| ||::| ||:|||:||  |  || |||||| |:|:||:||||||||||
Db   1437 KLIALGFKRFIEKWNRLDMFIVILSIAGIIFEEFEA-LELPINPTIIRVMRVLRIARVL 1495

Qy   1721 KLLKMAVGMRALLHTVMQALPQVGNIGLLFMLLFFIFAALGVELFGDLECDETHPCEGLG 1780
             ||||:|   ||  | :|||:|||||||::||||||||||||||||||||:||||||||||
Db   1496 KLLKMAKGIRSLLDTVGEALPQVGNLGSLFFLLFFIFAALGVELFGKLECSEDHPCDGLG 1555

Qy   1781 RHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSR-DCD------QESTCYNTVISPIYVSF 1834
             :||:||||||||||||:|:| |||||||||| :  |       |:  | : |  : | |
Db   1556 EHAHFRNFGMAFLTLFRIATGDNWNGIMKDALRDDCDSSDHCETNCCVDPIIAPCFFVIF 1615

Qy   1835 VLTAQFVLVNVVIAVLMKHLEESNKEAKERAELEAE 1870
             ||::|||:||||:|||||||||||| :  |:| | |
Db   1616 VLISQFVLNVVVAVLMKHLEESN---KRDAEGPAE 1648
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RESULT 14
US-10-627-370-2
; Sequence 2, Application US/10627370
; Publication No. US20040081988A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason M.
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;  APPLICANT: Castle, John C.
;  APPLICANT: Armour, Christopher D.
;  TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B
;  FILE REFERENCE: RS0202Y
;  CURRENT APPLICATION NUMBER: US/10/627,370
;  CURRENT FILING DATE: 2003-07-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 2
;  LENGTH: 2264
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-627-370-2

Query Match        14.0%;   Score 1680.5;  DB 15;  Length 2264;
Best Local Similarity  23.9%;  Pred. No. 1.2e-101;
Matches   623;  Conservative  349;  Mismatches   831;  Indels   801;  Gaps    82;

Qy    59  PGPGAAGASTEKDPGSADSEAEGLPYPALAPV----------VFFYLSQDSRPRSWCLRT  109
              :    ||||                             :::  :    |||||
Db    32  PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI  91

Qy   110  VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV  166
              ||||:|:|| |||||||||||:   ||  :||| |:::      || ||| |||||
Db    92  TEWPPFEYMILATIIANCIVLAL----EQHLPDGKTPMSERLDDTEPYFIGIFCFEAGI  147

Qy   167  KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA  222
              :||||:  |::| |:|||: || |||||||||:    || ||| ||  |  | ||||
Db   148  KIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTFDLR------TLRAVRVLRPLKL  202

Qy   223  INRVPSMRILVTLLLDTLPMLGNVLLCFVFFIFGIVGVQLWAGLLRNCFLPENFSLP  282
              ::  : |:|: |:     || || |:|:|| ||||||| ||||||  :|| |||
Db   203  VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF------P  255

Qy   283  LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSN  342
              :|                    :||||||| |||||   ::
Db   256  NSTDAEPV--------------------------GDFPCGKEAPARLCEGD  280

Qy   343  TTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF  401
              |||                          ||    : |||| :  |  |   | |
Db   281  TEC---REYWP---------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT  330

Qy   402  YNFIYFILLIIVGSSFMINLCLVVIATQFSETKQRES----------OLMREQRVRFLSNASTL  455
              :|: |||||:|||:||::| ||||::  ::                |   |  | |  :|
Db   331  WNWLYFIPLIIIGSFFMNLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIR----------  382

Qy   456  ASFSEPGSCYELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT  515
              :                                          |   |  ||| |
Db   383  ------------RELNGYLEWIFKAEEVMLAEED-----------------RNAEEKSPLDVLK  417

Qy   516  RSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS  575
              |
Db   418  RAATKKSRNDLIH-----------------------AEEGEDRFAD------------  440

Qy   576  GGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVVPTVHTSPPPEILK  635
               |                                   :||
Db   441  PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEP  469

Qy   636  DKALVEVAPSPGPPTLTSFNIPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG  695
              ||
Db   441  ------------LKSGKTESSSYF---------------------------------LCAVGSPFARAS--  452

Qy   696  SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF  755
              ||                           :||
Db   453  --MFRFF-----IRRMVKAQSFYWVVLCVVALNTLCVAMVHYNQPRRLITTLYFAEFVF  469

Qy   756  HYQQPQILDBALKICNYIFTVIFVFESVFKLVAPAFRRFFQDRWNQLDLAIVLLSIMGTI  815
              ||                                       :|||| :
Db   470  TSLFALEMLLKLLVVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ----QGGGLSVLRTFR  521

Qy   816  FYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL  870
              ||
Db   522  LGLFLTEMSIKMYGLGPRSYFRSSFNCFDFGVIVGSSVFEVVWAAIKPGSSFGISVLRALR  581

Qy   871  LMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDG  930
              :|:| |||::            ::::       :|:||| | ||| ||:|
Db   582  LLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFIVFALLGMQLFGGQFNFQDET  641

Qy   931  DTLPDRKNFDSLLWAIVTVFQILTQEDWNKVIYNGM----ASTSSWAALYFIALMTFGN  985
              :||   ||  |||:|: |||||||||||:|::::      ::   :||  ||| |||
Db   642  PT----TNFDTFPAILTVFQILTGEDWNAVMYHGIESQGVSKGMFSSFYFIVLTLFGN  697

Qy   986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSL  1045
              :  |       ::             ::
Db   698  YTLLNVFLAIAVDNLANAQELTKDEEMEEAA---------NQKIALQKAKEVAEV--SP  746

Qy  1046  LPPLLIHTAATPMSHPKSSSTGVGEA-----------------------------  1071
Db   747  MSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLR  806

Qy  1072  ------------------------------------LGSGSRRTSSSGSAEPGAA------  1097
                                                  :::            ::  ::
Db   807  PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHRHRDKDKTPAAGDQ  866

Qy  1098  -------PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL  1142
                     |:|:::   ||    :  :                 |    :: ::|:|
Db   867  DRAEAPKAESGEPGAREERPRPHRSHSKEAA--GPPEARSERGRGP----GPEGGRRHH  919

Qy  1143  LSGEGQESQDEE----------ESSEEDRASPAGSDHRHRGSLE---REAKSSFDLPDTL  1189
              ||                                          |:::|
Db   920  RRGSPEEAAEREPRRHRAHRHQDPSKECAGAKGERRARHRGGPRAGPREAESG-------  972

Qy  1190  QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----------RTLRTDDPQLDGDDNDE  1238
              :|||
Db   973  EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS  1032

Qy  1239  GNLSKGERIQAWVRSRLPACCRER--------DSW-----------------  1265
              |
Db  1033  GTVTVGP------MHTLPSTCLQKVEQPEDADNQRNVTRMGSQPPPDNTIVHIPVMLTG  1086

Qy  1266  ----------------------------SAYIPPPQSRRFRLLCHRI  1283
Db  1087  PLGEATVVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI  1146

Qy  1284  ITHKMFDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL  1343
              :: |: |:||:|: :   ::  :    |  |    | : |  |  ||||:|||  |:|
Db  1147  VTMRYFEVVILVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDL  1205

Qy  1344  GWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKIIGMLRVLRLRTIRPLRV  1402
              |                              ||: |||         |     | :
Db  1206  GLLLHPGAYFRDLWNILD---FIVVSGALVAPAFSGSKGKDINTIKSLRVLRVLRPLKT  1261

Qy  1403  ISRAQGLKLVVETLMSSLLKPIGNIVICCAFFIIFGILGVQLFKGKFYVCQGE-----D  1456
              |                                     |
Db  1262  IKRLPKLKAVFDCVVNSLKNVLNLIIVMLFMFIFAVIAVQLFKGKFYCTDESKELERD  1321

Qy  1457  TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD  1513
              ||                                                    |
Db  1322  CRGQYLDIYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE  1381

Qy  1514  QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRR  1573
              |
Db  1382  QGPSPGYRMELSIFYVVYFVVFPFFVNIFVALIIITF------QEQGDKVMSE---CS  1431

Qy  1574  LEKKRSREKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAME  1631
              |
Db  1432  LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMALNTVVLMMK  1491

Qy  1632  HYQQPQILDBALKICNYIFTVIFVFESVFKLVAPAFRRFFQDRWNQLDLAIVLLSIMGTI  1691
              ||
Db  1492  FYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL  1551

Qy  1692  LEEIB----------VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNL  1746
              ||
Db  1552  VTEIAETNNFINLS------------FLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYV  1602
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Query Match
Best Local Similarity   14.0%;   Score 1678;  DB 17;  Length 2327;
                        23.2%;   Pred. No. 1.8e-101;
Matches  620;  Conservative 378;  Mismatches 805;  Indels 872;  Gaps 87;

Qy   60 GPGAAGAGSTEKDPGSADSEAEGLP-------------------YPALAPV---      91
        |||
Db   23 GGGAGGAGG----PGQG-----GLPPGQRVLYKQSIAQRARTMALYNPI-PVKQNCPTVN  72

Qy   92 -VFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQ 150
         :|||||: : : .::  :: : ::: :.|  ::
Db   73 RSLFVFSEDNVVRKYAKRITEWPFFYMILATIIANCIVLAL---EQHLFDGDKTPMSE   128

Qy  151 AFDD----FIFAFFAVEMVKMVALG-IFGKKCYLGDTWNRLDFFVIAGMLEYS--LDL   203
        . ::    :|:.:|||:.:: ||  ||  : |  | ||: ||: ::|:
Db  129 RLDDTEPYFIGIFCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDL 188

Qy  204 QNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGVGVQ  263
        :| : ||||||:||||: : :|||||:|| ||:: |: ||:| :   |:|  |:|| :|
Db  189 R-----TLRAVRVLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGILLFFAILMFAIIGLE 243

Qy  264 LWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGE 323
              | |:  :|
Db  244 FYMGKFHKACF-----------PNSTDTFPV                              263

Qy  324 GGGGPPCSLDYETYNSSSNTTCVWNNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVI 383
        | ||| | |   : :   |:: ||:|       ||::||:|||||||::||:|:||:|.:
Db  264 --GDFPCGKDPPARQCDGDTEC-----REYWP--------GPNFGITNFDNILFAILTVFQCI 311

Qy  384 TLEGWVDIMYFVMD-AHSFYNFIYFILLIIVGSFFMINLCLVVIATOFSETKQRES---  438
        | |||.|||:|. | |  ||| |:||:||:|||||::|| ||:::|  ::.:: :
Db  312 TMEGWTDILYNTNDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLSGEFAKEREVENRRA   371

Qy  439 -QIMREQRVRFLSNASTLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAIGVRAGL 496
          :: :| : :: |  :
Db  372 FLKLRRQQQIE-----------RELNGYLEWITKAEEVMLAEED-                404

Qy  497 LSSPVARSGQEPGPSGSCTRSHRRLSVHHLVHHHHHHHHYHIGNGTLRVPRASPEIQDR  556
         :|  :.||:|||.|
Db  405 ------KNAEEKSPLDVLKRAATKKSRNDLIH------------AEEGEDR           437

Qy  557 DANGSRRIMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTV  616
                ::::|
Db  438 ------FVDL------                                            441

Qy  617 GSGGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLLETQSTGAC 676
Db  438 --------------                                              438

Qy  677 HSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSD 736
           | :::  :          ::.|
Db  442 ---CAVGSPFARAS----------------LKSGKTESSSYF------             464

Qy  737 LRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIE  796
          :::                      :|::: |:::::  |||:|||||::||||||||
Db  465 -----RRKEK--------MFRFF-----IRRMVKAQSFYWVLCVVALNTLCVAMV      502

Qy  797 YHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIV   856
         ::  |  :::  |:|| :||:| ||:|:| :||||||| || :  : ||||.||| |:
Db  503 HYNQPQRLTTALYFABFVFLGLFLITEMSLKMYLGLPRSYFRSSFNCDFGVIVGSIPEVV  562

Qy  857 GQ-----QGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFI  911
               :| |:| :||:||::||||::| :|::::||| : ||:::: |::|::|::|:||
Db  563 WAAIKPGTSFGISVLRALRLLRIFKVTKYWNSLRNLVVSLLNSMKSIISLLFLLFIVV   622

Qy  912 FSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----- 966
        |::||| |||  |  :: :   ::|:||| |  ||:||||||||:|||| |:| |
Db  623 FALLGMQLFGGQFNFQDETPT-----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGG 678

Qy  967 ASTSSWAALYFIALMTFGNYVLFNLLVALLVEGFQAEGDATKSESEPDFFSPSVDGDGR  1026
        .|:  :::|||:.|:|||||.| ||::|::|: : ||
Db  679 VSKGMFSSFYFIVLTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEA--------   729

Qy 1027 KKRLALVALGEHAELRKSLLPPLIIHTAATPMSHFKSSSTGVGEALGSGGR------   1077


Qy 1747 GLLFMLLFPIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNG 1806
        :|:::|||| |:.|||:||| :| ::|  .     ::  ||:| |:||||||:||  |:
Db 1603 CLLIAMLFFYAIIGMQVFGNIALDDD----TSINRHNNFRTFLQALMLLFRSATGEAWHE  1659

Qy 1807 IMKD--PSRDCDQE--STCVNTVISPIYFVSFVLTAQFV--------LVNV          1845
        ||    ||.||.:|   :|:::|:|||||||||::  ::
Db 1660 IMLSCLSNQACDEQANATECGSDFAYFYFVSFIFLCSFLRLVRMNMPISNEDMTVHFTST  1719

Qy 1846 VIAVLMKHLE------ESNKEAKEAELEAEL----ELEMKTLS--POQPHSP----LGSP 1889
        ::|:: |::|      |:::|::: :|::::||                    :
Db 1720 LMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDLLVPPHKPDEMTVGKV  1779

Qy 1890 F----LWPGVBGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPL-GPDLL 1944
             :::|       :|  : : .:        :|::   |::
Db 1780 YAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLF----HPLKATLEQTQPAVLRGARVF 1836

Qy 1945 TVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQ 2004
         :::|  :    |.|:  :
Db 1837 LRQKSST-----SLSNGAIQNQESGIKESV---SWGTQRTQDA--------         1872

Qy 2005 LPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD-------         2049
               :    : |   ::  : |||:  || :| |:|| : :
Db 1873 ----PHEA------RPPLERGHSTEIPVGRSGALAVDVQMQSITRRGPDGEP         1914

Qy 2050 --SLDVQLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQRSGIQSKVSKHIRLPAPC   2107
           :|:  .  : ||| :    :   ::||  : :  .: |  |
Db 1915 QPGLESQG--RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG-------THLCSTTP- 1964

Qy 2108 PGLEPSWAKDPPETRS------------SLELDTELSWISGDLLPSSQEEPLFP-     2149
                .  .   :   :|:|          :. |
Db 1965 ------DRPPPSQASSHHHHHRCHRRRDRKQRSLEKGPSLS-ADMDGAPSSAVGPGLPP  2016

Qy 2150 ------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPS----  2197
               :: : |  : :  ||||    :  :|.:    : :    :||
Db 2017 GEGPTGCRRERERRQERGRSQERRQFSSSSSEKQRF----YSCDRFGGREPPKPKPSLSSH 2073

Qy 2198 -------SLGGQPL-----------GGPGSRPKKKLSP-PSISIDDPPES         2227
               ::|| || :                 |  ::|  || : | :  :
Db 2074 PTSPTAGQEPGPHPQQSGSVNGSPLLSTSGASTPGRGGRRQLPQTPLTPRPSITYKTANS  2133

Qy 2228 ------QGSRPPCSPG-----------VCLRRRAPASD-----SKDPSVSSPLDSTA   2262
              ||:| ||.                  : ::||:::|      ||| |||| ::|
Db 2134 SPIHFAGAQTSLPAFSPGRILSRGLSREHNALLQRDPLSQPLAPGSRIGSDPYLGQRLDSEA 2193

Qy 2263 ASPSPKKDTLSL------------SGLSS                               2279
         :  |::|:|:|            |:|:|
Db 2194 SVHALPEDTLTFEEAVATNSGRSS                                    2217
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RESULT 15
US-10-735-883-38

; Sequence 38, Application US/10736883
; Publication No. US20040214238A1
; GENERAL INFORMATION:
; APPLICANT: LIPSCOMBE, Diane
; APPLICANT: BELL, Thomas
; APPLICANT: THALER, Christopher
; APPLICANT: CASTIGLIONI, Andrew
; TITLE OF INVENTION: NOCICEPTIVE NEURON-SPECIFIC CALCIUM CHANNEL ISOFORM AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: B0877.70026US00
; CURRENT APPLICATION NUMBER: US/10/736,883
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/443,474
; PRIOR FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 2327
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-736-883-38

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Qy   730  :|||  |  |: |    :                        :
          NQKLALQKAKEVAEV--SPMSAANISIAARQQNSAKARS--VWEQRASQLRLQNLRASCE  785

Qy  1078  ------------RTSSSGSAEPGAAHH------EMKCPPSARSSPHSPWSAASS  1113
                                              :    :: |||  |:
Db   786  ALYSEMDPEERLRYASTHVRPDMKTHMDRPLVVEPGRDGLRGPVGSKSKPEGTEATESA  845

Qy  1114  WTSRRSSRN------SLGRAP----------SLKRRSPSGE-----------  1138
          ||||  ||||                     : : |||||||
Db   846  DLPRRHHHRDRDKTSATAPAGEQDRTESETGAREERARPRRSHSKETPGADTQVRCE  905

Qy  1139  --RRSLLSGEGQESQDEE------------ESSEEDRAS---PAGSDH-RHRG--SLEREA  1179
            |::                         :|||
Db   906  RSRRHHRRGSPEEATEREPRHRAHRHAQDSSKEGTAPVLVPKGERRARHRGPRTGPREA  965

Qy  1180  KSSFD------------LPDTLQVPGLHRTASGRSSASE-----------HQDCNGKSAS  1216
          ::::
Db   966  ENNEEPTRRHRARHKVPPTLQPPE-REAAEKESNAVEGDKETRNHQPKEPHCDLEAIAVT  1024

Qy  1217  G-----RLARTL--RTDDPQLDGDDDND-----------------------  1237
Db  1025  GVGPLHMLPSTCLQKVDEQPEDADNQRNVTRMGSQPSDPSTTVHVPVTLTGPPGETPVVP  1084

Qy  1238  EGNI------SKGER------IQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIIT  1285
          ||:                  |||||  |:                   ::|| :||||
Db  1085  SGNMNLEGQAEGKKEAEADDVLRRGPRPIVPYS------SMFCLSPTNLLRRPCHYIVT  1137

Db  1286  HKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIPLTLSNYIFTAVFLAEMTVKVVALGW  1345
          :  |:|:| ||||| |: :::||    :|   :|:|||||| :::|:|||||| |: :::
Qy  1138  MRYFEMVILVVIALSSIALAAEDP-VRTDSFRNNALKYMDYIFTGVFTFEMVIKMIDLGL  1196

Db  1346  CFGEQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRLRTLRPLRVIS  1404
          ||:| ||||  ||||||:||:|:||:| :|:   ||::|||| |||:||||||:| :
Qy  1197  LLHPGAYFRDLWNILDFIVSGALVAFASSFMGGSKGKDINTIKSLRVLRVLRPLKTIK  1256

Db  1405  RAQGLKLVVETLMSSLKPIGNIVVICCAFFIIPGIIGVQLFKGKFFVCQGB------DTR  1458
          | : |||||  :   ||:|:|: ||| |||| ||:||||||||||||  :         |
Qy  1257  RLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCR  1316

Qy  1459  N-IITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQ  1515
          | || :||  ||  :| |  |:||| ||| ||:| :|  |:||||::: ::|||: ::||
Db  1317  GQYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDAIYEEQG  1376

Qy  1516  PIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRIRRLE  1575
          |  ::||   | ||:|:  :|:||:| ||    |||:||  :|| ::     |:: :::
Db  1377  PSPGFFMELSIFYVVFYVVFPFFVNIFVALIIITF------QEQGDKVMSE-----CSLE  1426

Qy  1576  KKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHY  1633
          |:  : ::  |    |||:  :   : |  :: |:::::|::||:|:| ||::|:|:: :
Db  1427  KNERACIDFAISAKPLTRYMPQNKSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFY  1486

Qy  1634  QQPQILDEALKICNYIFTVIFVPESVFKLIVAFAFRRFFQDRWNQLDLAIVLLSIMGITLE  1693
           : |  :|||:|||:||  :||  ||||||:|| :| ||:|:||:|| ||||| |||| |:
Db  1487  DAPYEYELMLKCLNIVFTSMFSMECILKIIAFGVLNYFRDAWNVFDFVTVLGSITDILVT  1546

Qy  1694  EIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLL  1753
          ||     | ||| ||||:||||||| |||:|: || ||||:|: | | ||||:||::||
Db  1547  EIANNF---IN---LSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAML  1600

Qy  1754  FFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWNGIMKD--P  1811
          |||:| :|:|:||::  |   |   | : :|||| | |::||||||| :||:  | |   |
Db  1601  FFIYAIIGMQVFGNIALDDD---TSINRHNNPRTFLQALMLLFRSATGEAWHEIMLSCLG  1657

Qy  1812  SRDCD----QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM-----------KH  1853
          ::: ||    |:  :   :|||||||||: ||| :|:|:|||:|           |:
Db  1658  NRACDPHANASEC-GSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHH  1716

Qy  1854  LEE-------------
          :|:
Db  1717  LDEFIRVWAEYDPAACGRISYNDMPEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISNE  1776

Qy  1857  ------SNKEAKEAELEAEL------ELEMKTLS--PQPHS  1884
               : :  ||| |||||       |:|
```

```
Db  1777  DMTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISSVWANLPQKTLDLLVPPHK  1836
          :|||                         :     :                :      :
Qy  1885  P-----LGSPF--LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVP  1936

Db  1837  PDEMTVGKVYAALMIFDFYKQNKTTRDQTHQAPGGLSQMGPVSLF---HPLKATLEQTQP  1893
          |||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Qy  1937  VPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWG----------  1980

Db  1894  AVLRGARVFLRQKSAT--SLSNGGAIQTQESGIKESL--SWGTQRTQDALYEARAPLE  1947
          :: |||:|:| |::                                     : :
Qy  1981  ------LPKAQSGSI-----------------------------------LSVHSQPADTSC  2001

Db  1948  RGHSAEIPVGQSGTLAVDVQMQNMTLRGPDGEPQPGLESQGRAASMPRLAAETQPAPNAS  2007
                  :||:                                  :||:|||:||:|||:
Qy  2002  ILQLPKDVHYLL-QPHGAPTWGAIPKLPPPG---------RSPLAQRPLRRQAAIRT  2048

Db  2008  --PMKRSISTLAPRPHGTQLCSTVLDRPPSQASHHHHHRCHRRRDKKQRSLEKGPSLSV  2065
            ||:                                   ::: :||||||||||||||
Qy  2049  DSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCP  2108

Db  2066  DP-------EGAPSTAAGPGLPHGEGSTACRRDRKQERGRSQERRQPSSSSSEKQRFY  2116
          ||                                                     :
Qy  2109  GLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCCYSVETQSCRRRPG  2168

Db  2117  SCDRFGSREPPQ---------------LMPSLSSHPTSP---------------  2140
          |:                         :||||| |||||
Qy  2169  FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPL---------GGPGSRPKKKLSP  2217

Db  2141  ----------TAALEPAPHPQ---GSGSVNGSPLMSTSGASTPGRGGRQLPQTPLTP  2185
                    :|||||||||||
Qy  2218  -PSIS--------IDPPESQGSRPPCSPG---------VCLRRRAPASD-------SKD  2251

Db  2186  RPSITYKTANSSPVHFAEGQSGLPAFSPGRLSRGLSEHNALLQKEPLSQPLAPGSRIGSD  2245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2252  PSVSSPLDSTAASPSPKKDTLSL--------SGLSS  2279

Db  2246  PYLGQRLDSEASAHTLPEDTLTFEEAVATNSGRSS  2280
          |||||||||||||||||||||||||||||||||||
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Search completed: November 18, 2004, 13:58:59
Job time : 208.328 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:21 ; Search time 50.7329 Seconds
                                      (without alignments)
                                      4337.375 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR..........KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Database :   PIR_79:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match	Length	DB	ID		Description
1	11657	96.9	2254	2		T09053		low voltage-activa
2	3553	29.5	1657	2		T15838		hypothetical prote
3	1720.5	14.3	1810	2		T31092		probable voltage-g
4	1676	13.9	2339	2		A42566		omega-conotoxin-se
5	1665.5	13.8	2259	2		S29236		calcium channel pr
6	1653.5	13.7	2272	2		C54972		voltage-dependent
7	1652.5	13.7	1891	2		T43262		calcium channel al
8	1652.5	13.7	2178	2		S29237		calcium channel pr
9	1650.5	13.7	2288	2		S41080		calcium channel al
10	1642	13.7	2223	2		A47447		calcium channel al
11	1640.5	13.6	2237	2		T45115		N-type calcium cha
12	1638	13.6	2251	2		B54972		voltage-dependent
13	1637.5	13.6	2270	2		A54972		voltage-dependent
14	1636	13.6	1993	2		T30902		sodium channel SCA
15	1632.5	13.6	2222	2		A37490		voltage-dependent
16	1632.5	13.6	2336	2		A45386		omega-conotoxin-se
17	1631	13.6	2181	2		A38198		calcium channel al
18	1628	13.5	1873	2		A30063		dihydropyridine re
19	1622	13.5	2161	2		JH0564		calcium channel al
20	1619.5	13.5	1911	2		T43048		calcium channel al
21	1616	13.4	1852	2		A37860		calcium channel pr
22	1614.5	13.4	1977	2		S54771		sodium channel alp
23	1613	13.4	2203	2		T42742		voltage-dependent
24	1610	13.4	2143	2		JH0427		voltage-dependent
25	1603	13.3	1610	2		A46227		probable voltage-d
26	1595.5	13.3	1783	2		T37258		calcium channel pr
27	1595	13.3	2166	2		S11339		voltage-dependent
28	1592.5	13.2	2139	2		A44467		voltage-dependent
29	1587.5	13.2	1646	2		JH0422		

30	1587.5	13.2	1873	2		A55645		calcium channel, v
31	1585.5	13.2	2016	2		A38195		sodium channel pro
32	1580	13.1	1917	2		C88728		protein C48A7.1 [i
33	1577.5	13.1	1559	2		T30535		calcium channel al
34	1574	13.1	2171	2		S05054		calcium channel al
35	1573	13.1	2108	2		S72458		sodium channel pro
36	1567.5	13.0	1687	2		S41742		calcium channel al
37	1565	13.0	1957	2		S68453		sodium channel pro
38	1557.5	12.9	2220	2		A45290		calcium channel pr
39	1556	12.9	2019	2		A33996		sodium channel pro
40	1551.5	12.9	1840	1		CHRTM1		sodium channel pro
41	1549	12.9	1976	2		I56555		sodium channel pro
42	1546.5	12.9	1983	2		A60054		sodium channel pro
43	1546	12.9	2262	2		T30890		calcium channel al
44	1544.5	12.8	1951	2		S00320		sodium channel pro
45	1544.5	12.8	2005	2		A46269		sodium channel alp

ALIGNMENTS

RESULT 1
T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09053
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox,
  Nature 391, 896, 1998
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium
A;Reference number: Z16538; MUID:98154730; PMID:9495342
A;Accession: T09053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2254 <PER>
A;Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Map position: 17
A;Note: CACNA1G
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel; voltage-gated ion channel

Query Match   96.9%;   Score 11657;   DB 2;   Length 2254;
Best Local Similarity   96.9%;   Pred. No. 0;
Matches 2219;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
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Db   30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy   122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKKCYLG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKKCYLG 149

Qy   182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLP 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLP 209

Qy   242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy   302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYTNCSAGEHN 361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYTNCSAGEHN 329

Qy   362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy   422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFERPGSCYEELLKYLVYILRKAAR 481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Qy  1552 EARRREEKRLRLREKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1621
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1530 EARRREEKRLRLREKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1589

Qy  1622 GLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA 1681
         |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  1590 GLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLVAFGRRRFFQDRWNQLDLA 1649

Qy  1682 IVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1650 IVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1709

Qy  1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1710 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1769

Qy  1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1861
         |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1770 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1829

Qy  1862 KEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1830 KEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889

Qy  1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1890 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1949

Qy  1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQCRPLR 2041
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1950 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQCRPLR 2009

Qy  2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2010 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2069

Qy  2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2161
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2070 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2129

Qy  2162 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2221
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2130 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2189

Qy  2222 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2281
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2190 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2249

Qy  2282 TDMDP 2286
         |||||
Db  2250 TDMDP 2254
```

```
Db   390 CLVVIATQFSETKQRESQLMEEQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy   482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGGSCTRSHRRLSVHHLVHHHHHHYHLGN 541
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGGSCTRSHRRLSVHHLVHHHHHHYHLGN 509

Qy   542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy   602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEIIKDKALVEVAPSPGPPTLTSFNIPPGPF 661
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEIIKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy   662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy   722 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   690 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy   782 IMIAILVNTLSMGIEYHQEPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN 841
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   750 IMIAILVNTLSMGIEYHQEPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN 809

Qy   842 IFDGVIVISVWEIVGQQGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKIMDNVATF 901
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   810 IFDGVIVISVWEIVGQQGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKIMDNVATF 869

Qy   902 CMLMLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870 CMLMLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy   962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

Qy  1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy  1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1109

Qy  1142 LLSGEQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1110 LLSGEQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy  1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy  1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy  1322 TLSNYIFTAVFLAEMTVKVKVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1290 TLSNYIFTAVFLAEMTVKVKVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

Qy  1382 TKILGMRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLG 1441
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1350 TKILGMRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLG 1409

Qy  1442 VQLFKGKPFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1410 VQLFKGKPFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy  1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529
```

RESULT 2
T15838
T15838 hypothetical protein C54D2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: T15838
R;Minx, P.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid C54D2.
A;Reference number: Z18415
A;Accession: T15838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1657 <MIN>
A;Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D
C;Genetics:
A;Gene: CESP:C54D2.5
A;Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 51
C;Superfamily: sodium channel protein

```
Query Match      29.5%;    Score 3553;    DB 2;    Length 1657;
Best Local Similarity      42.2%;    Pred. No. 1.3e-217;
Matches    800;    Conservative    234;    Mismatches 436;    Indels    426;    Gaps    42;

Qy   66 AGSTEKDPG---------SADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCN 112
                     :: ::::::||||||| :: :|| :||  ||  :  :  :||
Db   88 ASSSEASPSRWEGRQIEWNGNEEQIEEESE-LPYPGFAEPALRCFYQARPPRKWALQMVMS 146

Qy  113 PWFERVSMLVILLNCVTLGMFRPCED-IACDSQRCRILQAFDDFIFAFFAVEMVVKMVAL 171
         |||:|::| :|:|||||||||:|||    | ||||||||: || :|||||||:::||||
Db  147 PWFDRITMAVIMNCVTLGMYRPCEDGPDCDTYRCQILDIIDNCIFVFAFEMVIKIMAL 206

Qy  172 GIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQ--NVSFSAVRTVRVLRPLRAINRVPS 228
         |::|   ::|||||||||||:||:  |::||:|   |: ::||||||||||||| ||:|||
Db  207 GFYGPAAYMSDTWNRLDFFIVMAGIAEFVLHEYIGGNINLTAIRTVRVLRPLRAVNRIPS 266

Qy  229 MRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCF--LPENFS-----L 281
         ||||| ||||||||||||||||||||||||||||||||||||||    || : |     |
Db  267 MRILVNLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCVINLPKTISENQSAL 326

Qy  282 PLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSS 341
              : : || :   :   | |||| :||:   | :        |    :|:|:|||
Db  327 FNNVKLTRFYIPE-DTSLEYICSQPDANGLHTCSNLPPYTVD---GVKCNLTLDEYDKVT 382

Qy  342 NTTCVNWNQYYTNCSAG---------EHNPFKGAINFDNIGYAWIAIFQVIT 384
           :| ||| |  ||                | |:| |||||:||:||| :|:
Db  383 NDSCINWNIYNECQVNIYPSLMTIAISCFIKVMQRNPFQGSVSFDNIGFAWVAIFLVIS 442

Qy  385 LEGWVDIMYFVMDAHSFYNFYFIFLLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQ 444
         ||||.|||| |.|||||:|:||:|:|||| :||||||||||||||||:|||:||| ||:
Db  443 LEGWTDIMYYVQDAHSFWNWIYFVLLLIVIGAFFMINLCLVVIATQFAETKRRETERMLQE 502

Qy  445 RVRFLSNASTLASFSEPG---------SCYEELLKYIVIYILRKAARRLAQVSRAIGVRAG 495
         | :::   : ::   : :         :  :: :  :  ::     :
Db  503 RKMLLNRDSISCTGSEIGGASSKEEGDTVYAAFVRFIGHTFRRTKRAAKKKYTAY----- 557

Qy  496 LLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVVHHIVHHHHHHHYHLGNGTLRVPRASPEIQD 555
                :                  :
Db  558 ------MEERAERKSSERQQRRKSKL------------------DDMATILSRIEEKAED 592

Qy  556 RDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRT 615
          :
Db  593 EE----------DETTITRENGDDQIEQN------------------------------ 611

Qy  616 VGSGKVYPFTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGA 675
              :  :
Db  612 -GDGVRIKRVKIEEPKI-------------------------------------------- 628

Qy  676 CHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHS 735
               :                             :           :
Db  629 -----------------KIGNGNSNGPHYKHSSSDEES---DEDGEED 656

Qy  736 DLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMTAILVNTLSMGI 795
         :         : : :|      |: :    |:|  |:| :|     |:|:|||||||||
Db  657 QVYDGEEAKKK------STPSKL--WW--FREKIQKFVICDHFTRGILVAILVNTLSMGV 706

Qy  796 EYHQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGVIKNPYNIFDGVIVVISVWEI 855
         |||| | :  : :|: :|| ||||||||| :: :| | : |:|:|||||:|:|:|:|
Db  707 EYHQQPEIITVIILEYSNLFFTALFALEMLLKIIASGLFGYLADGFNLFDGGIVALSVLEL 766

Qy  856 VGQQGGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIL 915
         . : ::|||||||||||:|:|||||||||:| |||||:|:||||: | :|||:|:|||||
Db  767 FQEGKGGLSVLRTFRLLRILKLVRFMPALRYQLVVMLRTMDNVTVFFGLLVLFIFIFSIL 826

Qy  916 GMHLFGCKFASERD--GDTLP--DRKNPDSLLWAIVTVFQILTQEDWNKVLYNGMASTS 970
         || ||||||   :    :    |::: |:|::|:: |||||||||||| ||:|||| |
Db  827 GMLFGCKFCKVEEKFLGGLAKKCCERKNFDTLIWALIITVFQILTQEDWNMVLFNGMAQTN 886

Qy  971 SWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRL 1030
          |||||| ||||||||||||||||||||||| |    |:: ||:|  |||| || ||:|
Db  887 PWAALYFVALMTFGNYVLFNLLVAILVEGFQESKEEEKRQLEEDARKQAVEEEDERKREL 946


Qy 1031 ALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSSGSRRTSSGSAEPGAA 1090
         |:|
Db  947 ELII----------------------------------------AKTTSPAFNNGVA 963

Qy 1091 HHEMKC--PPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG---ERRSLL 1143
                :: ::|         :            :    :||:
Db  964 PAECTCQRPSSPEESP-SPRLLSANY----------------HPSPERKHSANLDAIIDKRLVL 1010

Qy 1144 SGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFPDLPDTLQVPGLHRTASGRSS 1203
                ::  : ||    :     | :|  :      : : :|
Db 1011 ------RNSAPPDR-SPV--SSGRDSRLNRHA--SLVLPVANGVP-- 1045

Qy 1204 ASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVSRRL-PACCRER 1262
          :       :  :  | : : :   :            :       :|
Db 1046 -YRRQRVHSWKASQELKQALAEEERKNEAKQN-------------------TFVRKLLKKTCLHNR 1091

Qy 1263 DSWSAYIFPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLT 1322
          :: :  :   : |:   :|: : :|||:|| : |:||||:||||| | | : ||:|
Db 1092 TEFSLFLMGPKNPLRIKCLQTTQKKWFDYTVLFPIGINCITLAMERPSIPPDSFERQFLH 1151

Qy 1323 LSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGT 1382
         :| ||||:: | || :|
Db 1152 ISGYIFTVIFTGEMMMK---------------------------------------------- 1168

Qy 1383 KILGMLRVLRLLRTLRPLRVISRAQGLKLVVETIMSSLKPIGNIVVICCAFFIFGILGV 1442
                             :          ||:|||||| ||| :|||:|||||
Db 1169 --------------------VSHRIPTLKPIGNIVLICCTFFIIFGILGV 1198

Qy 1443 QLFKGKFFVCQGEDTRNITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWV 1500
         |||||  : || | ::: | :|| |  : | ||:::||||||||||||||||:|||||
Db 1199 QLFKGMMYHCIGPEVGNVTTKADCIE-DYRNKWVNHRYNFDNLGQALMSLFVLSSKDGWV 1257

Qy 1501 DIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE 1560
         .|||.|:|||||| ||:  :| |:::||||||:|.|||||||||||||||||||| : |:
Db 1258 SIMYQGIDAVGVDVQPIENYNEWRMIYFISFLLLVGFFVLNMFVGVVVENFHKCKEALEK 1317

Qy 1561 EEARRREEKRLRLEKKRRSKEKQMAEAQCK------------------PYYSDYSRF 1600
         | ::: |:|:|:  :||:|:|| :: : |:                  |||:||  
Db 1318 EMREKEKEKRLKR-KLKRQKFEESMAGKRKKNRIVWAGSAIKSFSVERNYPYYHDYGHT 1376

Qy 1601 RLLVHHLCTSHYIDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVF 1660
         ||::|::.||:| || | |||| ||:.||||:|  | |:| ||| ||:|| ||| ||:
Db 1377 RLFLHGIVTSKYFDLAIAAVIGINVISMAMEFYMPMGLKYVLKALNYFFTAVFTLEAAM 1436

Qy 1661 KLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVL 1720
         || : .||||| ::|| ||: :|:|||.|| ||:|  | ||||||||||:||||||||||
Db 1437 KLIALGFKRFFIEKWNRLDMFTVILSIAGIIFEEFEA-LELPINPTIIRVMRVLRIARVL 1495

Qy 1721 KLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLG 1780
         |:|||| |:| |||||:|||||||||| ||:||||||||||||||| ||| | ||| ||||
Db 1496 KJLKMAKGIRSLLDTVGEALPQVGNLGSLFFLLFFIFAALGVELFGKLECSEDHPCDGLG 1555

Qy 1781 RHATPRNFGMAFLTLFRVSTGDNWNGIMKDPSR-DCD------QESTCYNTVISPIYFVSF 1834
          ||: :||||||||||||::|||||||||| .| |||      |:: | :|  :||||:|
Db 1556 EHAHFKNFGMAFLTLFRIATGDNWNGIMKDALRDDCDSSDHCETNCCVDPILAPCFFVIF 1615

Qy 1835 VLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAE 1870
         |||:||||.|||:||||||||||   : |:|| ||
Db 1616 VLISQFVLNVVVAVLMKHLEESN--KRDAEGPAE 1648
```

RESULT 3
T31092
probable voltage-gated sodium channel - Aiptasia pallida
C;Species: Aiptasia pallida
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T31092
R;White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.
A;Description: Structure of a putative sodium channel from the sea anemone Aiptasia palli
    submitted to the EMBL Data Library, January 1998
A;Reference number: Z20975
A;Accession: T31092
A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Molecule type: mRNA
A;Residues: 1-1810 <WHI>
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g27791840; PID:g27791841; PIDN:AAB9
C;Genetics:
A;Gene: NaI
C;Superfamily: sodium channel protein

Query Match     14.3%;  Score 1720.5;  DB 2;  Length 1810;
Best Local Similarity  25.8%;  Pred. No. 6.2e-101;
Matches  509;  Conservative 342;  Mismatches 694;  Indels 429;  Gaps 65;

Qy   110 VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF-AFFAVEMVVKM 168
Db   110 ITNQFFEFFILLTIIVVNCIFLAL------------RDAPEQPEYVFAAIYTFEMLLKI 155
Qy   169 VALG-IFGKKCVLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINVP 227
Db   156 IAKGLVMHEYAYLRDPWNWLDFVVVILGVTLVPNVANL--SGIRIFRVLRALRTISAVE 213
Qy   228 SMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDL 287
Db   214 GLKTMVNALLKSMKMLSDVLILTFFLCFVFALVGMQLFVGSLRNKCVLKPPLNTIDYDS 273
Qy   288 ---EPYYQTENEDBESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNT 343
Db   274 FVTNESHWVHHPDTDTPITC--------------GNSTSAGPCPLNY----------- 306
Qy   344 TCVNWNQYYTNCSAGEHNPPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN 403
Db   307 TCL-----ANIG-NNPNYGYTNLDNFGWAVITAFQLVTLDYWENVINYVLSSMGSWY 357
Qy   404 FIYFLLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGS 463
Db   358 IFYFFMVIFFGSFYLLNLVLAVVAVSY-----QOBVLALQDRENYYNNLKGVASLYSFHG 412
Qy   464 CYEBELLKYLVLYILRKAARRLAQVSRAIGVRAGL-LSSPVARSGQEPQPSGSCTRSHRRLS 522
Db   413 C-------VVPKLLRNSKSKTKSLASKCKMSFCVPCFSIGKQPEHSNG------- 453
Qy   523 VHHLVHHHHHHHYHLGNGILRVPRASPE---IQDRDANGSRRLMLPPPSTPTPSGGPP 579
Db   454 ----HASDNESSHASTG-GTIRVDSTAIEMKMLNDKNEVRTNGHSLPEPKT----- 499
Qy   580 RGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKAL 639
Db   500 SSFF------------------SVSSDN--SIH-------IRMNSS 518
Qy   640 VEVAPSPGPPTLTSF--NIPPGPFSSMHKLLETQSTGACHSSCKISSPCKADSGACGPD 697
Db   519 TEVMPQ-----TSKFDDNI------LTKTLDVKS-------SFLRKLSAISEQSS 555
Qy   698 SCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDACHSDLRDPHSRRRQRSLGPDAEPSS 757
Db   556 -----TDGVDNNENINNTQPQKSVSFIARV--------LTPRGSLARQTSTGSATHHKT 601
Qy   758 VI---AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELINALEISNIV 814
Db   602 ITKQDTKWNRIRRMISKIVLHGYMDTFITFCTWVNTLFLSLEYHNMDSNYLMVLEIGNKV 661
Qy   815 FTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWE------IVGQQGGLSVLRTF 869
Db   662 FTMVFLLEMILKITAFGKGYIKSRWNIFDGFIVVISMVDLMVELLVDDHDSGLSVLRTF 721
Qy   870 RLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD 929
Db   722 RLLRVFKLAQSWQTMNMLLSTIARSVGQLGNLTILVLGIVIYMLAVVGVQLFDCYYTTKNF 781
Qy   930 GDTLPDRKNFDSLLWAIVTVFQILLTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLF 989
Db   782 NGDVP-RWNFTDFWHSFMNIFRVLCGE-WIEPLYWCMRASTSWATLFLUTTLVIGNFLVL 839
Qy   990 NLIVAILVBGFQAEG---DATKSESEPDFFSPSVDGDGDRKKRKLAIVALGEHAELRKS-- 1044
Db   840 NLFLALLNAFARESLEQEAKKKTKKPSKFAQGV------SKLSR-ALRFRSTVSKTQ 891
Qy  1045 LLPPLIHTAATPMSHPKSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSP 1104
Db   892 ------GENATDGDK-----------APTVQNGL 917
Qy  1105 HSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGE------RRSLLSGEGQESQDEESSE 1158
Db   918 ESKTSDSAISTSSNASNAMISAVTAFQQGNKKGKLNRDTFRRLSLAIE------ 965
Qy  1159 EDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGR 1218
Db   966 -----TANSDSNTSNVLAMAASST-----------------SITGR 989
Qy  1219 LARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAVI-FPPQSRFR 1277
Db   990 ------QDHGTSDPPDPMTEVDECCPWCMNKMTCGCITR--WKASDGYRSWRNLR 1037
Qy  1278 LLCHRIITHKMPDHVVLVLIIFLNCITIAME-------RPKIDPHSAERIFLTLSNVIFTAV 1331
Db  1038 LAVKKFVEHYFEWTLIAIIMASSIALTFEDINLPSRPKL------KEYLQYLNIFFAVT 1091
Qy  1332 FLAEMTVKVALGWCFGEQAYLRSSWNVLDGLLLLISVIDILVSMVSDSGTK--IIGMLR 1389
Db  1092 FSIEFLLKVLGL----GVVSYFRNCWNCLDVLIVFPV---SSVIADSSNQDSSLSSLR 1143
Qy  1390 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIFGILGVQLFKGKF 1449
Db  1144 SLRTLRALRPLRAISRWEGMRVVVNSLLFAIPGIGNVLLVCMVFWLLIFSIMGVQFGGRF 1203
Qy  1450 FVCQEGDTRN------ITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMY 1504
Db  1204 FKCVDNNKERLPISIVQNRSECIQKGYRWVNSDINFDNSLNGFMALFQVATFEGWIEVMR 1263
Qy  1505 DGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE---- 1560
Db  1264 DAVDAREVDQQPSDGYNFSAYAYFVVFIIVGSFFTLNLFIGVIIDNFNRLKKKQYEDFGAL 1323
Qy  1561 ----EEARRREKRLRRLEKKRSKEKQMAEAQCKPYYSDY--SRFRLLVHHLCTSHYL 1613
Db  1324 DVLLTPSQRAWFGTIRKAATKPKKVISRPENSFMAWLFDVIHSSRFETLI-------- 1374
Qy  1614 DLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQD 1673
Db  1375 -MFF---ICLNILVMMIQHYGQKPAVEQALMIINLVFTGLFTLEAILRIVLRL-HYFRE 1429
Qy  1674 RWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALL 1733
Db  1430 PWNVFDFVIVILSILGIILEHLEYELFTTPSPF---VARVFRIGRLLRFYKGAKGIRRLL 1486
Qy  1734 HTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFL 1793
Db  1487 FALIISLPALLNIGALLFLIMFIYAIIGMSSFGYVK----KTGALDSVVNFETFGNSML 1541
Qy  1794 TLFRVSTGDNWNGIMKD----PSRDCDQE------STCYNTVISPIYFVSFVLTAQFVLVN 1844
Db  1542 LLFRLSTSAGWNDVLKPLLIKPPDCDKKLWCIPNGNCSTPWLAVVFTTFILFTTFLIIIN 1601
Qy  1845 VVIAVLMKHLEESNKEAKEAEAELEMKTLSPQFHSPLGSPFLWPGVEGVNSTDSP 1904
Db  1602 MYIAILLENLSQAH-EQEEVGVTDDLDMFY-------YHWERFD-- 1638
Qy  1905 KPGAPHTTAHIGAASGF---SLEHPTMVPHPEE-----VPVPLGPDLLTVRKSGVSRTH 1955
Db  1639 -PGATQYIPH-SALSDFVDGLDHFLRIPQPNKFACINLNIPIKQ----DRVH 1685
Qy  1956 SSSVAYTLMKSKMEQHCISTFPK 2007
Db  1686 CFDVMQALVRRVLGDIEEDGLG------ 1730
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RESULT 4
A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively splic
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: A42566
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC
Science 257, 389-395, 1992
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-typ
A;Accession number: A42566 MUID:92335886; PMID:1321501
A;Reference number: A42566
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2339 <WI1>
A;Experimental source: IMR32, hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:109168)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   13.9%;   Score 1676; DB 2; Length 2339;
Best Local Similarity   24.0%;   Pred. No. 6e-98;
Matches   638; Conservative   364; Mismatches   827; Indels   824; Gaps   88;

Qy   59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-------VFFYLSQDSRPRSWCLRT 109
               |||: ||| :|:: ||||||
Db   32 PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI 91

Qy   110 VCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV 166
               |||: | |: | || || | |: :| :| | ||||||
Db   92 TEWPPFEYMILATTIANCIVLALL---EQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI 147

Qy   167 KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA 222
                  || ||| | | || |||: | |: | | | | |:|
Db   148 KIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR----TLRAVRVLRPLKL 202

Qy   223 INRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP 282
               |::: : : | | ||||: | | | | |||| | :| | || | || |
Db   203 VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF------P 255

Qy   283 LSVDLEPYYCQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSN 342
                                                             |||
Db   256 NSTDAEPV--GDFPCQKEAPARLCEGD 280

Qy   343 TTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWTAIFQVITLEGWVDIMYFVMD-AHSF 401
                |: ||: : | ::| | : ||||: |
Db   281 TEC---REYWP------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT 330

Qy   402 YNFIYFILLIIVGSFFMINLCLVVIATOFSETKQRES------QLMREQRVRFLSNASTL 455
               |:|:| ||:| ||||:|| |||| :| |: |: : | || |:
Db   331 WNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE------ 382

Qy   456 ASFSEPGSCYEELLKYLVVLIRKAARRLAQVSRAIGVRAGLLSSPVARSQEPQPSGSCT 515
                      : | :: :: | :
Db   383 -----------RELNGYLEWIFKAEEVMLABED------RNAEEKSPLDVLK 417

Qy   516 RSHRRLSVHHLVHHHHHHHHHHYHIGNGTLRVPRASPEIQDRDANGSRRIMLPPSTPTPS 575
               | | |:
Db   418 RAATKKSRNDLIH---------------AEEGEDRFAD----------------- 440

Qy   576 GGPPRGABSVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSSKVYPTVHTSPPEEIIK 635
               | | | |||||| |
Db   441 -----------------LKSGKTESSSYF-------RRKEK----- 469

Qy   636 DKALVEVAPSGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG 695
                                       :: || :
Db   441 -----------------------------LCAVGSPFARAS----- 452

Qy   696 PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEP 755
               | || | | | :   : | |
Db   453 ----PDSCPYCARTGAGEPESADH-------RRMKKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLYFABFVF 521

Qy   756 SSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNIVF 815
               ::|| | | :   :   : | |
Db   470 --MFRFF---IRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLYFABFVF 521

Qy   816 TSLFALEMLLKLLVYGPFGYIQNPYNIFDGVIVISVWEIVG--QQQG--GLSVLRTFR 870
               |: |:: | |
Db   470 FYDAPYEYELMLKCLNIVFTSMSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL 521

Qy   871 LMRVLKLIVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFISLGMHLFGCKFASERDG 930
               |: |:|| | :   :| |: |:|| |
Db   522 LGLFLTEMSLKMYGLGPRSYPRSSFNCFDFGVIVGSVFEVVWAAIKPGGSFGISVLRALR 581

Qy   931 DTLPDRKNFDSLLWAIVTVFQILTOEDWNKVLYNGM---------ASTSSWAALYFIALMTFGN 985
               || | | | | | | | | | |: |: || |:||
Db   582 LLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFIVFALLGMQLFGGQFNFQDET 641

Qy   986 YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSL 1045
               | | : | : | : |:|
Db   642 PT----TNFDTFPAAILTVFQILTGEDWNAVMYHGLESQGGVSKCMFSSSYFIVLTLFGN 697

Qy   1046 LPPLIIHTAATPMSHPKSSSTGVGBA--------------- 1071
               |
Db   698 YTLLNVFLAIAVDNLANAQELTKDEEMEEAA-----NQKLALQKAKEVAEV--SP 746

Qy   1072 ----------------------LGSGRRTSSSGSAEPGAA----------HH------EMKCP----- 1097
                                     || : |: |
Db   747 MSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLR 806

Qy   1098 ----------------PSARSS---PHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSL 1142
                               |: | | : |: |||
Db   807 PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRDKDKTPAAGDQ 866

Qy   1143 LSGEGQESQDEE----------ESSEEDRASPAGSDHRHRGSLE---REAKSSFDLPDTL 1189
               | : | | | | |
Db   867 DRAEAPKAESGEPGAREERPRPHRSHSKEAA--GPPEARSERGRGP------GPEGGRRHH 919

Qy   1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA----RTLRTDPDQLGDGDDNDE 1238
               | : | |: ||
Db   920 RRGSPEEAAEREPRRHRAHRHQDPSKECAGAKGERRARHRGGPRAGPREAESG------- 972

Qy   1239 GNLSKGERIQAWVRSRLPACCRER-----------------DSW--------------- 1265
               |
Db   973 EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032

Qy   1266 ----------------------------SAYIFPPQSRFRLLCHRI 1283
                                           | |||:|
Db   1033 GTVTVGP----------MHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTG 1086

Qy   1284 ITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343
               : ||||| | | || | | | :| ||| :|| ||: |:||
Db   1087 PLGEATVPSGNVDLESQABQKKEVBADDVMRSGPRIVPYSSMFCLSPTNLLRRFCHYI 1146

Qy   1344 GWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRV 1402
               | | ||| | :| | :| |||| | | |||||||:||:| | |
Db   1147 VTMRYFEVVILVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFFEMVIKMIDL 1205

Qy   1403 ISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE-----D 1456
               | | | |: | ||| | | || |||||||||||||||: | |
Db   1206 GLLLHPGAYFRDLWNILD---FIVVSGALVAFAFSGSKGKDINTIKSLRVLRVLRPLKT 1261

Qy   1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD 1513
               | | | | | |: | | | ||||| | : | |
Db   1262 IKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERD 1321

Qy   1514 QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHOEEEARRREEKRLRR 1573
               | :| |||:
Db   1322 CRGGYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381

Qy   1574 LEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHLCTSHYLDLFITGVIGLNVVTMAME 1631
               | | | |: | | |
Db   1382 QGPSPGYRMELSIFVVVYFVPFFVNIFVALIIITF-----QEQGDKVMSE-----CS 1431

Qy   1632 HYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFQDRRWNQLDLAIVLLSIMGIT 1691
                   | | : |
Db   1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKIWTFVVSPPFEYFIMAMIALNTVLMMK 1491

Qy   1692 LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNL 1746
               |
Db   1692 TSLFALEMLLKLLVYGPFGYIQNPYNIFDGVIVISVWEIVG--QQQG--GLSVLRTFR 870

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Query Match              13.8%;  Score 1665.5;  DB 2;  Length 2259;
Best Local Similarity    23.8%;  Pred. No. 2.6e-97;
Matches         606; Conservative  379; Mismatches  844; Indels  719; Gaps  87;

Qy    62  GRAGAGSTEKDPGSADS--EAEGLPYPALA------------------------------PV--   91
Db     5  GEAAAGRPASGEGDSDQGRNLPGTPVPASGSAAAYKQSKAQARTMALYNPIPVRQNCFT       64

Qy    92  ---VFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFR--PCEDIACDSQRC     146
Db    65  VNRSLFIFGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR-     123

Qy   147  RILQAFDDFIFAFFAVEMVVKOWALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSIDLQN     205
Db   124  --LEKTEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFN     181

Qy   206  --VSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQ      263
Db   182  THVDLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLE     241

Qy   264  LWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGE     323
Db   242  FYSGKLIHRACFVNN--------SGVLEGF-------------------DPPHPC-----     268

Qy   324  GGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHNPPKGAINFDNIGYAWIAIFQVI     383
Db   269  --GVQGCPAGYE----------CKDW---------------IGPNDGITQFDNILFAVLTVFQCI  306

Qy   384  TLEGWVDIMYFVMDA-HSFYNFIYFIPLLLIIVGSFFMINLCLVVIATQFSETKQRESQLMR   442
Db   307  TMEGWTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERV-----    361

Qy   443  EQRVRFLSNASTLASSEPGSCYEELLKYLVYILRKAARRLAQVSRAI--GVRAGLLSSPV     501
Db   362  ENRRAFMK--------------------------LRRQQIERELNGYRAWIDKAEE      392

Qy   502  ARSGQEPQPGGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGS      561
Db   393  VMLAEENKNSGTSALEVLRRAT--------------IKRSRTEAMTRDSS--          428

Qy   562  RRLMLPPPSTTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKV     621
Db   429  ------------------------------FRHKE-------------              428

Qy   622  YPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCK    681
Db   429  -----------------DEHCVDIS---------------------------S         437

Qy   682  ISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPH    741
Db   438  VGTPLARASIKSAKVDGASY--------------------------------          462

Qy   742  SRRRQRSLGPDAEPSSVLAFWRLICDTFPRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQP   801
Db   463  --------------------RLLRISVRHAVKSQVFYWIVLSLIVALNTACVAIVHHNQP    501

Qy   802  EELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVLSVWEIVGQ-     858
Db   502  QWITHLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSPNCFDFGVTVGSIFEVVWAIFR    561

Qy   859  --QGGGLSVLRTFRLMRVLKLVRFLPAIQRQLVLMKTMDNVATFCMLLMLFIFISILG      916
Db   562  PGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFLFIVFALLG     621

Qy   917  MHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKLYNGM------ASTSS    971
Db   622  MQLFGGRF-NFNDG---TPSANFDTFPAAIMTVQILTGEDWNEVMYNGIRSQGGVSSGM    677

Qy   972  WAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSE-SEPDFFS----------    1017
Db   678  WSAVYFIVTLFGNYTLLNVLAIAVDNLANAQELTKDEQEEEEAFNQKHALQAKEVSP     737

Qy  1018  ------PSVDGDGDRKKRLAI-                                     1041


Db  1552  -------FLRFRAARLIKLLRQGYTIRILLWTFVQSFKALPYV               1602
Qy  1747  GLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNG  1806
Db  1603  CLLIAMLFFIYAIIGMVFGNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHE   1659

Qy  1807  IMKD--PSRDCDQE--STCYNTVISPIYFVFVLVNVVIAVLMKHLEESNKEAK         1862
Db  1660  IMLSCLSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS  1719

Qy  1863  ------EEAELEAELE------------LEM-KTLSPQPHSPLG------SPFLWPGV    1895
Db  1720  IIGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSP------PLGLGKKCPARVAYKRL 1775

Qy  1896  EGVNSTDSPKPGAPHTAHIGAASGFSLE--------------HPTMVPHPEEVPV-------  1937
Db  1776  VRMNMPISNEDMTVHFTSTLMALIRTALEIKLAPAQTKQHCDAELRKEISVVWANLPQK   1835

Qy  1938  -----PLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSGIL   1990
Db  1836  TLDLLVPPHKPDEMTVGKVYAA---LMIFDFY--KQNKTRDQMQQAPGGL--SQMGPVS    1888

Qy  1991  SVH--------SQPA-----------DTSCILQ----------LPKDVHYLLQ------P 2015
Db  1889  LFHPLKATLEQTQPAVLRGARVFLRQKSSTSLSNGGAINQESGIKESVSWQTQRTQDAP   1948

Qy  2016  HGAPTWGAIAPKLPPPGRGPLAQRPLRRQAAIRTDSLDVQ------------GLGSRE   2060
Db  1949  HEA-------RPPLERGHSTEIPVGRSGAI----AVDVQMQSITRRQPDQEPQPGLESGQ  1997

Qy  2061  DLLS--EVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDP  2118
Db  1998  RAASMPRLAAETQPVTDASPMKRSISTIAQRPRG-------THLCSTTP-------DRPP  2043

Qy  2119  PETRS---------------SLELDTELSWISGDLLPSSQEEPLFP-----------RDL  2152
Db  2044  PSQASSHHHHHRCHRRRDRKQRSLEKGPSLS--ADMDGAPSSAVGPGLPGEQPTQCRRER  2102

Qy  2153  KKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPS-----------    2197
Db  2103  ERRQERGRSQERRQPSSSSSEKQRF--YSCDRFGGREPPKPKPSLSSHPTSPTAGQEPG   2159

Qy  2198  -------SLGGQPL-------GGPGSR----PKKKLSP-PSIS------IDPPBSQGS   2230
Db  2160  PHPQGSGSVNGSPLLSTSGASTPGRGQRRQLPQTPLTPRPSITYKTANSSPIHFAQAQTS  2219

Qy  2231  RPPCSPG----------VCLRRRAPASD------SKDPSVSSPLDSTAASPSPKKDTLS   2273
Db  2220  LPAFSPGRLSRGLSEHNALLQRDPLSQPLAPGSRIGSDPYLQQRLDSEASVHALPEDTLT  2279

Qy  2274  L--------SGLSS                                             2279
Db  2280  FEEAVATNSGRSS                                             2292
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RESULT 5

S29236
calcium channel protein BII-1, brain - rabbit
calcium channel protein BII-1, brain - rabbit (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29236
R;Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
FEBS Lett. 308, 7-13, 1992
A;Title: Molecular cloning and characterization of a novel calcium channel protein from rabbit b
A;Reference number: S29236; MUID:93354772; PMID:1379552
A;Accession: S29236
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2259 <NII>
A;Cross-references: UNIPROT:Q02343; EMBL:X67855; NID:g1472; PIDN:CAA48040.1; PID:g1473
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

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Db  1785  ---MEVAEDMTVHFTSTLMALIRTALDIKIAKGADRQOLDSELOKETLAIWPHLSQKML  1841
Qy   738  MSAPNVPSIERDRRRRHHMSMWEPRSSHLRERRRHHMSVWEQRTSQLRRHMQMSSQEAL   797

Db  1935  ---VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQGSSILS 1991
Qy  1042  RKSLLPLIIHTAATPMS--HPKSSSTGV------GEALGSGSRRTSSSGSAEPGAAHHE  1093

Db  1842  DLLVPMKASD-LTVGKIYAA---MMIMDYYKQSKVKKQRRQL------EEQKNAPMF    1889
Qy   798  NKEEAAPPMNPLNPLSPLNPLNAHPSLYRRPRPMEGLALGLEKCEEEHVSRGGSLKGA   857

Db  1992  VHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPP------PGRSPLAQRPLRR   2042
Qy  1094  MKCPPS-----ARSSPHSPWSA----------SRRSSRNSLGR                 1126

Db  1890  QRMEPS------SLPQEI-IANAKALP---CLPQGPPAGLGGRSGCPAMSPLSPQIFQL  1938
Qy   858  LDCQRSPLSLGRREP--PWLARPCHGNCEPALQETAGGETVVTFEDRARHRQSQRRSRHR  915

Db  2043  QAAIRTD-------SLDVQGLGSREDLLSEVSGPSCPLTRSSSFW-----GGSS       2084
Qy  1127  APSLKRRSPSGERRSLLSGEGQESQDBEESSEDRASPAGSDHRHRGS------LERE    1178

Db  1939  TCMDPADDDGQFOFOQEQRSLVVTDPGSMRRSFSTIRD----KRSSSSWLEEFSMERSSDNT 1993
Qy   916  RVRTEAKESSSASRS-----RSVSQERSLDEGASTEGERDHEARGSHGGKEPTIHEEE   968

Db  2085  IQVVQQRSGIQS-KVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQ 2143
Qy  1179  AKSSFDLPDTLQVP-------GLHRTAS--------GRSSASEHQDCNGKSASGRL--  1219

Db  1994  YKSRRRSYHSSLRLSAH-RL------NSDSGHKSDTHRSG-GRERGRSKE           2035
Qy   969  RAQDLRRTDSLMVPKGSGLAGGLDEAGTPLVLSSPEGVGKEAAPTEQHADGSGEPALLGH 1028

Db  2144  EEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQP  2203
Qy  1220  ---ARTLRTDDPQL---------------------GNLSKGE--                1245

Db  2036  REHLLSADVSRCSSEE----RGAQADW-DSPERH                           2078
Qy  1029  VQLDVGRAISQSEPDLSCVTATTDKVTESTDVTVAIPDAEPIVDSTVVHIGNKTDGEAS  1088

Db  2204  LGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAP---ASDSKDPS-VSSPL  2258
Qy  1246  -----RIQAWVRSRLPACCRERDSWSA-YIFPPQSRFRLLCHRIITHKMPFDHV       1292

Db  2079  RQGTGSLSESSIPSVSDTSTPRHSRRQLPPVPP---KPRPLLSYSSLKQQPSNFSPPA  2133
Qy  1089  PFQEAEMKEAEQETEKQKKKERPASGKAMVPHSSMFIFSTSNPIRRACHYVVNLRYFEMC 1148

Db  2259  D-----STAASPSPKKDTLSLSGLSSDP                                 2281
Qy  1293  VLVIIFPLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAY 1352

Db  2134  DGSQGGSLLASPALESASAQVGLPESSDSP                               2161
Qy  1149  ILLIVIAASSIALAAEDPVLTNSERNRV-LRYFDYVFTGVFTFEMVIKMIDQGLIIQDGSY 1207

Qy  1353  LRSSWNVLDGLLVLLISVDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKL 1411
Db  1208  FRDLWNILDFVVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPLKTIKRLPKLKA 1267

Qy  1412  VVETLMSSLKPIGNIVVICCAFFIFGILGVQLFKGKFVC----QGEDTRN-----ITNK 1463
Db  1268  VFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFYFYCTDSSKDTEKECIGNYVDHE 1327

Qy  1464  SDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNP 1522
Db  1328  KNKMEVKGREWKRHEFHYDNIIWALLLTLFTVSTGEGWPQVLQHSVDVTEEDRGPSRSNRM 1387

Qy  1523  WMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRLEKKRRSKE  1582
Db  1388  EMSIFYVVYFVFVPFFFVNIFVALIIITF------QEQCDKMMEE---CSLEKNERACI 1437

Qy  1583  KQMAEAAQCKPYYSDYSR-FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILD 1640
Db  1438  DFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTVVLMMKYYSAPCTYE 1497

Qy  1641  EALKICNYIFTVIFVFESVFKLVAFAFARFRFFQQDRWNQLDLAIVLLSIMGITLEEIEVNLS 1700
Db  1498  LALKYLNIAFTMVFSLECVLKVIAFGFVNYFRDTWNIFDFITVIGSITBIVLTDSKLVNT 1557

Qy  1701  LPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAAL 1760
Db  1558  TGFNMSFLKLFRA---ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAII 1614

Qy  1761  GVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD-PSRDCD-  1816
Db  1615  GMQVFGNIRLDEESH----INRHNNFRSFFGSLMLLFRSATGEAWQEIMLSCLGEKGCEP 1670

Qy  1817  -----QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAK-------  1862
Db  1671  DTTAPSGQQESERCGTDLAYVVYFSFIFFCSFLMLNLFVAVIMDNFEYLTRDSSILGPHH 1730

Qy  1863  --EEAELEAELE------LEMKTL-SPQPHSPLG------SPFLWPGVEGVNST      1901
Db  1731  LDEFVRVWAEYDRAACGRIHYTEMYEMLTLMSP---PLGLGKRCPSKVAYKRLVLMN--  1784

Qy  1902  DSPKPGAPHTTAH------IGAASG------FSLEHETMV-PHPEE---            1934
```

RESULT 6

C54972

voltage-dependent calcium channel alpha 1E - mouse

```
C;Species: Mus musculus (house mouse)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mill
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel ε
A;Journal: J. Biol. Chem. 269, 22347-22357, 1994
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: C54972
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trai
A;Molecule type: mRNA
A;Residues: 1-2272 <WIL>
A;Cross-references: UNIPROT:061290; GB:L29346; NID:g522330; PIDN:AAA59206.1; PID:g522331
A;Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match         13.7%;  Score 1653.5;  DB 2;  Length 2272;
Best Local Similarity  23.4%;  Pred. No. 1.5e-96;
Matches 596;  Conservative 392;  Mismatches 835;  Indels 721;  Gaps 82;

Qy   73  PGSADSEA------EGLPYPALAPVV----------------------------FFY  95
Db   13  PGSGDGDSDQSRNRQGTPVPASGPAAAYKQSKAQARTMALYNPIPVRQNCFTVNRSLFI  72

Qy   96  LSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFR--PCEDIACDSQRCRILQAFD 153
Db   73  FGEDNIVRKYAKKLIDWPPFEYMLATIIANCIVLALEQHLPEDDKTPMSRR----LEKTE 129

Qy  154  DFIFAFFAVEMVKMVALG-IFGKKCYLGDTWNRLDFFIVAGMLEYSLDLQN--VSFSA  210
Db  130  PYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVLSGLLATAGTHFNTHVDLRA  189

Qy  211  VRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLR 270
Db  190  LRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYSGKLH 249

Qy  271  NRCFLPENFSLPLSVDLFPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPC  330
Db  250  RACFMNN-----SGILEGF------DPPHPC------------------GVQGC      274
```

```
Db  1105 ETKEEEEVEKKKQKKEKRETGKAMVPHSSMFIFSTNPIRRACHYIVNLRYFEMCLL  1164
         :|::    ::     |||||||   ::::|||||||
Qy  1296 IIFIMCTTIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMVKVVALGWCFGEQAYLRS 1355

Db  1165 VIAASSIALAAEDPVLTNSERNKV-LRYFDYVFTGVFTPEMVIKMIDQGLILQDGSYFRD 1223
         :|:::: ||||| :      :||||||
Qy  1356 SWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVE 1414

Db  1224 LWNILDFVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPLKTIKRLPLKLKAVFD 1283
         |||| |||||||||||
Qy  1415 TLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC----QGEDTRN------ITNKSDC 1466

Db  1284 CVVTSLKNVFNILLVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDTEKECIGNYVDHEKNK 1343
         :|::::|    ||||||||
Qy  1467 AEASYR-WTRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNINPWML 1525

Db  1344 MEVKGREWKRHEFHYDNIIWALLLTFTVSGEGWPQVLQHSVDVTEEDRGPSRSNRMEMS 1403
         :|::  |    ||||||||
Qy  1526 LYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEEARRREKRLRRLEKKRRSKEKQM 1585

Db  1404 IFYVVYFVVFPFFFVNIFVALIITF--------QEQGDKMEE---CSLEKNERACIDFA 1453
         :|::: |||||||||
Qy  1586 AEAQCKPYYSDYSR--FRILVHHLCTSHYLDLFITGVIGLNVTMAMEHYQQPIIDEAL 1643

Db  1454 ISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTVVLMMKYYTAPCYELAL 1513
         :||::  ::   |||||||||
Qy  1644 KICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEIEVNLSLPI 1703

Db  1514 KYLNIAFTMVFSLECVLKVIAFGFLNYFRDTWNIFDFITVGSITEILILTDSKLVNTSGF 1573
         |||:::    :||||||||
Qy  1704 NPTIIRIMRVLRIARVLKLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVE 1763

Db  1574 NMSFLKLFRA--ARLIKLLRQGYTIRILLWTTWFVQSFEKALPYVCLLIAMLFFIYAIIGMQ 1630
         |:::   |    ||||||||
Qy  1764 LFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD--PSRDCDQEST 1820

Db  1631 VFGNIKLDEESH---INRHNNFRSFFGSLMLLFRSATGEAWQEIMLSCLGEKGCEPDTT 1686
         :|:::        :||||||
Qy  1821 C--------YNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAK-----E 1863

Db  1687 APSGQNESERCGTDLAYVYFVSFIFFCSFLMNLFVAVIMDNFEYLTRDSSILGPHHLDE 1746
              ||||||
Qy  1864 RAELEABLE-----LEMKTL-SPQHSPLG------SPFLWPGVEGVNSTDSP 1904

Db  1747 FVRVWAEYDRAACGRIHYTEMYEMLTLMSP---PLGLGKRCPSKVAYKRLVLMN----- 1797
         :||::
Qy  1905 KPGAPHTTAH--------IGAASG-----------FSLEHPTMV--PHPEE----- 1934

Db  1798 MPVAEDMTVHFTSTLMALIRTALDIKIAKGGADRQOLDSELQKETLAIWPHLSQKMLDLL 1857
         :||:
Qy  1935 VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQGSSILSVHS 1994

Db  1858 VPMPKASD-LTVGKIYAA---MMIMDYYKQSKVKKQRQOL------EEQKNAPMFQRM 1905
         :||::   |
Qy  1995 QPADTSCIIQLPKDV-----HYLLQPHGAPTWGAIPLPPGRSPLAQRPLRRQAAIR 2047

Db  1906 EPS------SLPQEIIANAKALPYLQQD---PVSGLSGRSGYPSMSPLSPQEIFQLACM- 1955
         :|:
Qy  2048 TDSLDVQGLGSREDLLSEVSGPSCPL-----------TRSSSFW------- 2080

Db  1956 -DPADDGQFQEQQSLV--VTDPSSMRRSFSTIRDKRSNSSWLEBFSMERSSENTYKSRRR 2012
         :|:
Qy  2081 -----GGSSIQVQ-------QRSG----IQSKVSKIHRLP--APC--PGLEPSW---- 2114

Db  2013 SYHSSLRLSAHRLNSDSGHKSDTHRSGGRERGRSKERKHLLSPDVSRCNSEERGTQADWE 2072
         :|::
Qy  2115 ------AKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYVETQSCRRRPG 2168

Db  2073 SPERRQSRSGPSEGRSQTPNRQGTGSLSESSIPSISDTSTPRRSRRQLPPVPP----KPRPL 2129
         :||
Qy  2169 FWLDEQRHSIAVSCLDSGSGSQPRLCPSFPSSLGGQPLGGPGSRPKKK-LSPPSISIDPPES 2227
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Qy  331 SLDYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD 390
        ::    ||||||   :::|:
Db  275 PAGYE--------CKDW--------IGPNDGITQFDNILFAVLTVFQCITMEGWTT 314

Qy  391 IMYFVMDA-HSFYNFIYFILLIIVGSFFMINICLVVIATQFSETKQRESQLMREQRVRFL 449
        :::     |||||||||
Db  315 VLYNTNDALGATWNWLYFIPILIIIGSFFVLNLVLGVLSGEFAKERERV--ENRRAFM 369

Qy  450 SNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAI-GVRAGLLSSPVARSGQEP 508
        :|:
Db  370 K---------------LRRQQQIERELNGYRAWIDKAEEVMLAEEN 400

Qy  509 QPSGSCTRSHRRLSVHHLVHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPP 568
        :|:
Db  401 KNSGTSALEVLRRAT---------IKRSRTEAMTRDSS-------- 429

Qy  569 PSTPTPSGPPRGAESVHSFYHADCHLEPVRCQAPPPRCIPSEASGRTVGSGKVYPTVHTS 628
        :|:
Db  430 ---------------------------------FRHKE 429

Qy  629 PPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSK 688
        :|:
Db  430 ----DEHCVDLS----------SVGTPLAR 445

Qy  689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVVEFTQDAQHSDLRDPHSRRRQRS 748
        :|:
Db  446 ASIKSTKVDGASY------ 463

Qy  749 LGPDAEPSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL 808
        ::|  :||||||
Db  464 -----RLLRLSIRHMVKSQVFYWIVLSVVALNTACVAIVHHNQPQWLTHLL 509

Qy  809 EISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGL 863
        ||:: ||||||||
Db  510 YYAEFLFLGLIFLLEMSLKMYGMGPRLIYFHSSFNCPDFGVTVGSIFEVVWAIFRPGTSFGI 569

Qy  864 SVLRTFRLMRVLKLKLJVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCK 923
        |||:::|:|||||||:|
Db  570 SVLRALRLLRIFIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFLFIVVFALLGMQLFGGR 629

Qy  924 FASERDGTLPDRKNFDSLLMIAIVTVFQILTQEDWNKVLYNGM------ASTSSWAALYFI 978
        :|:      ||:|:|||||||||||
Db  630 F-NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNEVMVNGIRSQGGVVSGMWSAIYFI 685

Qy  979 ALMTFGNYVLFNLLVAILVEGFQAEGDATKSE-SEPDFFS----------P 1018
        ||:||||||    ||||
Db  686 VITLFGNYTLLNVFLAIAVDNLANAQELTKDEQEBEEAFNQKHALQKAKEVSPMSAPNMP 745

Qy  1019 SVDGDGDRKKRLAL------ 1048
         :|:
Db  746 SIERDRRRRHHMSMWEPRSSLRERRRHHMSVWEQRTSQLRRHMQMSSQAINKEEAPP 805

Qy  1049 LIIHTAATPMS----------HP----KSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPP 1098
         :||  ::
Db  806 MNPLNPLNPLSPLNPLNAHPSLYRRPRPIEGLALGLGLEKCEEERISRGGSLKGDIGGLT 865

Qy  1099 SARSSPHSPWSAAS--SW------TSRRSSRNSLGR 1126
         :|:
Db  866 SALDNQRSPISLGKREPPWLPRSCHGNCDPIQQEAGGGETVVTFEDRARHRQSQRRSRHR 925

Qy  1127 APSLKRRSPSGERRSLLSGEGQESSQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDL 1185
         :|::
Db  926 RVRTEGKDSASASRS-RSASQERSLDEGVSVEGEKEHEPHSSHRSKEPTIHEEERTQDLR 984

Qy  1186 -PDTLQVP-----GL----HRTASGRSSASEHQDCNGKSASGRL------ 1219
         ::|
Db  985 RTNSLMVPRGSGLVGALDEAETPLVQPQPELEVGKDAALTEQEABGSSEQALLGDVQLDV 1044

Qy  1220 --ARTLRTD-------DPQLD----GDDDNEGNLSKG 1244
         :||:
Db  1045 GRGISQSEPDLSCMTANMDKATTESTSVTVAIPDVDFLVDSTVVNISNKTDGBASPLKEA 1104

Qy  1245 E-RIQAWVRSRLPACCRERDSWSA------YIFPPQSRFRLLCHRIITHKMFDHVVLV 1295
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Db    2130 LSYSSLMRHTGGISPPPDGSE----------GGSPLASQALESNSACLTESSNSLHPQQG 2179

Qy    2228 QGSRPP---CSPGVCLRRRAPASD 2248
                |    |  :|:   |||
Db    2180 QHPSPQHYISEPYIALHEDSHASD 2203

RESULT 7
T43262
calcium channel alpha-1 chain, L-type - Stylophora pistillata
C;Species: Stylophora pistillata
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43262
R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J
Gene 227, 157-167, 1999
A;Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylo
A;Reference number: Z22375; MUID:99148007; PMID:10023047
A;Accession: T43262
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1891 <ZOC>
A;Cross-references: UNIPROT:O97017; EMBL:U64465; NID:g4204978; PIDN:AAD114
C;Genetics:
A;Gene: CACHL
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match       13.7%;    Score 1652.5;  DB 2;  Length 1891;
Best Local Similarity   24.8%;    Pred. No. 1.4e-96;
Matches   523;    Conservative 331;   Mismatches 623;    Indels 633;    Gaps   60;

Qy     115 FERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF-AFPAVEMVKMVALG- 172
               |::  |:  | | : ||   |   | |||:  |:  ::| :  ::|| | :|::
Db      83 FDVMILITIFANCAAILAAFAEPLPE-KDSSEINDNLEVAEYVFLAVFTMEAVLKIIAYGF 140

Qy     173 IFGKKCYLGDTWNRLDFFIVIAG---MLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPS 228
           ||:  |  :|  :|||: |  ||     |: |:| :  || |:: ||:|| ||:|::|
Db     141 LFHPGAYLRNGWNILDFVIVVGLATILVKATLSSGSFDVKALRAFRVLRPLRLRVSGVPS 200

Qy     229 MRILVTLLLDTLPMLGNVLLCFFVVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLE 288
           ||::    :| :  |:   ::|  |||: |::: || :|  ||  :|  ||  |  :|
Db     201 LQVVLNSIIKALIFLFHIALLVVFVIIYAIIGVELFMGRLHKTCY--DNVTGAESFE-E 257

Qy     289 PYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNW 348
                               ||   | ||:   |  ::::|:  ::  |
Db     258 PH---------------------PCS-----SGSSGFQCDKA 273

Qy     349 NQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDA-HSFYNFIYF 407
           |||:| |: : ::  |:|::|:| |: | :   | |||:|| :::: | :  | |:|
Db     274 AGQV--CEGGWKGPNHGITNFDNIGLACMTVFQCITLEGWTDVLYWINDAVGNSWPWVYF 331

Qy     408 ILLIIVGSFFMINICLVVIATQFSETKQR----ESQLMREQR------- VRFLSNAS 453
           :||:|:|||:|:|| |:||  ::                  :::        | :::
Db     332 VTLIIWGSFFVINLVGVLSGEFAKEKARRQKSGEFQKFREKQQVEDAYNGYLDWITQAE 391

Qy     454 TLASFSEPGSCYEELLKYLVIYLLRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGS 513
                                    |  ::        :  |
Db     392 DIEGDSESSGDES--------KASKK----------TSSRQSRT----EDIEM 423

Qy     514 CTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPT 573
           | ||||   |||| |:                  |: |   |:  ||  | | |
Db     424 IDRNERQDSI------SQHDTHHY---------------------- 441

Qy     574 PSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEI 633
           :   | : |  | : |: |  | |: ::           :   | |
Db     442 IVCNTVVLMMQYYQEPKLYTRVLDGFNIGFTAVFLLECILAFLKIIAFKPKNYFTDRWNLFDF 441

Qy     634 LKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGA 693
                                      :  ::::||:  |  :   :|| |
Db     442 GWCHNEKKV--------- 450

Qy     694 CGPDSCCPYCARTCAGEPESADHVMPDSDSEAVPFTQDAQHSDLRDPHSRRRQRSLGPDA 753
                                      || :      |   | | :  || |  |: |
Db     451 LKKWHHRRQTE------ 461
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```
Db     754 EPSSVLAPWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 813
                    | ||:   |   ||: |  | |: ||:: |  ||:: |  :||  |  :|
Db     462 LRKAVKTQAFYWIVIVVVFLNSLTLALEHYDQPDWLTKFLDIANK 506

Qy     814 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVV----- ISVWEIVGQGQGGLSVLRT 868
           :   ||| | : ||:   | |    |::|:|  | :           |  |   | |: |
Db     507 LFLGIFTIEMVKMYCLGFHGYFASLFNRFDCLVVISSLLELAITEALKQPPIGISVLRC 566

Qy     869 FRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASER 928
           : |:|:|::||   |   |::::|: : |||  :| ||:| :|  :|| :  :| : |
Db     567 IRLLRIFKVTRYWSSLSNIVASLLNSMRSIAGLLLLLSLFMLICSLLGMQIFGGKF-NT 624

Qy     929 DGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMAS---------- TSSWAALYFIALM 981
           | | :|    :|| |  ||:|||:|| ||||  | |:               ::  | |:::|
Db     625 DDDEIP-RSNFDSFWRALITVFQIITGEDWNAVMYDGIRAWGIGEGGSAIAILYFIFLV 683

Qy     982 TFGNYVLFNLLVALLVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAEL 1041
                |  :::| |||| |||   |  ||: |                        ||::|
Db     684 VVGNYILLNVFLAIAVDNLADAENLTEMEEE--------------------- EKARE 724

Qy    1042 RKSLLPPLLIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCCPPSAR 1101
           :||:                                                ::|:: ||:
Db     725 KEAL------------------------------KMKGSVDSQG------ RIDQDGAIVPN--- 749

Qy    1102 SSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQQESQDEEESSEEDR 1161
            :::|                         || |  :                  ::|:|:
Db     750 ----HS------------SASRSNVTLDKSTQELHSTG------ 771

Qy    1162 ASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLAR 1221
                                     ::          | ||:
Db     772 ----------------------------TLNGNGVARTAS------- HDDVEAQS--- 791

Qy    1222 TLRTDDPQLDG---------DDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRF 1276
              :: || |                    |    :  :  :  |
Db     792 ---TDISEIVGSKSAVSNNNESASASSSDDID---RAPMP---- PESALFIFSPTNIF 839

Qy    1277 RLLCHRIITHKMFDHVVIVIIFLNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEM 1336
           |: | |: :|  | |:    :: | |    :|:  :|  :| :|    :  |  |  : |
Db     840 RVVCYKIATNTYFVNFILCLIIVSSILLAAEDP-LNASAKRNQVLNVFDYFFTSVFTFEI 898

Qy    1337 TVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRVLRLLRT 1396
           |  :::   |   |  :|: |||:| ||:|| :|| :|::: |:     |:||:|:| | :
Db     899 LVKFISYGLLILHKGSFCRSAFNLLDLLVVSVSISLR--------- TSQFSVVRILRVLRV 952

Qy    1397 LRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGED 1456
           |||| | |:|:|  :::  : || | ||:|||: |  |:|: | |: ||  | | ||:|
Db     953 LRPLRAINRAKGLKHVVQSVFVAVKTIGNIKLVTMLFQFLFAVIGVQLFKGTFFSCNDE- 1011

Qy    1457 TRNITNKSDCAEASY----------- RWVRHKYNFDNLGQALMSLFVLASKDGWV 1500
           :     |||  | :                   : :| :||  | |:|| : | ||
Db    1012 --KILTAEEC-QGNYIDFKGPGLSNPVVKEREWRRHDFNFDNVGNAMLTLFTVMFEGWP 1068

Qy    1501 DIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE 1560
           || :| |  |: |:| ||||  | : | :|:: |:  ::  :||| :  : |
Db    1069 GILENSIDSTEVDKGPNQNNRPWVAIYYIIIIIAFFMVNIFVGFVIVTF-------- 1119

Qy    1561 BEARRREEKRLRLEKKRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGV 1620
            ::  ||:|  |:: :    |  :| ||       :||  | ||:   ||| |:  :||
Db    1120 -QSEGREEFKGCELDKNQRQCIEFALKAKPLKRYIPENRLQFHIWPVVTSQAFEYLLIFAF 1178

Qy    1621 IGLNVVTMAMEHYQQPQILDEALKICNYIPTVIFVFESVFKLVAFAFRRFFQDRWNQLDL 1680
           | |||| | |:|  |   ||||:|::|: |:| ||  |  ||||| |:|  ||||| ||
Db    1179 IVCNTVVLMMQYYQEPKLYTRVLDGFNIGFTAVFLLECILAFLKIIAFKPKNYFTDRWNLFDF 1238

Qy    1681 AIVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVM--- 1737
                      |  | ::|:  |::| |:::|| |||||: | |: |  :|  || :
Db    1239 IIVVGSIIDITMNEVSSEQMFAFG--- FFRLFRALRLVKLLNQSGGIKTLLWTFIKSF 1293

Qy    1738 QALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFR 1797
           ||||     | ::  :|  :| :|:   || :|     |
Db    1294 QALPYV---ALLIVMFFIYAVIGMQMFGRIAINSD---- TAINRNNNFQTFPQSLMVLFR 1347
```

```
Qy   1798  VSTGDNWNGIMK------------------DPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVI 1847
                 ::||.|           ||||    :.: .||::|.:||.||||
Db    269  --GVQGCPAGYE----------------------CKDW------------IGPNDGTQFDNILFAVLTVFQCI 306

Qy   1348  SATGENWQQIMLACTHRDDVKCDQNADPQEPSGLCGSDFAIYFYFVSFYSICSFLIINLFV 1407
                                                      :||||   :::|   |:|:|||||||
Db    384  TLEGWVDIMYFVMDA-HSFYNFIYFIFLLIIVGSFFMINLCLVVIATQFSETKQRESQLMR 442

Qy   1848  AVLMKFHLEESNKEAKEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPG 1907
                 |||| :|: .||
Db    307  TMGWTTVLYNTNDALGATWNWLYFIFPLIIIGSFFVLNIVLGVLSGEFAKERERV----- 361

Qy   1408  AVIMDNFDYLTRD------------WSILGPHHL---DEYVRVWSEYDPD 1442
                 |||| .|:|||               |:||:||       .:|||:||::
Db    443  EQRVRFLSNASTLASFSEPGSCYEELLKYLVILRKAARRLAQVSRAI-GVRAGLLSSPV 501

Qy   1908  APHTTAHIGAASGFSLEHPTM----VPHPEE----VPVPLGPDLLTVRKSGV------- 1951
                 |: ::|:                  |:|:|                 ||:.
Db    362  ENRRAFMK-----------------------------LRRQQQERELNGYRAWIDKAEE 392

Qy   1443  AHGCVKHVDIVTVLKRIAPPLGPGKFCPHREACKRLVTMNMG-----LTKDGMVDFNATL 1497
                                     :|:                        |:.||:|||:|
Db    502  ARSGQEPGPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGS 561

Qy   1952  -----SRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQGSGSILSVHSQPADTSCIIQL 2005
                      :|:.                                     |:|  .
Db    393  VMLAEENKNSGTSALEVLRRAT-----------------------IKRSRTEAMTRDSS-- 428

Qy   1498  FGLIRSSLNIKRPEGKGSIDKANEEVRNIILRIW--PKT-SMELLDKVVQPSGVRDDVTV 1554
                 |
Db    562  RRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKV 621

Qy   2006  PK-DVHYLLQ---------------------------PHGAPTWGAIPKLPP-PGRSPLAQPRPLRRQAA 2045
                 |. :||:||
Db    429  ---------------------------------------------------------------- 428

Qy   1555  GKFYATYLIQEYFRRFKARQKAQNQANEPHGNSTMALQAGLRTLHGLGPQLRRAISGQLG 1614
                 |:|:||.:||  :|::||
Db    622  YPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMKLLETQSTGACHSSCK 681

Qy   2046  I------RTDSLDVQGLGSREDLLSEVS-GPSCPLTRSSSF-----WGGSSIQVQQ 2089
                                                :.|.:
Db    429  ---------------------------DEHCVDIS------------------------S 437

Qy   1615  SDDDELFLKEDDSQKAHDKGFWESLKSAVSVSPRHSFRRSASFRLSAFLGKNGSGLETKK 1674
                                       |:                     |:||::
Db    682  ISSPCSKADSGACGPDSCPYCARTGAGEPSSADHVMPDSDEAVYEFTQDAQHSDLRDPH 741

Qy   2090  RSGIQSKVSK 2099
                 |.|::|:||
Db    438  VGTPLARASIKSAKVDGASY----------------------------FRHKE------ 462

Db   1675  KSSSMSNLSE 1684
                                            |:||.:..|:|:|.|.|::|.::|::|.
Db    742  SRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQP 801

Qy
           RLLRISVRHAVKSQVFYWIVLSLVALNTACVAIVHHNQP 501
Db    463
```

```
RESULT 8
S29237
calcium channel protein BII-2, brain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29237
R;Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
FEBS Lett. 308, 7-13, 1992
A;Title: Molecular cloning and characterization of a novel calcium channel from rabbit b
A;Reference number: S29236; MUID:92354772; PMID:1379952
A;Accession: S29237
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2178 <NII>
A;Cross-references: UNIPROT:Q02343; EMBL:X67856; NID:g1474; PIDN:CAA48041.1; PID:g1475
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

Query Match     13.7%;  Score 1652.5;  DB 2;  Length 2178;
Best Local Similarity  23.8%;  Pred. No. 1.7e-96;
Matches  601;  Conservative 376;  Mismatches  850;  Indels 699;  Gaps 83;
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Qy     62  GAAGAGSTEKDPGSADS--EAEGLPYPALA--------------------------PV------- 91
                                                                     |
Db    802  EELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQ-- 858

Qy      5  GEAAAGRPASGEGDSDQGRNLPGTPVPASGSAAAYKQSKAQRARTMALYNPIPVRQNCFT 64
                                                                     |:||:|: :||
Db    502  QWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAIFR 561

Qy     92  ---VFFYLSQDSRPRSWCLRTVCNPWERVSMLVILLNCVTLGMFR--PCEDIACDSQRC 146
                                     |:|     ::|||.:|.|:|
Db    859  --QGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSILG 916

Qy     65  VNRSLFIFGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR-- 123
                                          :|  ||:|::|::||.::|.|:|.|  |.|
Db    562  PGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFIVVFALLG 621

Qy    147  RILQAFDDFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN 205
                                       ::||
Db    917  MHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGM--------ASTSS 971

Qy    124  -LEKTEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVLSGILATAGTHFN 181
                                                        :||
Db    622  MQLFGGRF-NFNDG--TPSANFDTFPAAIMTVFQIITGEDWNEVMYNGIRSQGGVSSGM 677

Qy    206  --VSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIGVGVQ 263
                                                                |:||
Db    972  WAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSE-SEPDFFS----------- 1017

Qy    182  THVDLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLE 241
                                                            ::||
Db    678  WSAVYFIVLTLFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEAFNQKHALQKAKEVSP 737

Qy    264  LWAGLLRNRCFLPENFSLPLSVDLEPYYCQTENEDESPFICSQPRENGMRSCRSVPTLRGE 323
                                                                        ::|
Db   1018  ----------------PSVDGDGDRKKRLAL---------------------VALGEHAEL 1041

Qy    242  FYSGKLHRACFVNN---------DPFHPC----------------- 268
                                                 ::|.
Db    738  MSAPNVPSIERDRRRRHHMSMWEPRSSHLRERRRRHHMSVWEQRTSQLRRHEHQMSSQEAL 797

Qy    324  GGGGPPCSLDYEFYNSSSNTTCVNWNQYYTNCSAGEENPFKGAINFDNIGYAWIAIFQVI 383
                                                              |||.|  |||.|: ::|
Db   1042  RKSLLPPLLIHTAATPMS--HPKSSSTGV-----GEALGSGSRRTSSSGSAEPGAAHHE 1093
```

```
Db    798  NKEEAPPMNPLNPLNPLSPLNPLNAHPSLYRRPRPMEGLALGLEKCEEEHVSRGGSLKGA 857

Db   1094  MKCPPS--------ARSSPHSPWSA-------------SRRSSRNSLGR 1126

Db    858  LDCQRSPLSLGRREP--PWLARPCHGNCEPALQETAGGETVVTFEDRARHRQSQRRSRHR 915

Db   1127  APSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPAGSDHRHRGS----------LRRE 1178

Db    916  RVRTEAKESSSASRS-----------RSVSQERSLDEGASTEGERDHEARGSHGGKEPTIHEEE 968

Db   1179  AKSSFDLPDTLQVP---------GLHRTAS----------GRSSASEHQDCNGKSASGRL-- 1219

Db    969  RAQDLRRTDSLMVPKGSGLAGLDEAGTPLVLSPEGVKEAAPTEQHADGSGEPALLGH 1028

Db   1220  -----------ARTLRTDDPQL------------------DGDDDNDE------GNLSKGE-- 1245

Db   1029  VQLDVGRAISQSEPDLSCVTATTDKVTTESTDVTVAIPDAEPLVDSTVVHIGNKTDGEAS 1088

Db   1246  --------RIQAWVRSRLPACCRERDSWSA-YIFPPQSRFRLLCHRIITHKMFDHV 1292

Db   1089  PFQEAEMKEAEQETEKQKKKERPASGKAMVPHSSMFIFSTSNPIRRACHYVVNLRYFEMC 1148
```

```
Qy   2259 DSTAAS 2264
          ||||
Db   2149 DSTGGA 2154

RESULT 9
S41080
calcium channel alpha-1 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S41080
R;Coppola, T.; Waldmann, R.; Borsotto, M.; Heurteaux, C.; Romey, G.; Mattei, M.G.; Lazdur
FEBS Lett. 338, 1-5, 1994
A;Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Evidence f
A;Reference number: S41080; MUID:94139884; PMID:8307146
A;Accession: S41080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2288 <COP>
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match             13.7%;  Score 1650.5;  DB 2;  Length 2288;
Best Local Similarity   23.8%;  Pred. No. 2.4e-96;
Matches   632;  Conservative 367;  Mismatches 783;  Indels 875;  Gaps    94;

Qy    60 GPGAAGAGSTEKDPGSADSEAEGLP----------------------YPALAPV-              91
          ||
Db    23 GGGAGGAG-------PGQG-------GLPPGGQRVLYKQSIAQRARTMALYNPI-PVKQNCFTVN    72

Qy    92 -VFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQ        150
          :::       :||
Db    73 RSLFVFSEDNVVRKYAKRITEWPPFEYMILATIIANCIVLAL---EQHLPDGDKTPMSE        128

Qy   151 AFDD----FIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDL       203
                    ::::       :::      ||||    :      ||::
Db   129 RLDDTEPYFIGIFCFEAGIKIIALGLGVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDL       188

Qy   204 QNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCCFVFFIFGIVGVQ       263
          ::       :     |
Db   189 R-----TLRAVRVLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFGIGLE       243

Qy   264 IWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGE       323
                         :   |   :
Db   244 FYMGKFHKACF--------------------PNSTDTEPV-                          263

Qy   324 GGGGPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVI       383
                                                    ||
Db   264 -GDFPCGKDFPARQCDGDTEC---REYWP---------GPNFGITNFDNILFAILTVFQCI       311

Qy   384 TLEGWVDIMYFVMD-AHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES----       438
          ||
Db   312 TMEGWTDILYNTNDAAGNTWNWLYFIPLIIIGSFFMNLVLGVLSGEFAKERERVENRRA       371

Qy   439 --QLMREQRVRFLSNASTLASFSEPGSCYEBLLKYLVYILRKAARRLAQVSRAIGVRAGL       496
                                                        RELNGYLEWIFKAEEVMLAEED---
Db   372 FLKLRRQQQIB-                                                       404

Qy   497 LSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDR       556
          ::  ::
Db   405 ----------KNAEKSPLDVLKRAATKKSRNDLIH------------AEEGEDR           437

Qy   557 DANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTV       616
Db   438 ----------------------------------------------------------------     437

Qy   617 GSGKVYPTVTHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGAC       676
Db   438 --------------------FVDL---------------------------------------     441

Qy   677 HSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVVEFTQDAQHSD       736
          ::
Db   442 ---CAVGSPFARAS------------------------LKSGKTESSSYF-               464
```

```
Qy   1293 VLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAY     1352
           :|:||  |:     ||:||    :    ||:|||  ||| ::     ||||| |
Db   1149 ILLVIAASSIALAAEDPVLTNSERNRV-LRYFDYVFTGVFTFEMVIKMIDQGLILQDGSY     1207

Qy   1353 LRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKL     1411
           |||:|||||  |:|:|:||| |::  ::||| :  :|||:|| ||| ||||::||||| |
Db   1208 FRDIWNIILDFVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPLKTIKRLPLKLA     1267

Qy   1412 VVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKFFVC----QGEDTRN-----ITNK     1463
           |    |:::|   |   |   ||  ||:|| ||||||||| |    ||:
Db   1268 VFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDTEKECIGNYVDHE     1327

Qy   1464 SDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNP     1522
           :||    || |:: |  : |:|| :    ||  |||| ::  :  || :  ||     |
Db   1328 KNKMEVKGREWKRHEFHYDNIIWALLLTFTVSTGEGWPQVLQHSVDVTEEDRGPSRSNRM     1387

Qy   1523 WMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARRREEKRLRRLEKKRSKE     1582
           |    |:||:  |    || :     |   :::      ||
Db   1388 EMSIFYVVYFVVFPFFFVNIFVALIIITF------QEQGDKMMEE---CSLEKNERACI     1437

Qy   1583 KQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILD     1640
                  :||        ::  |||| |   ||:|||||| | ::|  ::||   ||:
Db   1438 DFAISAKPLTRTXMPQNRHTFQYRVWHFVSPSFEYTIMAMIALNTVVLMMKYYSAPCTYE     1497

Qy   1641 EALKICNYIFTVIFVFESVFKLVAFAPRRFFQODRWNQLDLATVLLSIMGITLLEEIVNLS     1700
                |||    ::   || :  :      :
Db   1498 LALKYLNIAFTMVFSLECVLKVIAFGFVNYFRDTWNIFDFITVIGSITEIVLTDSKLVNT     1557

Qy   1701 LPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAAL     1760
           | |  |:|  ||  ::  |||   :     ||:|   |      ||| || ::|:|||
Db   1558 TGFNMSFLKLFRA---ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAII     1614

Qy   1761 GVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD--PSRDCD-     1816
           |:||||  ||  ::   |:|            |:|||:|:||:|||
Db   1615 GMQVFGNIRLDEESH---INRHNNFRSFFGSLMLLFRSATGEAWQEIMLSCLGEKGCEP     1670

Qy   1817 ------QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAK---          1862
Db   1671 DTTAPSGQQESERCGTDLAYVYFVSFIFFCSFLMLNLFVAVIMDNFEYLTRDSSILGPHH     1730

Qy   1863 --EEABLEAELE-----------LEMKTL-SPQPHSPLG----------SPFLWPGVEGVNST     1901
                                :  |     |            ||:| |
Db   1731 LDEFVRVWAEYDRAACGRIHYTEMYEMLTLMSP----PLGLGKRCPSKVAYKRLVLMN---     1784

Qy   1902 DSPKPGAPHTTAH---------------IGAASG----------FSLEHPTMV--PHPEE---     1934
                                                   :
Db   1785 ---MPVAEDMTVHFTSTLMALIRTALDIKIAKGGADRQQLDSELQKETLAIWPHLSQKML     1841

Qy   1935 ---VPVPLGPDLLITVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILS     1991
               :  |  | :|
Db   1842 DLLVPMPKASD-LTVGKIYAA---MMIMDYYKQSKVKKQRRQL------EEQKNAPMF     1889

Qy   1992 VHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLP----------PGRSPLAQRPLRR     2042
                                                  |     |
Db   1890 QRMEPS-----SLPQEI-IANAKALP----CLFQGPPAGLGRGSGCPAMSPLSPQIFQL     1938

Qy   2043 QAAIRTD------------SLDVQGLGSREDLLSEVSGPSCPLTRSSSFW-----------GGSS     2084
                                 ::    :
Db   1939 TCMDPADDGQFEQRSLVVTDPGSMRRSFSTIRD----KRSSSSWLEEFSMERSSDNT       1993

Qy   2085 IQVQQRSGIQS-KVSKHIRLPAPCGLEPSWAKDPPETRSSLELDTELSWISGDLLPPSSQ     2143
                           :                     :|
Db   1994 YKSRRRSYHSSLRLSAH-RL----------NSDSGHKSDTHRSG-GRERGRSKE          2035

Qy   2144 EEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSSQPRLCPSPSSLGGQP     2203
           ::
Db   2036 REHLLSADVSRCSSEE-----RGAQADWDSPERHPSRSDSPEGRSQSPRSRQGTGSLSESSIP     2091

Qy   2204 LGGPGSSRPKKKLSPPSISIDPPBSQGSRSPPC----SPGVCLRRRAPASDSKDPSVSSPL     2258
           ||||| |       :           ||: |
Db   2092 SVSDTSTPRQQWGPQEEGVLLHPHQGCWPCRDRRWMPG---RRGWSGEKSHSPLPHCGR     2148
```

```
Qy   737  LRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGRIMIAILVNTLSMGIE  796
Db   465  -----RRKEK------MRFFF-----IRRMVKAQSFYWVVLCVVANTLCVAMV          502

Qy   797  YHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIIFDGVIVISWEIV    856
Db   503  HYNQPQRLTTALYFAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCDFGVIVGSIFEVV    562

Qy   857  GQ------QGGGLSVLRITFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFI  911
Db   563  WAAIKPGTSFGISVLRALRLLRLFKVTKYWNSLRNLVVSLLNSMKSIISLLFLLFLFIVV   622

Qy   912  FSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIILTQEDWNKVLYNGM-----  966
Db   623  FALLGMQLFGGQPNFQDETPT----TIFDTFPAAILTVFQIILTGEDWNAVMHGIESQGG   678

Qy   967  ASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDR  1026
Db   679  VSKGMFSSFYFIVLTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEAA---------   729

Qy  1027  KKRLALAVLALGEHAELRKSLLPPLLIHTAATPMSHPKSSSTGVGEALGSGSR-------  1077
Db   730  NQKLALQKAKEVAE-----VSPMSAANISIAAQQNSAKARSWEQRASQLRLQNLRASCE    784

Qy  1078  --------------RTSSSSGAEPGAAHH----------EMKCPPSARSSPHSPWSAAASS  1113
Db   785  ALYSEMDPEERLRYASTRHVRPDMKTHMDRPLVVEPGRDGLRGPVGSKSKPEGTEATESA   844

Qy  1114  WTSRSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASP--------A  1165
Db   845  DLPRHHHHRH--DRDKTSATAPAG---------GEQDRTESTETGPREEARPRRSHSKETP  895

Qy  1166  -----HRHRRGSLE-----------------------------------SWA         1176
Db   896  GADTVRCERSRRHRRRGSPEEATEREPRCHRAHRHAQDSSKEGTVPVLVPKGERRARHR    955

Qy  1177  --------REAKSSFD----------LPDTLQVPGLHRTAS--------GRSSASEHQDCNG  1212
Db   956  GPRRTGPREARENNEEPTRRHRARHKVPPTLQPP--EREAAEKESNPVEGDKETRNHQPKEP  1013

Qy  1213  KSASGRLART--------------LRTDDPQLDGDDDND---------               1237
Db  1014  HCDLEAIAVTDVGPLHMLFSTCLQKVDEQPEDADNQRNVTRMGSQPSDPSTTVHVPVTLT  1073

Qy  1238  --------EGNL-----SKGER------IQAWVRSRLPACCRERDSWSAYIFPPQSR     1275
Db  1074  GPPGETPVVPSGNMNLEGQAEGKKEAEADDVLRRGRPIVPYS------SMFCLSPTNL    1126

Qy  1276  FRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAE  1335
Db  1127  FRRFCHYIVIMVRYLEMVILVVIALSSTALAAEDP-VRTDSFRNNALEYMDYIFTGVFTCE  1185

Qy  1336  MTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISIVDILVSMV-SDSGTKLLGMLRVLRLL  1394
Db  1186  MVIKMIDLGLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSKGKDINTIKSLRVL   1241

Qy  1395  RTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQG  1454
Db  1242  RVLRPLKTIKRLPKLKPVFDSVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTD  1301

Qy  1455  E------DTRN--IITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYD  1505
Db  1302  ESKELERDCRGQLYDYEKEEVEAQPRQWKKYDFHYDNVLWALLLTFLTTVSTGEGWPMVLKH  1361

Qy  1506  GLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARR   1565
Db  1362  SVDATYEEQGPSPGFRRMELSILVVYFVVFPFFFVNIFVALIIITF------QEQGDKVM  1415

Qy  1566  REEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGL  1623
Db  1416  SE----CSLEKNERACIDFAISAKPLTRYMPQNKQSFQYKTWTFVVSPPFEYFIMAMIAL  1471

Qy  1624  NVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLAIV  1683
Db  1472  NTVVLMMKFYDAPYEYEYLMLKCLNIVFTSMFSMECILKIIAFGVLNYFRDAWNVFDFVTV  1531

Qy  1684  LLSIMGITILEEIE-----VNLSLPINPTIIRMVLRIARVLKLLKMAVGMRALLHTVMQ   1738
Db  1532  LGSITDILVTEIAETNNFNLS--------FLRLFRAARLIKLLRQGYTIRILLWTFVQ    1582

Qy  1739  ALPQVGNIGLLFMLLFFIFAALGVELFGDLECEDTHPCEGLGRHATFRNFGMAFLTLFRV  1798
Db  1583  SFKALPYVCLLIAMLFFIYAIIGMQVFGNSALDDD---TSINRHNNFRTFLQAIMLLFRS  1639

Qy  1799  STGDNWNGIMKD--QESTCYNTVISPIYFVYFVSFVLTAQFVLVNVVIAVLMKH        1853
Db  1640  ATGEAWHEIMLSCLDNRACDPHANASEC-GSDFAYFYFVSFIFLCSFLMLNLFVAVIMDN  1698

Qy  1854  LEESNKEAK----------EEAELEAELE----------LEM-KTLSPQPHSPLG------  1887
Db  1699  FEYLTRDSSILGPHILDEFIRVWAEYDPAACGRISYNDMFEMLKHMSP---PLGLGKKKC  1754

Qy  1888  -SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPLGP-DLLT  1945
Db  1755  PARVAYKRLVRMNMPISNEDMTVHFTSTLMALIRTALE----------IKLAPADEMT   1802

Qy  1946  V-----------------RKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSIL  1990
Db  1803  VGKVYAALMIFDFYKQNKTTRDQTHQAPG------------GL-SQMGPVS           1840

Qy  1991  SVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR---PLRRQAAIR  2047
Db  1841  LFHPLKAT----------LEQTQPAVLRGA----------RVFLRQKSATSLSNGGAIQ   1879

Qy  2048  TDSLDVQGLGSR----------EDLLSEVSGP----------SCPLTRSSSFWGGSSIQVQQR  2090
Db  1880  T----QESGSRSRCPGGRGTQDALYEGRAPLERDHSKEIPVGQS---GTLLVDVQMQ     1930

Qy  2091  S----GIQS-KVSKIHRLPA-PCPGLEP                                  2115
Db  1931  NMTLRGPDGDPQPGLESQGRAASMLRLAAETQPAPNASPMKRSISTLAPRPDGTQLCSTV  1990

Qy  2116  KDPP-----------------------ETRSSLELDTE--LSWISGDLLPSSQEEPLF   2148
Db  1991  LDRPPPSQASHHHHHCHRRRDKKQRSLEKGGSLSVDPEGAPSTAAAGPGLPHGEGSTAC  2050

Qy  2149  PRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSC-LDSGSQPRLCPSPS---------  2197
Db  2051  RRDRKQERGRSQE--RRQPSSSSSEKQRF--YSCDRLGAGS-PQLMPSLSHPTSPAAA   2104

Qy  2198  ----------SLGGQPL----------GGPGSRPKKKLSP-PSIS--------IDPPE   2226
Db  2105  LEPAPHPQGGSGVNGSPLMSTSGAITPGRGGRRQLPQTPLTRPSITYKTANSSPVIHFAE  2164

Qy  2227  SQGSRPPCSPG------------VCLRRRAPASD------SKDPSVSSPLDSTAASPSPKK  2269
Db  2165  GQSLPAFSPGRLSRGLSEHNALLQKEPLSQPLAPGSRIGSDPYLGQRLDSEASAHTLPE  2224

Qy  2270  DTLSL------SGLSS      2279
Db  2225  DTLTFEEAVATNSGRSS     2241
```

RESULT 10
A47447
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)
C;Species: Discopyge ommata
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47447
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Dis
A;Reference number: A47447; MUID:93248175; PMID:7683405
A;Accession: A47447
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA

A;Residues: 1-2223 <HOR>
A;Cross-references: UNIPROT:P56699
A;Note: sequence extracted from NCBI backbone (NCBIP:130671)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   13.7%;   Score 1642;   DB 2;   Length 2223;
Best Local Similarity 24.0%; Pred. No. 8.1e-96;
Matches 598; Conservative 373; Mismatches 841; Indels 682; Gaps 78;

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Qy    37 RRMERAPRSRDSPVASRSSTTCPGPGAAGAGSTEKDPGSADSEAEGLPYPA-----LAPV   91
         :: : :::   : :  :::     :            :         :     :: :::
Db    21 RSRHQVPVTGETAVAAAAAVVAGAAQQSAGFKQTRAQRARTMALYNPIPVRHNCLTPANR   80

Qy    92 VFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFR--PCEDIACDSQRCRIL  149
         :: ::    ::     : ::  ::   :::::::::::: :  ::  :     :  ::
Db    81 SLFLFGEDNIVRKSARRVIEWPPFEYMIATIIANCVVLALEQHLPNGD--KTPMAKSL   137

Qy   150 QAFDDFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSF  208
         :   :::  :: :   :::::::  :    ::  :  ::::::::::::::   :  :
Db   138 EQTEPYFIGIFCFEAGIKIVALGFVFHKGSYLRNGWNVMDFIVVLSGLL--ATAATHFNL  195

Qy   209 SAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGL  268
         : :: ::::::: :::  ::  ::::  :  ::  : :::::: :::::::::::: :
Db   196 RTLRAVRVLRPIKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEPYYGK  255

Qy   269 LRNRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGP  328
         : : :   ::  ::  :  : :
Db   256 LHRTCYTDDAAAEELDLQF-----------------------------------------  274

Qy   329 PCSLDYETYNSSNNTCVNMNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGW   388
         ::      :    : :  :      :       :      :    : ::::::: :::::
Db   275 PCGTQEPTRLCPNGTVCSYW-----------IGPNDGITQFDNILFALLTVFQCITMEGW  323

Qy   389 VDIMFVFMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVR  447
          ::  :  ::  ::  : ::::::::::::::::: :::: :::: ::::
Db   324 TTILVNTDDALGAMNNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERV----ENRRS   378

Qy   448 FLSNASTLASFSEPGSCYEELLKYLVYILRKAAARRLAQVSRAI-GVRAGLLSSPVARSGQ  506
         ::                      :::: ::
Db   379 FLK-----------------------------LRRQQIERELNGYRAWIDKAEEVMLLE   409

Qy   507 EPQPSGSCTRSH--RRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRL   564
         :                ::::
Db   410 ENKNAGEKSALHVLRRAFIK----------------KGRMEM------IQTESSEDQ---  444

Qy   565 MLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPT   624
                 ::
Db   445 ----YTEISSVVGSPLARASIKS-----------------------------   462

Qy   625 VHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISS  684
                      : :
Db   463 ------------------------------TKLLLEGSS-------------   470

Qy   685 PCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEPTQDAQHSDLRDPHSRR  744
         :
Db   471 ------------------------------------------YFRR   474

Qy   745 RQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEEL  804
         :: ::                  ::                : :::: ::
Db   475 KERMI---------RI---SIRHMVKSHAFYWIVLGLVALNTVCVAVVHYDQPLWL   518

Qy   805 TNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIV----GQQ   859
          : :   ::::: :  ::  ::::  :         :    : :
Db   519 SNFLYYAEFTFLGLFSSEMFLKMYGCGPRLYFHSSFNCFDCGVIIGSIFDVVWTIIRPET  578

Qy   860 GGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHL  919
           : ::::  ::::: ::::  : : :::::: ::  : ::   :: ::::::: :::::
Db   579 SFGISVLRALRLLRIFKITKYWASLRNLVVSLRNLIVVSSMKSIISLLFLLFLFIVVFALLGMQL  638

Qy   920 FGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTGEDWNKVLYNGMAS-----TSSWAA  974
         ::   :          :  :    :::::::::::::::::  :::: :       :  ::
Db   639 FGGQFNFEE--GTPP--TNFDTFPAAIITVFQLLTGEDWNEVMYNGIKSQGGVNSGMWSS  694

Qy   975 LYFIALMTFGNYVLFNLLVAILLVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRIALVA 1034
         :||: : ||||| | || ||: :: ::          ::
Db   695 VYFIVLTLFGNYTLLNVFLAIAVDNLANAQELTKEQEEE--------------EA   736

Qy  1035 LGEHAELRKSLLPPLLHTAATPMSHPKSSST------------------GVGEALGSGSRRTSSSGS 1084
         : :  : ::    :
Db   737 INQKHALQKA----------KEVSPMSAPGPFSTEREFRRHKHMSIWEARTSQLRRRMQMSS  788

Qy  1085 AE------PGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRS---- 1134
         :        :    :  ::    ::    ::     ::::::::  : ::
Db   789 REALFTDALQGLEGSRYRRHRSRIFEAESLRRLAEQQAAESHQLGEVGRREAFKSRSLRN  848

Qy  1135 ---PSG-ERRSLLSGEGQE-----SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDL 1185
             ::   :: : :::         :  :   :    ::::
Db   849 SWQPAGPDKRSSSIKVNGEQQRALGRSVEAGASFRMAEPIRARRYR-SLYKEAK--MGL   905

Qy  1186 PDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQ 1229
          :   :   :: :  :   :  :  :: :    : : : :  :
Db   906 EESAETSLSRRPGGNKEGRLLQQLCE-EQESGQLTQTPEVMDAQGQMKAFSWQGEPHSSS  964

Qy  1230 ----LDGDDNDEGNLSK----------------------GERIQA--WVRSRL 1255
               : :: :::::                       ::: :
Db   965 MTRTPDVDTDPSGGNLEKESGRTPENGKESANTSEQVNEQSWNLNLQLNQQATPGDREL 1024

Qy  1256 PACCRERDSWSAYIFPPQS 1274
                  :     :
Db  1025 TTGTRDTKQDKTQEQTEIDVDCENTETPMDSLVTPGNAYSSSSSVKEDEKKSKAIIPYTS 1084

Qy  1275 RF------RLLCHRIITHKMFDHVVIVIIFLNCITIAMERKIDPHSAERIFLTLSNY 1326
         :        :: ||  : :::  : ::::::::::: ::   :  : || : : ::
Db  1085 MELFRKTNPIRRVCHFIVNLRYFEMCILLVIAASSVALAAEDP-IHKDSARNQVLRYFDY 1143

Qy  1327 IFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKIL 1385
         :||:||  ||  |: : | ||    :   ::||:|| :|: :    : :: :::
Db  1144 VFTGVFTFEMVIKMIDIGLVFHEGSYFRDVWNILDFIVVSGALVAFTNLIGGSSGDI 1203

Qy  1386 GMLRVLRLLRTLRPLIVRSRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILGVQLF 1445
          | : ||| ||:|||:   :   :|::  :| :| ||| || ::   ||:|  : |||
Db  1204 NTIKSLRVLRVLRPLKTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLF 1263

Qy  1446 KGKFFVCQGEDTRNITNKSDCAEASYRWVRHK----------YNFDNLGQALMSLFVL 1493
         |||||:|      : ||:||| ||   :           :   :   : || ::|||
Db  1264 KGKFFYC--TDSSKMT-KQDC-RGQFVLYRQRTKLSIENGNVTTFHYDNVVWALLTLFTV 1319

Qy  1494 ASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHK 1553
          : :||  :: :    | ::||:: |  | :  :: ||:|: ||  |:::  |:| ||
Db  1320 STGEGWPQVLQHSVDVDTEADQGPIPGNRMEMSIFYIVYFVFPFFPVNIFVALIIITF-- 1377

Qy  1554 CRQHQEEEARRREEKRLRELEKKRRSKEKQMAEAQQCKPYYSDYSR--FRLLVHHLCTSH 1611
                 :   :: ::  :      :  : |   :::   ::    ||:: : :
Db  1378 ------QEQGDKMLEES---SLEKNERACIDFAISAKPLTRYMPQNRQTFQYRVRWQFVVSP 1429

Qy  1612 YLDLFITGVIGLNVTMAMEHYQQPILDEALKICNYIFTVIFVIFFSVFKLVAFAPRRFF 1671
          : |: :  : ||| ::   : :  :::| | |: || ::: :| ||||:|    ||:
Db  1430 SFEYTILTMIALNTVVLMMKHSPPGFASVLKLMNIAFTITFLECILKIIAFGFLNYF 1489

Qy  1672 QDRWNQLDLAIVLLSIMGITLEEIE--VNLSLPINPTIIRMRVLRIARVLKLLKMAVG 1728
          | ||| |  :|:: ::  :     :   :|| | :  : :::: |:|| :|||::::
Db  1490 RDSWNVFDFVTVVGSISEIIVTECNLKFVNLS------FLKLFRAARLIKLLRQGIT 1540

Qy  1729 MRALLHTVMQALPQVGNLGLFMLLFFIPAALGVELFGDLECDETHPCEGLGRHATFRNF 1788
          ||:: ||:| ||    |: ::: :: |: | ::|||:      ||  ::: ::: ||
Db  1541 IRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQLFGNIGLDDHTP---INRHNNFHTF 1597

Qy  1789 GMAFILFRVSTGDNWNGIMKD-PSRDCD--QESTCYNTVISPIYFVSFVLTAQFVLVN 1844
          :|:  |:|::||:||  || :  :  |   : :|    :::|| ||: | :|: ::|
Db  1598 FNALMLLFRSATGESWQEIMLACLSGKECEGTREPSC-GTDVAYFVFVSFIFLCSFLMLN 1656

Qy  1845 VVIAVLMKHLEESNKEAK--------------EEAELEAELE 1883
          ::||:: :: ::  :                 ::|:: ::|
Db  1657 LFVAVIMDNFEYLTRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTDMQMLTIMSP---- 1713

Qy  1884 SPLGSPFLWPGV----------------EGVNSTDSPKPGAPHTTAHIGAASGFSLEHPT 1927
```

```
Db   1714  -PLGLGLKKCPSKVAYKRLVLMLMNMPVTEDKTVHFT-STLMGLIRTALQIKLARGGA----- 1766
                |||              :|: ||   ||        : |      ||   :||
Qy    283  LSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSN 342

Db   1928  MVPHPEVPVPLGPDLLTVRKSGVSRTHSL--PNDSYMCRNGSTAERSLGHRGWGLPKAQ 1985
                 : |   ||               :: :                    : :||
Qy    256  ------------------------------------GDFPCGKEAPARLCEGD 280

Db   1767  ---DKQQLDAELRKEIMTIWPHLSQKTLDLLVPMHTY------SDLTVG------KIY 1809
                ||:||:|   |  |||| ||||||  |||||       |   ||       :| |
Qy    343  TTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWGDIMYFVMD-AHSF 401

Db   1986  SGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR----PLR 2041
                |:|| :   ::                   :       ||||  ::    : ||
Qy    281  TEC---REYWP---------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNTNDAAGNT 330

Db   1810  AAMMIMDYYKQSKNKKYQKLQEE------------------------QSRTPMFQRMEASLP 1848
                :::|||||||:|:::|:||||                      ||| | |: ||||
Qy    402  YNFIYFILLIVGSFFMINLCLVVIATQFSETKQRES---------QLMREQRVRFLSNASTL 455

Db   2042  RQAAIRTDSLDV--QGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSK 2099
                : ||| || :    | || || :: || ||  |   :||| |  : ||  :|: ||:
Qy    331  WNMLYFIPLIIIGSFFMLNLVLGVLSGEFAKERRVENRRAFLKLRRQQQIE--------- 382

Db   1849  PQIISSTKGLPYLQTGTGPDVDSRSEFT-PLVPLPPVMFQQGRTSSQGEEIHKQRPKELK 1907
                |  |:  |           :| :     || || ::   ::|| :  ::||:|
Qy    456  ASFSEPGSCYEELLKYLVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCT 515

Db   2100  HIRLPAP-----------------CPGLEPSWAKDPPETRSSLEL----DTELSWISGDLL 2139
                :  | |                 | || :      : :||| :    ||  | | ||
Qy    383  ------------------RNAEEKSPLDVLK 417

Db   1908  KIKLEYPHYGHYLPIENQGRAVSMPRLEIESAEDTSPLKRSLSTFAANHSNSTWLNEYSL 1967
                :||  :||  |  ::   |   | ||  ::  ::   |||   ::  | | |: :|
Qy    516  RSHRRLSVHLVHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSPTPS 575

Db   2140  PSSQEEPLPPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSL 2199
                |                   ||| || |
Qy    418  --------------RAATKKKSRNDLIH----------------AEEGEDRFAD 440

Db   1968  ---ERAGPEDLYKRWS----------LRP--PSRSSN 1992
                   :| |  :||
Qy    576  GGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRIVGSGKVYPTVHTSPPPEILK 635

Db   2200  GGQPLGGPGSRPKKKLSPPSISI--------DPPESQG-----SRPPCSPGVCLRRRAPAS 2247
                |  |   ||   : |  ::         | |         | |  | |
Qy    441  ----------------------------------DKALVEVAPSPGPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACG 695

Db   1993  AGSRERG-RSRERKHILSPERSVCSTGQCAHPSQHRGLDQRLSRSP-SPGYSHRPREQVN 2050
                |                    |
Qy    452  ----------------------------------LCAVGSFPARAS---------- 452

Db   2248  DSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2281
                | |
Qy    696  PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEP 755

Db   2051  SSVS--ESPVPSSSGTSSPPKQGQRQLPQTPSKP 2081
                |
Qy    453  -------------------------------LKSGKTESSSYF 469

Qy    756  SSVLAFWRLICDTFRKIVDSKYFGRGIMIALLVNTLSMGIEYHEQPELTNALEISNIVF 815
                :         | |     |||||  :||| : :::  | :||  ||| |  |
Db    470  --MFRFF---------IRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLYFAEFVF 521

Qy    816  TSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQ-----QGGLSVLRTFR 870
                ||| | |: :|| ||||   ||  ||| || |:| ||| |      ||| |: ||
Db    522  LGFLTEMSLKMYGLGPRSYRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGISVLRALR 581

Qy    871  LMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDG 930
                |||:|:|  | || ||||  |::|:   : |  ||:| |   | | :|    |
Db    582  LLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLLFLFLFIVFALLGMQLFGGQFNFQDET 641

Qy    931  DTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----ASTSSWAALYFIALMTFGN 985
                :  |::||  |||  |  || |||:||||||  |     ||    | ::  :|| ||
Db    642  PT----TNFDTFPAAILTVFQIITGEDWNAVMHGIESQGGVSKGMFSSFYIVLTLFGN 697

Qy    986  YVLFNLLVAILVEGFQAEGDATKSESEPDFFSSPVDGDGDRKKRLALVALGEHAELRKSL 1045
                || :| |: | |
Db    698  YTLLNVFLAIAVDNLANAQELTKDEEEMEEAA-------------NQKLALQKAKEVAEV--SP 746

Qy   1046  LPPLIIHTAATPMSHPKSSSTGVGEA---------------------------- 1071
                :
Db    747  MSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLR 806

Qy   1072  ----------------LGSGSRRTSSSGSSAEPGAA---------HH----EMKCP----- 1097
                                |                         ||    |||
Db    807  PDMKTHLDRPLVVELGRDCGARGPVGGKARPEAEAPEGVDPPRRHHHRDKDKTPAAGDQ 866

Qy   1098  -----PSARSS---PHSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGERRSL 1142
                     |                   |  | | | :|
Db    867  DRAEAPKAESGEPGAREBRPRPHRSHSKEAA--GPPEARSERGRGP------GPGGRRHH 919

Qy   1143  LSGEGQESQDEE--------------ESSEEDRASPAGSDHRHRGSLE---REAKSSFDLPDTL 1189
                |
Db    920  RRGSPEEAAEREPRRHRAHRHQDPSKECAGAGKRRARHRGGPRAGPRBAESG------ 972

Qy   1190  QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA---------RTLRTDDPQLDGDDDNDE 1238
                |
Db    973  EEPARRHRARHKAQPAHEAVEKETTEKEAEBAIVEADKEKELRNHQPREPHCDLETS 1032
```

RESULT 11
T45115
T45115   N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Maroufi, A.; McCu
    Science 257, 389-395, 1992
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-typ
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: A42566
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2237 <WIL>
A;Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PIDN:g1797
A;Experimental source: cell line IMR32; neuroblastoma
C;Genetics:
A;Note: CCHL1A2
C;Function: calcium influx
A;Description: voltage-dependent calcium channel protein alpha-1 chain
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   13.6%;   Score 1640.5;   DB 2;   Length 2237;
Best Local Similarity   23.5%;   Pred. No. 1e-95;
Matches 614;   Conservative 350;   Mismatches 815;   Indels 839;   Gaps 82;

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Qy     59  PGPGAAGAGSTEKDPGSADSRAEGLPYPALAPV----------VFFYLSQDSRPRSWCLRT 109
                |    |                            |
Db     32  PGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI 91

Qy    110  VCNPWFERVSMLVLLNCVTLGMFRPCEDIACDSQRCRILQAFDD----FIFAFFAVEMVV 166
                | | |      |              |               | |:    |
Db     92  TEWPPFEYMILATIIANCIVLAL-----EQHLPDGDKTPMSERIDDTEPYFIGIFCFEAGI 147

Qy    167  KMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA 222
                | | |    | |||       | ||| |:   |      | :: |  :| |||:
Db    148  KIIALGFVFHKGSYLRNGWNVMDFVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL 202

Qy    223  INRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP 282
                |:| |:    |   || | |:   |       |  |  | :|||  |  : |
Db    203  VSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-------P 255
```

```
Qy  2032 ------------THLCSTTP-------------------------------      2032
                  ::                                :||
Db  2076 ------------DRPPPSQASSHHHHRCHRRRDRKQRSLEKGPSLS-AD        2076
Qy  2136 GDLLPSSQEEPLFP---------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDS 2186
Db  2077 MDGAPSSAVGPGLPPGEGPTGCRERERQERGRSQERRQPSSSSSEKQRF--YSCDRF     2133
Qy  2187 GSQ--PRLCPSPSSLGGQPLGG--PGSRPK----------KKLSP---PSISIDPPESQ-- 2228
Db  2134 GGREPPKPKPSLSSHPTSPTAGQEPGPHPQAGSAVGFPNTTPCCRETPSASPWLALELA   2193
Qy  2229 ------GS----RPPCSPGVCLRRRAPASDSKDPSVSSP                       2257
Db  2194 LTLTWGSVWTVRPLSTP--CLRTRSLSRRIWPPTRAAP                        2229
```

RESULT 12

B54972

voltage-dependent calcium channel alpha 1E-1 - human

C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Accession: B54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mill
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel ε
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: B54972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2251 <WIL>
A;Cross-references: GB:L29384; NID:g495867; PIDN:AAA59204.1; PID:g495868
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

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Query Match             13.6%;  Score 1638;  DB 2;  Length 2251;
Best Local Similarity   23.7%;  Pred. No. 1.5e-95;
Matches  600;  Conservative  391;  Mismatches  818;  Indels  724;  Gaps  86;
```

```
Qy   73 PGSADSEA------------EGLPYPALA-----------------PV-------VFFY   95
Db   12 PGSGDGDSDQSRNRQGTPVPASGQAAAYKQTKAQRARTMALYNPIPVRQNCFTVNRSLFI  71
Qy   96 LSQDSRPRSWCLRTVCNPWPFERVSMLVILLNCVTLGMFR--PCEDIACDSQRCRIIQAFD 153
Db   72 FGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR---LEKTE  128
Qy  154 DFIFAFFAVEMVKVMVALG-IFGKKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN--VSFSA 210
Db  129 PYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVLSGILATAGTHFNTHYDLRT   188
Qy  211 VRTVTRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLR  270
Db  189 LRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYSGKLH  248
Qy  271 NRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPC   330
Db  249 RACFMNN-------SGILEGF-------DPPHPC                            273
Qy  331 SLDYETYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINPDNIGYAWIAIFQVITLEGWVD   390
Db  274 PAGYE--------CKDW--------IGPNDGITQFDNILFAVLTVFQCITMEGWTT      313
Qy  391 IMYFVMDA-HSFYNFIYFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESOLMREQRVRFL 449
Db  314 VLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERV-----ENRRAFM  368
Qy  450 SNASTLASFSEPGSCYEELLKYLVYILRKCAARRLAQVSRAI-GVRAGLLSSPVARSGQEP 508
Db  369 K-------------LRRQQQIERELNGYRAWIDKAEEVMLAEEN                  399
Qy  509 QPSGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPP    568
Db  400 KNAGTSALEVLRRAT---------------IKRSRTEAMTRDSS---------         428
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Qy  1239 GNLSKGERIQAWTRSRLPACCRER----------DSW-------------          1265
Db  1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPDPNTIVHIPVMLTG  1086
Qy  1266 ----------------------------------SAYIFPPQSRFLLCHRI          1283
Db  1087 PLGEATVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLLSPTNLLRRFCHYI 1146
Qy  1284 ITHKMFDHVLVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343
Db  1147 VTMRYFEVVILVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDL 1205
Qy  1344 GWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMV--SDSGTKILGMLRVLRLLRTIRPLRV 1402
Db  1206 GLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGGSKGKDINTIKSLRVLRVLRPLKT 1261
Qy  1403 ISRAQGLKLIVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFYCVCQGE------D 1456
Db  1262 IKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFYCTDESKELERD  1321
Qy  1457 TRN--ITNKSDCAEASYR-WVRHKYNPDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD 1513
Db  1322 CRGQYLDYEKEVEAQPRQWKKYDFHYDNVLWALLITLFTVSTGEGWPMVLKHSVDATYEE 1381
Qy  1514 QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRR  1573
Db  1382 QGPSPGYRMELSIFYVYVVVFPFFFNIFVALIIITF------QEQGDKVMSE----CS   1431
Qy  1574 LEKKRRSKEKQMAEEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1631
Db  1432 LEKNERACICDFAISAKPLTRYMPQNRQSFQYXKTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491
Qy  1632 HYQQPOILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGIT  1691
Db  1492 FYDAPYEYELMKCLNIVFTSMFMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIL    1551
Qy  1692 LEEIE----VNLSLPINPIIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPVQGNL  1746
Db  1552 VTEIAETNNFINLS---------FLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYV 1602
Qy  1747 GLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNG 1806
Db  1603 CLLIAMLFFIYAIIGMQVFGNIALDDD------TSINRHNNPRTFLQALMLLFRSATGEAWHE 1659
Qy  1807 IMKD--PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM-------      1851
Db  1660 IMLSCLSNQACDEQANATECGSPAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS  1719
Qy  1852 --------KHLEE-------------------------------------          1856
Db  1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMN 1779
Qy  1857 -----------SNKEAKEAELEAEL-------------ELEMKTLS-             1879
Db  1780 MPISNEDMTVHFTSTLMALIRTALEIKLAPAGTKQHCQDAELRKEISVVWANLPQKTLDl 1839
Qy  1880 -POPHSP---LGSPF-----LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVP 1930
Db  1840 LVPPHKPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLF---HPLKAT 1896
Qy  1931 HPEEVPVPL-GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI 1989
Db  1897 LEQTQPAVLRGARVFLRQKSST----SLSNGGAIQNQESGIKESV---SWGTQRTQDA-- 1947
Qy  1990 LSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD 2049
Db  1948 PHEA-----------RPPLERGHSTEIPVGRSGALAVD                        1974
Qy  2050 SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSG                  2092
Db  1975 VQMSITRRGPGDGEPQPGLESGQ--RAASMPRLAAETQPVTDASPMKRSISTLLAQRPRG 2031
Qy  2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS----------SLEDTELSWIS          2135
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Qy   569  PSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTS  628
Db   429  ------------------------------------------------------------  428

Qy   629  PPPEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSK  688
          :::                                              ::|: :
Db   429  ----------DEHCVDIS-----------------------------SVGTPLAR       444

Qy   689  ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVEFTQDAQHSDLRDPHSRRQRS     748
              :::
Db   445  ASIKSAKVDGVSY------------------------FRHKE------               462

Qy   749  LGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALLVNTLSMGIEYHEQPEELTNAL   808
          ||:|                    :|:       :  | :::||: :|:|::| |:  :
Db   463  ------------RLLRISIRHMVKSQVFYWIVLSLVALNTACVAIVHHNQPQWLTHLL     508

Qy   809  EISNIVFTSLFALEMLLKLLVGPFGYIKNPYNIFDGVIVVISVWEIVGQ------QGGGL   863
          : : ::|  :| |||::|: |||  :  |  |:   ||:  |:| | |        :|
Db   509  YYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAIFRPGTSFGI   568

Qy   864  SVLRTFRLMRVLKLVRFLLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCK  923
          ||||  ||:|::|::|:                  ::    |  ||:|:| |||:|||| :
Db   569  SVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFLFIVFALLGMQLFGGR     628

Qy   924  FASERDGDTLPDRKNFDSLLWAIVTVFQLITQEDWNKVLYNGM----ASTSSWAALYFI    978
          |  :  ||        | : : :||:|||||| |:|| : ||:         ||| ||||
Db   629  F-NFNDG---TPSANFDIFPAAIMTVFQLITGEDWNEVMYNGIRSQGGVSSGMWSAIYFI    684

Qy   979  ALMTFGNYVLFNLLIVAILVEGFQAEGDATKSE-SEPDFFS----------------P   1018
           : ||||| | |:| :||:: : |   : ||::  | :                   |
Db   685  VLTLFGNYTLLNNVFLAIAVDNLANAQELTKDEQEEEAFNQKHALQKAKEVSPMSAPNMP  744

Qy  1019  SVDGDGDRKRKLAIVALGEHAELRKSL----------------LPPLIHTAATPM-S    1059
          |::  ||:::                    |||:: :::::| :
Db   745  SIERRRRRHHMS-VWEQRTSQLRKHMQMSSQEALNREEAPTMNPLNPLNPLSSLNPLNA    803

Qy  1060  HP----------KSSSTGV--------------GEALGSGGRRTS----SSGSAEPG   1088
          ||          ::
Db   804  HPSLYRRPRAIEGLALGLALEKFEERISRGGSLKGDGGDRSSALDNQRTPLSLGQREPP    863

Qy  1089  -AAHHEMKCPPSARSSPHSPWSAAASWTSRSRRNSLGRAPSLKRRSPSGERRSLLSGE   1146
Db   864  WLARPCHGNGCDPTQQEA--GGGEAVVTFEDRARHRQSQRRS---RHRRVRTEGKESSSAS  918

Qy  1147  GQESQDEEESSEEDRASPAGSDHRHRG------SLEREAKSSFDLPDTLQVPGLHRTAS   1199
          | :|  | ::
Db   919  RSRSASQERSLDEAMPTEGEKDHELRGNHGAKEPTIQEERAQDLRRTNSLMVSRGSGLAG   978

Qy  1200  GRSSAS--------------EHQDCNGKSASGRLAR------------------T     1222
          |  :|
Db   979  GLDEADTPLVLPHPELEVGKHVVLTEQEPEGSSEQALLGNVQLDMGRVISQSEPDLSCIT  1038

Qy  1223  LRTD-----------DPQLDG----------------------DDDNDEGNLSK       1243
Db  1039  ANTDKATTESTSVTVAIPDVDPLVDSTVVHISNKTDGEASPLKEAEIREDEEEVEKKKQK  1098

Qy  1244  GERIQAWVRSRLPACCRERDSWSAYIPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCIT   1303
          | |: :                                 :|  : : ::||:||:
Db  1099  KEKRETG-KAMVPHS-----------SMFIFSTTNPIRRACHYIVNLRYFEMCILLVIAASSIA  1150

Qy  1304  IAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEQAYLRSSWNVLDGL   1363
          :| :  | |  || :|  | ||:|||:|  |:|:||:  |  ||:|||: :  ||||::
Db  1151  LAAEDPVLTNSERNKV-LRYFDYVFTGVFTFEMVIKMIDQGLILQDGSYFRDLWNILDFV  1209

Qy  1364  LVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKP  1422
          :|  :|    |||  ::|  |:||:|||||:|||||||| : |:    || |||| |::
Db  1210  VVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPLKTIKRLPKLKAVFDCVVTSLKN    1269

Qy  1423  IGNIVICCAFFIIFGILGVQLFKGKFVC--QGEDIRN----ITNKSDCAEASYR-W     1473
          : |::|  :|:::||:: |||||||| :      |:         |:|  : ::  |
Db  1270  VFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDTEKECIGNYVDHEKNKMEVKGREW  1329

Qy  1474  VRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLL  1533
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Db  1330  KRHEFHYDNIIWALLLTLFTVSTGEGWPQVLQHSVDVTEDRGPSRSNRMEMSIFYVVVFV  1389
          ||::::||| ||::|| :||:|::|::::|||:|:|                   VVVVFV 1389

Db  1534  IVARFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRSEKQMAEAAQCKPY   1593
          :||:|| ::||||:|::|:|                                     1593

Db  1390  VPFPFFVNIFVALIIITF------QEQGDKMMEE--CSLEKNERACIDFAISAKPLTR   1439
          |::::| ||:||:|||:                                        1439

Db  1594  YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPOILDEALKICNYIFT  1651
          :|:|||   ||:| |  :::                                     1651

Db  1440  YMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTVVLMKYYSAPCTYELALKYLNIAFT   1499
          ::||:||                                                  1499

Db  1652  VIFVFESVFKLVAFAFRRFFQDRWNQLDIAIVLLSIMGITLEEIEVNLSLPINPTIRIM   1711
          |||:|::                                                  1711

Db  1500  MVFSLECVLKVIAFGFLNYFRDTWNIFDFITVIGSITEIILTDSKLVNTSGFNMSFLKLF  1559
          ||:                                                     1559

Db  1712  RVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECD  1771
          :|:|:||||:||::|                                          1771

Db  1560  RA--ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVFGNIKLD   1616
          |                                                       1616

Db  1772  -ETHPCEGLGRHATIFRNFGMAFLILFRVSTGDNWNGIMKD--PSRDCDQPSTC-      1821
          :||                                                     1821

Db  1617  EESH---INRHNNFRSFFGSLMLLFRSATGEAWQEIMLSCLGEKGCEPDTTAPSGQNEN   1672
          |:||                                                    1672

Db  1822  --YNTVISPIYFVSFVLTAQFVLNVVIAVIMKHLEESNKEAK----EEAELEAEL      1871
           :::                                                    1871

Db  1673  ERCGTDLAYYVFVSFIFFCSFLMLNLFVAVIMDNFEYLITRDSSILGPHHLDEFVRVWAEY  1732
          ||                                                      1732

Db  1872  E------LEMKTL-SPQPHSPLG--------SPFLWPGVEGVNSTDSPKPGAPHTT      1912
          |                                                       1912

Db  1733  DRAACGRIHYTEMYEMLTLMSP--------PLGLGKRCPSKVAYKRLVLMN-----MPVAEDMT 1783
          :||                                                     1783

Db  1913  AH------IGAASG--------------FSLEHPTMV--PHPEE---VPVPLGPD      1942
          ||                                                      1942

Db  1784  VHFTSTLMALIRTALDIKIAKGADRQQLDSELQKETLAIWPHLSQKMLDLLVPMPKASD   1843
          |                                                       1843

Db  1943  LLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCI  2002
          :|||:|:                                                  2002

Db  1844  -LTVGKIYAA--MMIMDYYKQSKVKKQRQQL------EEQKNAPMFQRMEPS-        1886
                                                                  1886

Db  2003  LQLPKDV-------HYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRRQAAIRTDSLDVQG  2055
          ::                                                      2055

Db  1887  -SLPQEIANAKALPYLQQD---PVSGLSGRSGYPSMSPLSPQDIFQLACM--DPADDGQ   1940
          :                                                       1940

Db  2056  LGSREDLLSEVSGPSCPL--------TRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPC  2107
          |                                                       2107

Db  1941  FQERQSLIV--VTDPSSMRRSFSTIRDKRSNSSW------LEEFSMERSS-         1981
          ::                                                      1981

Db  2108  PGLEPSWAKDPPETRSSLELDT-ELSWISG---DLLPSSQEEPLFPRDLKKCYSVETQSC  2163
          ||                                                      2163

Db  1982  -ENTYKSRRRSYHSSLRLSAHRLNSDSGHKSDTHPSGGRERRRSXERKHLLSPDVSRC   2038
                                                                  2038

Db  2164  ---RRRPGFWLDEQRHSIAVSCLDSGSQPRLCPSPSSLGGOPLGGPGSRPKKKLSPPS   2219
          :                                                       2219

Db  2039  NSEERGTQADWESPERRQS--------RSFSEGRSQTPNRQGTGSLSESSIPS       2083
          :                                                       2083

Db  2220  IS--IDPPESQGSRPPCSPG--------VCLRRRA------PASDSKD-PSVVSPLDSTAA  2263
          ::                                                      2263

Db  2084  VSDTSTPRRSRRQLPPVPPKPRPLLSYSSLIRHAGSISPPADGSEEGSPLTSQALESNNA  2143
          :                                                       2143

Qy  2264  ------SPSPKK                                               2269
          :                                                       2269

Db  2144  WLTESSNSPHPQQ                                              2156
```

RESULT 13

A54972

voltage-dependent calcium channel alpha 1E-3 - human

C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54972
R;Williams, M.E.; Marrubio, L.M., Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mi
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel

```
A:Reference number: A54972; MUID:94350992; PMID:8071363
A:Accession: A54972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2270 <WIL>
A:Cross-references: UNIPROT:Q15878; GB:L29385; NID:g495869; PIDN:AAA59205.1; PID:g495870
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match        13.6%;   Score 1637.5;  DB 2;   Length 2270;
Best Local Similarity 23.6%; Pred. No. 1.6e-95;
Matches 601; Conservative 394; Mismatches 815; Indels 741; Gaps 87;

Qy     73 PGSADSEA------EGLPYPALA----------------------------PV------VFFY   95
                                                                 :| |:  ||||
Db     12 PGGSDGDSDQSRNRQGTPVPASGQAAAYKQTKAQRARTMALYNPIPVRQNCFTVNRSLFI   71

Qy     96 LSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFR--PCEDIACDSQRCRILQAFD  153
           ||:|| :.|: .||: ::|::|:  .: ||||||| ::     |::: :| | .::.:
Db     72 FGEDNIVRKYAKKLLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR--LEKTE  128

Qy    154 DFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN--VSFSA  210
           ||| |::|||:|:|:||:| :: |  ||||||||||:| ||:|:||.||.|:    ||.|
Db    129 PYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFNTHVDLRT  188

Qy    211 VRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFVFFIFGIVGVQLWAGLLR   270
           | ||||||| |.: :| |. :   ::   .| :.|::| |.:| |:|| |: :.:|
Db    189 LRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYSGKLH  248

Qy    271 NRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPC   330
           ..| :    .|||| ::.|                                      :
Db    249 RACFMNN------SGILEGF------DPPHPC----------------------GVQGC  273

Qy    331 SLDYETYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD  390
           ...   |::    .||.|  :.                :|||:| ::|.|:|:| ||::
Db    274 PAGYE------CKDW------------------IGPNDGITQFDNLFAVLTVFQCITMEGWTT  313

Qy    391 IMYFVMDA-HSFYNFIYFPILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFL  449
           :||.|:|| ||||:|: | |:| ||| ||::|| |:|:.: :     ::::||.:.|  :
Db    314 VLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERV----ENRRAFM  368

Qy    450 SNASTLASFSEPGSCYEELLKYLVVLRKAARRLAQVSRAI-GVRAGLLSSPVARSGQEP  508
           .            |: | | | |.| ::.  :|:    |  | ::  :.:  :
Db    369 K-----------------------LRRQQQIERELNGYRAWIDKAEEVMLAAEEN  399

Qy    509 QPSGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPP   568
           . :. |   : |:..:||                :|| || .|  |:.|:|||:|||
Db    400 KNAGTSALEVLRRAT---------------------------IKRSRTEAMTRDSS----  428

Qy    569 PSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTS  628
           .                               :|||:.|:    :.|  |: |
Db    429 ----------------------------------FRHKE------------------  428

Qy    629 PPPILKDKALVEVAPSPGPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSK   688
                :                                                :| ::|
Db    429 ----DEHCVDIS-----------------------------SVGTPLAR  444

Qy    689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS  748
           :: |  |:.     .|:                      :  |:.| .:| ::.||.:|
Db    445 ASIKSAKVDGVSY----------------------------------PRHKE------  462

Qy    749 LGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL  808
                    :  | |::| :|.| | :||  ||.|:::|| :.|.|||.||.:|  :|.:
Db    463 ------RLLRISIRHMVKSQVFYWIVLSLVALNTACVAIVHHNQPQWLTHLL  508

Qy    809 EISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGL  863
           ||:|:|:| ||| |:|||:||  || :.| | :|||  | :|| ||: |       |: |
Db    509 YYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAAIFRPGTSFGI  568

Qy    864 SVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCK  923
            |:|:  |:||:||:||:|   ::|:.|||:        |:::: : |:|| |.:|||
Db    569 SVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLLFLFLFIVVFALLGMQLFGGR  628

Qy    924 FASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFI  978
           |.||||                .: .::||:::|||| | ||        :.|  |:| |
Db    629 F-NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGVSSGMWSAIYFI  684
```

```
Qy    979 ALMTFGNYVLFNLLVAILLVEGFQAEGDATKSE-SEPDFFS------------------ 1018
           |::||||:||||||.:.|:  |  |..:                               |
Db    685 VLTLFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEEAFNQKHALQKAKEVSPMSAPNMP  744

Qy   1019 SVDGDGDRKKRIAL-------------------------VALGEH--AELRKSL----  1045
           | |:| :|  |:                            |:||:   |:|::
Db    745 SIERDRRRHRHHMSWEPRSSHLRERRRHHMSVWEQRTSQLRKHMQMSSQEALNREEAPT  804

Qy   1046 ---LPPLIHTAATPM-SHP-----------------------KSSSTGV----GEALGSGSRRT 1079
              ::|::|:.|:|  |:|                       |.| : |     ||:||:|.|
Db    805 MNPLNPLNPLSSLNPINAHPSLYRRPRAIEGLALGLALEKFEEERISRGGSLKGDGGDRS  864

Qy   1080 S----------------------SSGSAEPG--AAHHEMKCPPSARSSPHSPWSAASWTSRSSRNSLGRAP 1128
           |                       .||:.| |   | ::|  |:| :  .|.||:.: .:||:.|:. :|
Db    865 SALDNQRTPLSLGQREPPWLARPCHGNCDPTQQEA--GGGEAVVTFEDRARHRQSQRRS-  921

Qy   1129 SLKRRSPSGERRSLLSGEGQESQDEESSEDRASPAGSDHRHG-----------SLEREAKS 1181
           |  ||.: .| |:||   :.|:    |:|   : :| .|:||              ::| |
Db    922 --RHRVRTEGKESSSASRSRSASQERSLDEAMPTEGEKDHELRGNHGAKEPTIQEERAQ  979

Qy   1182 SFDLPDTLQVPGLHRTASGRSSAS---------------------------EHQDCNGKSASGRLAR-- 1221
           ||:|   |:| .|  ::..| ::|                            .|.:.  :.::.|:|
Db    980 DLRRTNSLMVSRGSGLAGGLDEADTPLVLPHPELVGKHVVLTEQEPEGSSEQALLGNVQ 1039

Qy   1222 ---------------------------------------------------DPQLDG-  1232
                                                              ||| :
Db   1040 LDMGRVISQSEPDLSCITANTDKATTESTSVTVAIPDVDPLVDSTVVHISNKTDGEASPL 1099

Qy   1233 -------------DDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIIT 1285
                        :::: :.| : :| |:|.::|| ||   :.||:|:||:|| || |: |::||
Db   1100 KEAEIREDEEEVEKKQKKEKRETG-KAMVPHS-------SMFIFSTNPIRRACHYIVN 1151

Qy   1286 HKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGW 1345
           |:: ::|:|::::|||.||||.| |:| ||::|: |:||:|:|.||||.|||.|:|||.|
Db   1152 LRYFEMCILLVIAASSIALAAEDPVLTNSERNKV-LRYFDYVFTGVFTFEMVIKMIDQGL 1210

Qy   1346 CFGEQAYLRSSWNVLDGLLVLLVSVIDI-LVSMVSDSGTKILGMRVLRLLRTLRPLRVIS 1404
           |:|.:|.|:|.|.|||:||::|:: :|  :|:|:::||.|:|||:|:|:||::|||:|:
Db   1211 IIQDGSYFRDLWNILDFVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPLKTIK 1270

Qy   1405 RAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC--QGEDTRN--- 1459
           | .|::|:|::|:.||:| |||:::. ||::|| ||||:||:|||| |   .|:..
Db   1271 RLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFYCTDSSKDTEKECI 1330

Qy   1460 ---ITNKSDCAEASYR-WVRHKYNFDNLGQAIMSLFVLASKDGWVDIMYDGLDAVGVDQQ 1515
              ::|:|:|| ||:| ||||::.||:|:.:: ||| : ||:.||: |||.|:  || ||
Db   1331 GNYVDHEKNKMEVKGREWKRHEFHYDNIIWALLLTFVVSTGEGWPQVLQHSVDVTEEDRG 1390

Qy   1516 PIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREKRLRRLE 1575
           ||:.::||:|||||.|: :|.|::|||||.||: ||||  :  |::|   |:||:|:|:|
Db   1391 PSRSNRMEMSIFYVVYFVFFPFFVNFVALIIITF------QEQGDKMMEE----CSLE 1440

Qy   1576 KKRRSKEKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVTMAMEHY 1633
           |::|:.|::.:  :|  :|||:||    :|::||:|||||: |:  |::| :||:|: |
Db   1441 KNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTVVLMMKYY 1500

Qy   1634 QQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFPPQDRWNQLDLAIVLLSIMGITLE 1693
           :||:|||:||:|||||:|.:|| |:|||:|| :   |  |||||::| || |: |.|.||
Db   1501 SAPCTYELALKYLNLAFTMVFSLECVLKVIAFGFLNYFRDTWNIFDFITVIGSITEIILT 1560

Qy   1694 EIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLL 1753
           | :| |:.|: |.||| || :|:||.|| :|||    | ||:| | ||: . ::| |:|
Db   1561 DSKLVNTSGFNMSFLKLFRA----ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAML 1617

Qy   1754 FFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD--- 1810
           ||:  .|| |::| :::| :   .| |:  :   |  :.:|: |:::|:.:|:  ::
Db   1618 FFIYAIIGMQVFGNIKLDEESH----INRHNNFRSFFGSLMLLFRSATGEAWQEIMLSCL 1673

Qy   1811 PSRDCDQESTC----------------------YNTVLSPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
           |:|:|::.||                          | | ::| | :: ::
Db   1811 FASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFI  978
```

```
Db   1674  GEKGCEPDTTAPSGQNENERCGTDLAYVYFVGFIFFCSFLMLNLFVAVIMDNFEYLTRDS  1733
Qy    283  LRQKCVLNPVPELGTNITHDEWDNDWVNNESHWQKDFYDEWQ--VC                325

Qy   1862  K-------ERAELEAELE------LEMKTL-SPQPHSPLG------SPFLWPG          1894
Db    320  LRGEGGGGPPCSLDYETNSSSNTTCV-NWNQYYTNCSAGEHNPFKGAINFDNIGYAWIA   378

Db   1734  SILGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTLMSP----PLGLGKRCPSKVAYKR  1789
Qy    326  --GNGTGAGKCG--NGTINGTAEWLCLPNIGQ----------NPNHDFTSFDNFGMALLC  371

Qy   1895  VEGVNSTDSPKPGCAPHTTAH-------IGAASG-------FSLEHPTMV--P         1930
Db    379  IFQVITLEGWVDIMYFVMDAHSFYNFIYPILLIIVGSFFMINLCLVVIATQFSETKQRES  438

Db   1790  LVLMN-----MPVAEDMTVHFTSTLMALIRTALDIKIAKGGADRQQLDSELQKETLAIWP  1844
Qy    372  AFRLMTQDFWESLYHLVLRAVGSAHCLYFVLVILLGSFYLVLNLLAIVAMSYDET-QKQD  430

Qy   1931  HPEE------VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKA  1984
Db    439  QLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYLRKAARRIA-QVSRAIGVRAGLL   497

Db   1845  HLSQKMLDLLVPMPKASD-LTVGKIYAA--MMIMDYYKQSKVKKQRCQL------EE     1892
Qy    431  QADAEEEA---------AERQE--------EEARKEALSIMTKSPSNSSWNNDFEAGVR-  472

Qy   1985  QSGSILSVHSQPADTSCILQLPKDV------HYLLQPHGAPTWGAIPKLPPPGRSPLAQ   2037
Db    498  SSPVARSGQPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRD    557

Db   1893  QKNAPMFQRMEPS------SLPQEIIANAKALPYIQQD--PVSGLSGRSGYPSMSPLSP  1943
Qy    473  ---TAGDKAEKERLSLTSDHSATSAHLKPSRLNQKRH------SLSLP-GSPYIHRRN   521

Qy   2038  RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPL-------TRSSSFWGGGSIQVQQ  2089
Db    558  ANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVG  617

Db   1944  QDIFQLACM--DPADDGQFQERQSLV--VTDPSSMRRSFSTIRDKRSNSSW------LEE 1993
Qy    522  SRGSGQYSWRKPVPTAKRS----------------------PYCPDR              545

Qy   2090  RSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDT-ELSWISG---DLLPSSQEE 2145
Db    618  SGKVYPTVHTSPPPEILKDKALVEVAPSPGPPLTSF------NIPPG--PFSSMHKLLET 670

Db   1994  FSMERSS-----------ENTYKSRRRSYHSSLRLSAHRLNSDSGHKSDTHPSGGRE    2039
Qy    546  QPLVHHTLENILPLP-FADDSAAV------TPSSEDLCNFSFIRNMPNGRRFSFASQRRPDGT 600

Qy   2146  PLFPRDLKKCYSVETQSC---RRRPGFWLDEQRRHSIAVSCLDSGSGQPRLCPSPSSLGG 2201
Db    671  QSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGE----------PESA-D      714

Db   2040  RRRSKERKHLLSPDVSRCNSEERGTQADWESPERRQS-------RSPSEGRS         2084
Qy    601  GRSGRRSS--FASNHSRASRTSRG-------------SGGGDRTKTQTLLNFKKGKVPDVLD 649

Qy   2202  QPLGGPGSRPKKKLSPPSIS--IDDPESQSRPPCSPG------VCLRRRA-----PAS   2247
Db    715  HVMPDSDSEAVYEFTQDAQHSDLRDPHSRRR-------QRSLGPDAEPSSVLA        760

Db   2085  QTPNRQGTGSLSESSIPSVSDTSTPRRSRQLPPVPPKPRPLLSYSSLIRHAGSISPPAD  2144
Qy    650  KSKLDDDQDSV--SSGGSGHCPEKDKASESNPFLSHSPGGPNVEMKDVMVLKDILDQASG 707

Qy   2248  DSKD--PSVSSPLDSTAA--------SPSPKK                              2269
Qy    761  -----------FWRLIC---------DTFRKI                              789

Db   2145  GSEEGSPLTSQALESNNAWLTESSNSPHPQQ                               2175
Db    708  HRRSFVSMTSIHQRTMKDIMWKYFCWDCHPNFQKLQRLVSLFIMDAFVDLFITICILVN   767

Qy    790  TLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVV  849
Db    768  TAFMAMEHYDMEDDLKAVSNAANLVFTAIFAVBAFLKIALSPVIYFKDGWNIFDSIIVA   827

Qy    850  ISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFI  909
Db    828  LSLMELSMTKLPGLSVLRAFRLLRVFKLAKSWPTLNMLIAIVGRTMGALGNLIIVLGIII  887

Qy    910  FIFSILGWHLFGCKFAS-ERD----------GDTLPDRKNFDSLLWAIVTVFQILTQEDW  958
Db    888  FIFAVMGQQLFSSDYKTYEREIDAWGNVTINKDKMP-RWNFNDFLHSPMIVFRVLCGE-W  945

Qy    959  NKVLYNGMASTSSWAAL-YFIALMTFGNYVLFNLLVLNLVVGNLVVLNLFLALLLSFGSESLQRSESDDEPDFF 1016
Db    946  IESMW-GCYLVSGWACVPFLLTYVVGNLVVLNLFLALLLSFGSESLQRSESDDEPSKI   1004

Qy   1017  SPSVDGDGDRKKRLA------LVALGEHAELRKSLLPLIIHTAATPMSHPKSSSTGVG   1069
Db   1005  AEAI-----DRFKRFGNWVKVKIIVCIKVLQRQKNWRPP--------PTTGQS       1045

Qy   1070  EALGSGSRRTSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAAASWTSRRRSSRNSLGRAPS 1129
Db   1046  EVNG------KDPAVVDGTVSMEKTPDDFPDGPCCPAQAAIC                   1082

Qy   1130  LKRRSPSGERRSLLSGBGGEQESQDEEESSEEDRASPAGSDRHRGSLEREAKSSFDLPDTL 1189
Db   1083  SAKKDLKSPSGS-HSNSGS                                          1100

Qy   1190  QVPGLHRTASGRSASASEHQDCNGKSAGSGRLARTLRTDPQLGDGDDNDEGNLSKGERIQA 1249
Db   1101  SHCSSCSSLSESAQTKKID---LEADHEINEVEI---V                       1132

Qy   1250  WSAYIFPPQSRFRLLCHRIITHKMPDHVV                                1293
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RESULT 14

T30902

sodium channel SCAP1 alpha chain - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
R;Reference number: Z20929; MUID:97238630; PMID:9115644
A;Accession: T30902
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1993 <DYE>
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C;Superfamily: sodium channel protein

Query Match   13.6%; Score 1636; DB 2; Length 1993;
Best Local Similarity   25.8%; Pred. No. 1.7e-95;
Matches 518; Conservative 348; Mismatches 702; Indels 442; Gaps 69;

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Qy     94  FYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGM--FRPCEDIACDSQRCRIIQA  151
Db    ...

Qy    119  FLLSPFNFIRRAIYILVHPIFSLLVMMTILVNCVFMAITSYTP--------------PA  164

Qy    152  FDDFIF-AFFAVEMVKMVALGIFGKK-CYLGDTWNRLDFFIV-IAGMLEYSLDLQNVSF   208

Qy    165  FVEHIFLGIYTVBAVVKVLSRGFVLKPFTYLRDPWNWLDFFVISIAYMTVKSFGNL--   222

Qy    209  SAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIRGIVGVLAWGL  268

Qy    223  QALRTFRVLRALKTISVIPGLKTIVGALLEAVRFLRDVWNWLDFFVLSIFALIGMQLYSGA  282

Qy    269  LRNRCFLPENFSLPLS-------VDLEPYYQTENEDESPFICSQPRENGMRSCRSVPT   319
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Db   1133 YVKFPDDCFCYMCTKRCPWCVKVEKSKIGRAWWA--------VRCFFYRLTENKYFDSFI 1184

Qy     94 FYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFR--PCEDIACDSQRCRILQA 151
           :  ||:   :  |    :   ::||  ||||||| :|: :        :  ::|    |
Db     21 FIFGEDNIVRKYAKKLLIDWPPFEYMLATIIANCIVLALEGHLPEDDKTPMSRR----LEK 77

Db   1294 LVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVPLAEMTVKVVALGWCFGEQAYI 1353
Qy   1185 IAMLLASSCALALEDAYLHEKPLIKEILEYLDKVFTAIPIIEMLIKWLA----FGFKTYF 1240

Qy   1354 RSSWNVLDGLLVLISVIDILVSM-VSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLV 1412
Db   1241 TDAWCWLDFTIVMLSIVMLVADILTASEEGGSMSWMKSMRTLRALRPLRAVSRWEGMRVV 1300

Qy   1413 VETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFVCQGE----DTRNITNKSDCA 1467
Db   1301 VNALFKAIPSICNVLLVCLVFWLIFGIMGVQLFGNGKFHACRDEKGDKYPREEVPNKTVCI 1360

Qy   1468 EASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLY 1527
Db   1361 DKGYNWTNAQINFDHVLSAYLALFQVATYKGWIDIMNNAIDSTEIGQQPSREENVIMYLF 1420

Qy   1528 FISFLLIVAFFVLNMFVGVVVENFH--KCRQHQEEEEARRREEKRLRRIEKKRRSKEKQM 1585
Db   1421 FVLFIVPCSFFTLNLFIGVIIENFSQKKKAGGSLEMFTEDQKKYYNAMKRMQSKSPQ- 1479

Qy   1586 AEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKI 1645
Db   1480 -KSIPRPKY---KLAGLIFDITTDQKFDIAIMVIIIINMLTMMFEHHGMSAQMKNIIGI 1534

Qy   1646 CNYIFTVIFVIFESVFKJVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINP 1705
Db   1535 FNLIFITTIFTABCVLKLIGLRW--YYFKIPWNVFDFVVVLSILASSLSEFFD--SFFISP 1591

Qy   1706 TIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELF 1765
Db   1592 TLLRVIRVFRVGRVLRLIVKSAKGIRTLLFSMAVSLPALFNIGLLLGLIMFIYAIMGMNFF 1651

Qy   1766 GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTV 1825
Db   1652 --MGAEQKY---GLDDAFNFDTFLRSFILLFQMCTSAGWSDVLNGLIARCAPEGTCKDYN 1706

Qy   1826 ISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELAELEMKTLSPQHSP 1885
Db   1707 VATIYLATYLVVSFLVVVNMYIAVILENFSQATED--EQQGLTPD-DFDMYEKWEKYDP 1763

Qy   1886 LGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF--SLEHPTMVPHPE----EVPVP 1938
Db   1764 KASKYI-------------------PLDQLSDFVDYLEEPLRLPKPNHFILVKLDIP 1801

Qy   1939 LGP---------DLLTVRKSGVSRTHSLP 1958
Db   1802 ICENDRCYCRDILDALTKNFLGTGETSDIP 1831
```

RESULT 15

A37490

voltage-dependent calcium channel alpha 1E - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A37490
R;Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A;Title: Structure and functional expression of a member of the low voltage-activated ca
A;Reference number: A37490; MUID:93262464; PMID:8388125
A;Accession: A37490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2222 <SOO>
A;Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:132101)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   13.6%;   Score 1632.5;   DB 2;   Length 2222;
Best Local Similarity   23.6%;   Pred. No. 3.3e-95;
Matches 587;   Conservative 389;   Mismatches 819;   Indels 697;   Gaps 81;

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Qy  1087 ------------------------PGAAHHEMKCPPSARSSPHSPW-----SAASSWTSRRS  1119
Db   814 LTSVLDNQRSPLSLGKREPPWLPRSCHG--NCDPTQQEFGGGETVVTFEDRARHRQSQRR    871
Qy  1120 SRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREA   1179
Db   872 SRHRRVRTEGKESASASRSR---SASQERSLDEGVSIDGEKEHEPQSSHRSKEPTIHEE    927
Qy  1180 KSSFDL--PDTLQVP---GL--------HRTASGRSSASEHQDCNGKSASGRL         1219
Db   928 ERTQDLRRTNSLMVPRGSGLVGALDEAETPLVQPQPELEVGKDAALITEQEAEGSSEQALL   987
Qy  1220 A-------RTLRTDDPQL----------------------------------DG-       1232
Db   988 ADVQLDVGRGISQSEPDLSCMTTNMDKATTESTSVTVAIPDVDPLVDSTVVNISNKTDGE   1047
Qy  1233 ----------DDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCH   1281
Db  1048 ASPLKEAETKEEEEEVEKKQKKEKRETG-KAMVPHS--------SMFIFSTTNPIRKACH   1099
Qy  1282 RIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVV   1341
Db  1100 YIVNLRYFEMCILLVIAASSIALAAEDPVLTNSERNKV-LRYFDYVFTGVFTFEMVIKMI   1158
Qy  1342 ALGWCFGEQAYLRSSWNVLDGLLLVLLSVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPL  1400
Db  1159 DQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPL   1218
Qy  1401 RVISRAQGLKLVVETIMSSLKPIGNIVVICCAFFIFGILGVQLFKGKFFVC--QGEDTR   1458
Db  1219 KTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDTE   1278
Qy  1459 N------ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG   1511
Db  1279 KECIGNYVDHEKNKMEVKGREWKRHEFHYDNIIWALLTLFTVSTGEGWPQVLQHSVDVTE   1338
Qy  1512 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREKRL   1571
Db  1339 EDRGPSRNRMEMSIFYVVYVVFPFFVNIFVALIIITF-------QEQGDKMMEE---     1388
Qy  1572 RRLEKKRRSKBKQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMA   1629
Db  1389 CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTVVLM   1448
Qy  1630 MEHYQQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMG  1689
Db  1449 MKYYSAPWTYELALKYLNIAFTMVFSLECVLKVIAFGFLNYFRDTWNIFDFITVIGSITE   1508
Qy  1690 ITLEEIEVNLSLPINPTIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLL   1749
Db  1509 IILTDSKLVNTSGFNMSFLKLFRA--ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLL   1565
Qy  1750 FMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIM   1808
Db  1566 IAMLFFIYAIIGMQVFGNIKLDEESH----INRHNNFRSFFGGSLMLLFRSATGEAWQEIM   1621
Qy  1809 KD--PSRDCDQESTC--------YNTVISPIYFVVSFVLTAQFVLVNVVIAVLMKHLEES   1857
Db  1622 LSCLGEKGCEPDTTAPSGQNESERCGTDLAYYYFVSFIFFCSFLMLNLFVAVIMDNFEYL   1681
Qy  1858 NKEAK-------EEAELEAELE-------------LEMKTL-SPQHSPLG------SPF   1890
Db  1682 TRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTLMSP-----PLGLGKRCPSKV  1737
Qy  1891 LWPGVEGVNSTDSPKPGAPHTTAH------------IGAASG----------FSLEHPTM  1928
Db  1738 AYKRLVLMN-----MPVAEDMTVHFTSTLMALIRTALDIKIAKGGADRQQLDSELQKETL   1792
Qy  1929 V--PHPEE-----VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWG   1980
Db  1793 AIWPHLSQKMLDLLVPMPKASD-LTVGKIYAA----MMIMDYYKQSKVKKQRQQL------  1842
Qy  1981 LPKAQSGSILSVHSQPAD-TSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRP   2039

Db  1843 --EEQKNAPMFQRMEPSSLPQEIISNAKALPYLQQD---PVSGLSGRSGYPSMSPLSPQE   1897
Qy  2040 LRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPL-------TRSSSFW------------   2080
Db  1898 IFQLACM--DPADDGQFQEQQSLV--VTDPSSMRRSFSTIRDKRSNSSWLEEFSMERSSE   1953
Qy  2081 ----------QRSG--IQSKVSKHIRLP--APC----                        2107
Db  1954 NTYKSRRRSYHSSLRLSAHRLNSDSGHKSDTHRSGGRERGRSKERKHLLSPDVSRCNSEE   2013
Qy  2108 PGLEPSW------AKDPPETRSSLELDTELSWISGDLLPSQEEPLFPRDLKKCVSVET    2160
Db  2014 RGTQADWESPERRQSRSPSEGRSQTPNRQGTGSLSESSIPSISDTSTPRRSRRQLPPVPP   2073
Qy  2161 QSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKK-LSPPS   2219
Db  2074 ---KPRPLLSYSSLMRHTGGISPPPDGSE-----------------GGSPLASQALESNSACLTESS  2120
Qy  2220 ISIDPPESQGSRPP---CSPGVCLRRRAPASD                             2248
Db  2121 NSLHPQQGQHPSPQHYISEPYLALHEDSHASD                             2152
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Search completed: November 18, 2004, 13:34:36
Job time : 94.7329 secs

OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.
GenCore version 5.1.6

Run on: November 18, 2004, 13:06:30 ; Search time 254.167 seconds
                                         (without alignments)
                                         5177.235 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR.........KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : UniProt 02:*
           1: uniprot_sprot:*
           2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11657	96.9	2254	1	CCAG_RAT	O54898 rattus norv
2	11657	96.9	2254	2	AAG35186	Aag35186 rattus no
3	11532	95.9	2288	2	Q9WUB8	Q9wub8 rattus norv
4	11372.5	94.6	2295	2	Q9WUT2	Q9wut2 mus musculu
5	11263	93.6	2248	2	Q6PFV8	Q6pfv8 mus musculu
6	11263	93.6	2248	2	AAH57399	Aah57399 mus muscu
7	10732.5	89.2	2377	1	CCAG_HUMAN	O43497 homo sapien
8	6809.5	56.6	1389	2	Q6ZPX4	Q6zpx4 mus musculu
9	6809.5	56.6	1389	2	BAC98104	Bac98104 mus muscu
10	6226	51.8	2359	1	CCAH_RAT	Q9eq60 rattus norv
11	6222	51.7	2353	1	CCAH_HUMAN	O95180 homo sapien
12	6190	51.5	2365	1	CCAH_MOUSE	O88427 mus musculu
13	5418	45.0	2223	1	CCAI_HUMAN	Q9p0x4 homo sapien
14	5354	44.5	1835	1	CCAI_RAT	Q9z0y8 rattus norv
15	4750.5	39.5	1994	2	Q7Z6S8	Q7z6s8 homo sapien
16	4188.5	34.8	1762	2	Q7PQV4	Q7pqv4 anopheles g
17	4137.5	34.4	2893	2	Q9W433	Q9w433 drosophila
18	3856.5	32.1	1837	2	Q967R4	Q967r4 caenorhabdi
19	3849	32.0	1852	2	Q7Z002	Q7z002 caenorhabdi
20	3849	32.0	1852	2	AAR25651	Aar25651 caenorhab
21	3830	31.8	1844	2	Q7YZR6	Q7yzr6 caenorhabdi
22	3830	31.8	1844	2	AAR25653	Aar25653 caenorhab
23	3824.5	31.8	1885	2	Q7Z003	Q7z003 caenorhabdi
24	3824.5	31.8	1885	2	AAR25652	Aar25652 caenorhab
25	3665	30.5	1460	2	Q80TU2	Q80tu2 mus musculu
26	3665	30.5	1418	2	Q7JPB4	Q7jpb4 caenorhabdi
27	2941.5	24.5	1418	2	AAR30210	Aar30210 caenorhab
28	2813.5	23.4	1942	2	Q869H0	Q869h0 lymnaea sta
29	2098.5	17.4	1211	2	Q8MQ95	Q8mq95 caenorhabdi
30	1727	14.4	541	2	Q6PE92	Q6pe92 mus musculu
31	1727	14.4	541	2	AAH58206	Aah58206 mus muscu
32	1720.5	14.3	1810	2	O44930	044930 aiptasia pa
33	1678	14.0	2327	1	CCAB_MOUSE	055017 mus musculu
34	1674	13.9	2339	1	CCAB_HUMAN	Q00975 homo sapien
35	1673	13.9	2331	2	Q9TT4	Q9tta4 bos taurus
36	1666.5	13.9	1599	2	Q7PNK9	Q7pnk9 anopheles g
37	1665.5	13.8	2259	1	CCAE_RABIT	Q02343 oryctolagus
38	1661	13.8	2333	2	O89089	089089 rattus norv
39	1660	13.8	2295	2	Q923K6	Q923k6 rattus norv
40	1656	13.8	2304	1	Q9BMQ4	Q9bmq4 blattella g
41	1653.5	13.7	2272	1	CCAE_MOUSE	Q61290 mus musculu
42	1652.5	13.7	1891	2	O97017	097017 stylophora
43	1650	13.7	2312	1	CCAE_HUMAN	Q15878 homo sapien
44	1649.5	13.7	1984	2	Q28644	Q28644 oryctolagus
45	1646.5	13.7	1847	2	Q6RKB0	Q6rkb0 brachydanio

ALIGNMENTS

RESULT 1
CCAG_RAT
ID   CCAG_RAT   STANDARD;   PRT;   2254 AA.
AC   O54898;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.1).
GN   Name=Cacna1g;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=98154730; PubMed=9495342;
RA   Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
RA   Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT   "Molecular characterization of a neuronal low-voltage-activated T-type
RT   calcium channel.";
RL   Nature 391:896-900(1998).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC   entry of calcium ions into excitable cells and are also involved
CC   in a variety of calcium-dependent processes, including muscle
CC   contraction, hormone or neurotransmitter release, gene expression,
CC   cell motility, cell division and cell death. The isoform alpha-1G
CC   gives rise to the T-type calcium currents. T-type calcium channels
CC   belong to the "low-voltage activated (LVA)" group and are strongly
CC   blocked by nickel and mibefradil. A particularity of this type of
CC   channels is an opening at quite negative potentials and a voltage-
CC   dependent inactivation. T-type channels serve pacemaking functions
CC   in both central neurons and cardiac nodal cells and support
CC   calcium signaling in secretory cells and vascular smooth muscle.
CC   They may also be involved in the modulation of firing patterns of
CC   neurons which is important for information processing as well as
CC   in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression
CC   in heart; low expression in placenta, kidney and lung.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC   hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC   positively charged transmembrane segment (S4). S4 segments
CC   probably represent the voltage-sensor and are characterized by a
CC   series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC   channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC   family.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its

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DR   EMBL; AF027984; AAC67372.1; -.
DR   PIR; T09053; T09053.
DR   RGD; 68942; Cacna1g.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW   Ionic channel; Multigene family; Phosphorylation; Repeat;
KW   Transmembrane; Voltage-gated channel.

FT   REPEAT       68    398       I.
FT   REPEAT      730    968       II.
FT   REPEAT     1242   1519       III.
FT   REPEAT     1564   1822       IV.
FT   DOMAIN        1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    101       S1 of repeat I.
FT   DOMAIN      102    119       Extracellular (Potential).
FT   TRANSMEM    120    141       S2 of repeat I (Potential).
FT   DOMAIN      142    150       Cytoplasmic (Potential).
FT   TRANSMEM    151    170       S3 of repeat I.
FT   DOMAIN      171    175       Extracellular (Potential).
FT   TRANSMEM    176    193       S4 of repeat I.
FT   DOMAIN      194    213       Cytoplasmic (Potential).
FT   TRANSMEM    214    234       S5 of repeat I (Potential).
FT   DOMAIN      235    370       Extracellular (Potential).
FT   TRANSMEM    371    395       S6 of repeat I (Potential).
FT   DOMAIN      396    744       Cytoplasmic (Potential).
FT   TRANSMEM    745    765       S1 of repeat II (Potential).
FT   DOMAIN      766    778       Extracellular (Potential).
FT   TRANSMEM    779    800       S2 of repeat II (Potential).
FT   DOMAIN      801    806       Cytoplasmic (Potential).
FT   TRANSMEM    807    825       S3 of repeat II (Potential).
FT   DOMAIN      826    833       Extracellular (Potential).
FT   TRANSMEM    834    857       S4 of repeat II.
FT   DOMAIN      858    868       Cytoplasmic (Potential).
FT   TRANSMEM    869    889       S5 of repeat II (Potential).
FT   DOMAIN      890    940       Extracellular (Potential).
FT   TRANSMEM    941    965       S6 of repeat II (Potential).
FT   DOMAIN      966   1251       Cytoplasmic (Potential).
FT   TRANSMEM   1252   1274       S1 of repeat III (Potential).
FT   DOMAIN     1275   1292       Extracellular (Potential).
FT   TRANSMEM   1293   1313       S2 of repeat III (Potential).
FT   DOMAIN     1314   1323       Cytoplasmic (Potential).
FT   TRANSMEM   1324   1343       S3 of repeat III (Potential).
FT   DOMAIN     1344   1357       Extracellular (Potential).
FT   TRANSMEM   1358   1379       S4 of repeat III.
FT   DOMAIN     1380   1389       Cytoplasmic (Potential).
FT   TRANSMEM   1390   1413       S5 of repeat III (Potential).
FT   DOMAIN     1414   1490       Extracellular (Potential).
FT   TRANSMEM   1491   1516       S6 of repeat III (Potential).
FT   DOMAIN     1517   1578       Cytoplasmic (Potential).
FT   TRANSMEM   1579   1599       S1 of repeat IV (Potential).
FT   DOMAIN     1600   1613       Extracellular (Potential).
FT   TRANSMEM   1614   1635       S2 of repeat IV (Potential).
FT   DOMAIN     1636   1642       Cytoplasmic (Potential).
FT   TRANSMEM   1643   1661       S3 of repeat IV (Potential).
FT   DOMAIN     1662   1675       Extracellular (Potential).
FT   TRANSMEM   1676   1699       S4 of repeat IV.
FT   DOMAIN     1700   1713       Cytoplasmic (Potential).
FT   TRANSMEM   1714   1734       S5 of repeat IV (Potential).
FT   DOMAIN     1735   1794       Extracellular (Potential).
FT   TRANSMEM   1795   1822       S6 of repeat IV (Potential).
FT   DOMAIN     1823   2254       Cytoplasmic (Potential).
FT   DOMAIN      290    295       Poly-Gly.
FT   DOMAIN      496    506       Poly-His.
FT   DOMAIN     1527   1530       Poly-Glu.
FT   SITE        354    354       Calcium ion selectivity and permeability
FT                               (By similarity).
FT   SITE        924    924       Calcium ion selectivity and permeability
FT                               (By similarity).
FT   SITE       1465   1465       Calcium ion selectivity and permeability
FT                               (By similarity).
FT   SITE       1770   1770       Calcium ion selectivity and permeability
FT                               (By similarity).
FT   CARBOHYD    173    173       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    246    246       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    310    310       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    322    322       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   1427   1427       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   1430   1430       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   1666   1666       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   2254 AA;  250405 MW;  697BBE06360CF0F6 CRC64;
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Query Match             96.9%;  Score 11657;  DB 1;  Length 2254;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 2219;  Conservative 0;  Mismatches 0;  Indels 6;  Gaps 0;

Qy     62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
               ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     30  GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML  89

Qy    122  VILLNCVTLGMFRPCEDIACDSQRCRILQAPDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90  VILLNCVTLGMFRPCEDIACDSQRCRILQAPDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy    182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy    242  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy    302  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    270  ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy    362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy    422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy    482  RLAQVSRAIGVRAGLLSSPVARSGQPPQPSGGCTRSHRRLSVHHLVHHHHHHHYHLGN 541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    450  RLAQVSRAIGVRAGLLSSPVARSGQPPQPSGGCTRSHRRLSVHHLVHHHHHHHYHLGN 509

Qy    542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    510  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy    602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEIIKDKALVEVAPSPGPPTLTSFNIPPGPF 661
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    570  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEIIKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy    662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy    722  SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690  SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy    782  IMIAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN 841
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1922  SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1890  SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL  1949

Qy  1982  PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLIAQRPLR  2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1950  PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLIAQRPLR  2009

Qy  2042  RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI  2101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2010  RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI  2069

Qy  2102  RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ  2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2070  RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ  2129

Qy  2162  SCRRRPGFWLDEQRRHSIAVSCLLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS  2221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2130  SCRRRPGFWLDEQRRHSIAVSCLLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS  2189

Qy  2222  IDPPESQSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP  2281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2190  IDPPESQSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP  2249

Qy  2282  TDMDP  2286
          |||||
Db  2250  TDMDP  2254
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RESULT 2
AAG35186
ID   AAG35186;          PRELIMINARY;       PRT;   2254 AA.
AC   AAG35186;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Calcium channel alpha-1-G subunit.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=brain;
RX   PubMed=11073957;
RA   McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA   Baillie D.L., Stea A., Snutch T.P.;
RT   "Molecular and functional characterization of a family of rat brain T-
RT   type calcium channels.";
RL   J. Biol. Chem. 276:3999-4011(2001).
DR   EMBL; AF290212; AAG35186.2; -.
SQ   SEQUENCE 2254 AA; 250405 MW; 697BBE06360CF0F6 CRC64;
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Query Match       96.9%;  Score 11657;  DB 2;  Length 2254;
Best Local Similarity 99.7%;  Pred. No. 0;
Matches 2219;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy  62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML  121
        | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30  GRQGPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML  89

Qy  122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  90   VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG  149

Qy  182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVTRVRVLRPLRAINRVPSMRIIVTLLLDTLP  241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVTRVRVLRPLRAINRVPSMRIIVTLLLDTLP  209

Qy  242  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  269
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Db  750  IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLIVYGPGYIKNPYN  809

Qy  842  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  810  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  869

Qy  902  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKV  961
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  870  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKV  929

Qy  962  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  1021
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  930  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD  989

Qy  1022  GDGDRRKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS  1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  990   GDGDRRKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS  1049

Qy  1082  SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS  1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1050  SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS  1109

Qy  1142  LLSGEGGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR  1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1110  LLSGEGGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR  1169

Qy  1202  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWYRSRLPACCRE  1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1170  SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWYRSRLPACCRE  1229

Qy  1262  RDSWSAYIFPPQSRFRLLCHRIIThKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1230  RDSWSAYIFPPQSRFRLLCHRIIThKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL  1289

Qy  1322  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG  1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1290  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG  1349

Qy  1382  TKIILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILG  1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1350  TKIILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILG  1409

Qy  1442  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1410  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1469

Qy  1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1470  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE  1529

Qy  1562  EARRREEKRLRRLEKKRRSKEKQMAEAAQQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI  1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1530  EARRREEKRLRRLEKKRRSKEKQMAEAAQQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI  1589

Qy  1622  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVFESVFKLVAFARRFFQDRWNQLDLA  1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1590  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVFESVFKLVAFGFRRRFFQDRWNQLDLA  1649

Qy  1682  IVLLSIMGITLLEEIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRALLHTVMQALP  1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1650  IVLLSIMGITLLEEIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRALLHTVMQALP  1709

Qy  1742  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTG  1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1710  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTG  1769

Qy  1802  DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA  1861
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1770  DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA  1829

Qy  1862  KEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1830  KEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF  1889
```

Qy 1382 TKILGMLRVIRLLRTLRPLRVISRAQGLKLIVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1350 TKILGMLRVIRLLRTLRPLRVISRAQGLKLIVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy 1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy 1562 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFLLVHHLCTSHYLDLFITGVI 1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1530 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFLLVHHLCTSHYLDLFITGVI 1589

Qy 1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVFPESVFKLVAFAFRRFFQDRWNQLDLA 1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1590 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVFPESVFKLVAFAFRRFFQDRWNQLDLA 1649

Qy 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1709

Qy 1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1710 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1769

Qy 1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYVSFVLTAQFVLNNVIAVLMKHLEESNKEA 1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1770 DNWNGIMKDTLRDCDQESTCYNTVISPIYVSFVLTAQFVLNNVIAVLMKHLEESNKEA 1829

Qy 1862 KEEAELEAELELEMKTLSPQHSPLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 1921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1830 KEEAELEAELELEMKTLSPQHSPLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 1889

Qy 1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1890 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1949

Qy 1982 PKAQGSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1950 PKAQGSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2009

Qy 2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2010 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2069

Qy 2102 RLPAPCPGLBPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2070 RLPAPCPGLBPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2129

Qy 2162 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKKLSPPSIS 2221
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2130 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKKLSPPSIS 2189

Qy 2222 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLLDSTRAASPKKKDTLSLSGLSSDP 2281
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2190 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLLDSTRAASPKKKDTLSLSGLSSDP 2249

Qy 2282 TDMDP 2286
          |||||
Db 2250 TDMDP 2254

RESULT 3
Q9WUB8
ID   Q9WUB8   PRELIMINARY;   PRT;   2288 AA.
AC   Q9WUB8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   T-type calcium channel isoform.

Qy   302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy   362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy   422 CLVVIATQFSETKQRESOLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   390 CLVVIATQFSETKQRESOLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy   482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN 541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN 509

Qy   542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy   602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPTLTSFNIPPGPF 661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPTLTSFNIPPGPF 629

Qy   662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCCPYCARTGAGEPESADHVMPDSD 721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCCPYCARTGAGEPESADHVMPDSD 689

Qy   722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy   782 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   750 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN 809

Qy   842 IFDGVIVVLSVWEIVGQQGGGLSVLRTFRIMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   810 IFDGVIVVLSVWEIVGQQGGGLSVLRTFRIMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy   902 CMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   870 CMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy   962 LYNGMASTSSWAALYFIALMTFGNVVLFNLLIVAIIVEGFQAEGDATKSESEEPDFFSPSVD 1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   930 LYNGMASTSSWAALYFIALMTFGNVVLFNLLIVAIIVEGFQAEGDATKSESEEPDFFSPSVD 989

Qy 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy 1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPSGERRS 1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPSGERRS 1109

Qy 1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy 1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy 1262 RDSWSAYIFPPQSRFPLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1230 RDSWSAYIFPPQSRFPLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy 1322 TLSNYIFTAVFLAEMTVKVFLAEMTVKVFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1290 TLSNYIFTAVFLAEMTVKVFLAEMTVKVFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

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OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=20081696; PubMed=10615950;
RA   Zhang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
RA   Wu S., Berggren P.O., Li M.;
RT   "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
RT   cells.";
RL   Diabetes 49:59-64(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
DR   EMBL; AF125161; AAD26858.1; -.
DR   GO; GO:016021; C:integral to membrane; IEA.
DR   GO; GO:005891; C:voltage-gated calcium channel complex; IEA.
DR   GO; GO:005261; F:cation channel activity; IEA.
DR   GO; GO:005245; F:voltage-gated calcium channel activity; IEA.
DR   GO; GO:006816; P:calcium ion transport; IEA.
DR   GO; GO:006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M-channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; CACHANNEL.
DR   PRINTS; PR01167; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
SQ   SEQUENCE   2288 AA;  253476 MW;  B89DB5A1D81757F CRC64;

Query Match            95.9%;  Score 11532;  DB 2;  Length 2288;
Best Local Similarity  97.7%;  Pred. No. 0;
Matches 2206;  Conservative   18;  Mismatches   1;  Indels   34;  Gaps    2;

Qy     62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
          ||  | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy    122 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy    182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy    242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy    302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    270 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy    362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy    422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy    482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN 541
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN 509

Qy    542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy    602 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSNIPPGPF 661
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    570 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSNIPPGPF 629

Qy    662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy    722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy    782 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    750 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy    842 IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    810 IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy    902 CMLLMLFIFFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 CMLLMLFIFFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy    962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE------------------ 1003
          |||||||||||||||||||||||||||||||||||||||||
Db    930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEEIGKREDASGQLSCIQLP 989

Qy   1004 -----GDATKSESEEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPM 1058
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 VNSQGGDATKSESEEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPM 1049

Qy   1059 SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPFSARSSPHSPWSAASSWTSRR 1118
          || |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1050 SLPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKSPFSARSSPHSPWSAASSWTSRR 1109

Qy   1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQSGQDEEESSEEDRASPAGSDRHRGSLERE 1178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQSGQDEEESSEEDRASPAGSDRHRGSLERE 1169

Qy   1179 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDE 1238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDE 1229

Qy   1239 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1289

Qy   1299 LNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 LNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1349

Qy   1359 VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1409

Qy   1419 SLKPIGNIVICCAFFIIFGILGVDQQPIMNHNPWMLLYFISFLLIVAFF 1478
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 SLKPIGNIVICCAFFIIFGILGVDQQPIMNHNPWMLLYFISFLLIVAFF 1469

Qy   1479 NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1529

Qy   1539 VLNMFVGVVVENFHKCRQHQEEEARRREKRLRLEKKRR---------SKEKQMAE 1587
          ||||||||||||||||||||||||||||||||||||||         :  :
Db   1530 VLNMFVGVVVENFHKCRQHQEEEARRREKRLRLEKKRRNLMLDDVIASGSSASAASE 1589

Qy   1588 AQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN 1647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
SQ   SEQUENCE   2295 AA;  253957 MW;  FE817D054ED26984 CRC64;

Query Match             94.6%;  Score 11372.5;  DB 2;  Length 2295;
Best Local Similarity   96.1%;  Pred. No. 0;
Matches 2178;  Conservative  12;  Mismatches  34;  Indels  43;  Gaps  4;

Qy     62  GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML  121
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     30  GRQGPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML  89

Qy    122  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDIFAFFAVEMVKMVALGIFGKKCYLG   181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90  VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDIFAFFAVEMVKMVALGIFGKKCYLG   149

Qy    182  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP  241
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150  DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLP  209

Qy    242  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210  MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF  269

Qy    302  ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN  361
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    270  ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN  329

Qy    362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  421
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL  389

Qy    422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR  481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR  449

Qy    482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCCTRSHRRLSVHHLVHHHHHHHYHLGN   541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    450  RLAQVSRAVGVRAGLLSSPVARGGQEPQPSGSCSRSHRRLSVHHLVHHHHHHHYHLGN   509

Qy    542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSSGGPPRGAESVHSFYHADCHLEPVRCQ  601
           |||||||||||||||||| ||| |||||| |||||||||||||||||||||||||||||
Db    510  GTLRVPRASPEIQDRDANGSRWLMLPPPSTPTPSSGGPPRGAESVHSFYHADCHLEPVRCQ  569

Qy    602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  661
           ||| |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    570  APPPRSPSEASGRTVGSGKVYPTVHTSPPPEMLKDKALVEVAPSPGPPTLTFNIPPGPF  629

Qy    662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHEMPDSD  689

Qy    722  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVIAFWRLICDTFRKIVDSKFYPGRG  781
           ||||||||||||||| |||| ||| ||||||||| |||||||||||||||||||||||||
Db    690  SEAVYEFTQDAQHSDLRDPH-RRRRPSLGPDAEPSSVLAFWRLICDTFRKIVDSKFYPGRG  748

Qy    782  IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN  841
           ||||||||||||||||||||||||||||||||||: ||||||||||||||||||||||||
Db    749  IMIAIIVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN  808

Qy    842  IFDGVIVVISWEIVSQQGGGLSVRTFRLMRVLVLKLVRFLPALQRQIVVLMKTMDNVATF  901
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809  IFDGVIVVISWEIVSQQGGGGLSVLRTFRLMRVLVLKLVRFLPALQRQIVLMKTMDNVATF  868
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Db   1590  AQCKPYYSDYSRPRLLVHHLCTSHYLDLPITGVIGLNVVTMAMEHYQQPQILDEALKICN  1649
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1648  YIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDIAIVLLSIMGITLEEIEVNLSLPINPTI  1707
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650  YIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTI  1709

Qy   1708  IRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD  1767
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710  IRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD  1769

Qy   1768  LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVIS  1827
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770  LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVIS  1829

Qy   1828  PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMKTLSPQPHSPLG   1887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1830  PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMKTLSPQPHSPLG   1889

Qy   1888  SPPLWPGVEGVNSTDSPKPGAPHTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVR   1947
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1890  SPPLWPGVEGVNSPDSPKPGAPHTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVR   1949

Qy   1948  KSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSIILSVHSQPADTSCILQLPK  2007
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1950  KSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSIILSVHSQPADTSCILQLPK  2009

Qy   2008  DVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVS  2067
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2010  DVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVS  2069

Qy   2068  GPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCGLEPSWAKDPPETRSSLEL  2127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2070  GPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCGLEPSWAKDPPETRSSLEL  2129

Qy   2128  DTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSG  2187
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2130  DTELSWISGDLLPSSQEEPLSPRDLKKCYSVETQSCRRRPGSWLDEQRRHSIAVSCLDSG  2189

Qy   2188  SQPRLCPSPSSLGQPLGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPAS  2247
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2190  SQPRLCPSPSSLGQPLGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPAS  2249

Qy   2248  DSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP  2286
           |||||||||||||||||||||||||||||||||||||||
Db   2250  DSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP  2288
```

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RESULT 4
Q9WUT2
ID   Q9WUT2          PRELIMINARY;      PRT;   2295 AA.
AC   Q9WUT2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Voltage-gated calcium channel, alpha-1-G subunit.
GN   Name=Cacna1g;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99189326; PubMed=10087148;
RA   Klugbauer N., Marais E., Lacinova L., Hofmann F.;
RT   "A T-type calcium channel from mouse brain.";
RL   Pflugers Arch. 437:710-715(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
DR   EMBL; AJ012569; CAB40793.1; -.
DR   MGD; MGI:1201678; Cacna1g.
DR   GO; GO:0005886; C:plasma membrane; IDA.
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Qy   1940 GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT 1999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1949 GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADT 2008

Qy   2000 SCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSR 2059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 SCIIQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSR 2068

Qy   2060 EDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP 2119
          |||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db   2069 EDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGQSKVSKHIRLPAPCPGLEPSWAKDPQ 2128

Qy   2120 ETRSSLEIDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSI 2179
          ||||||||||||||||||||||||||||||||:|||||||:||||||||:||||||||||
Db   2129 ETRSSLEIDTELSWISGDLLPSSQEEPLSPRDLKKCYSVEAQSCRRRPGSWLDEQRRHSI 2188

Qy   2180 AVSCLDSGSQPRLCPSPSSLGGQPLGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVC 2239
          |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db   2189 AVSCLDSGSQPRLCPSPSSLGGQPLGPGSRPKKKLSPPSISIDPPESQGSQGPRPPCSPGVC 2248

Qy   2240 LRRRAPASDSKDPSVSSPLDSTAASPSPKKDTISLSGLSSDPTDMDP 2286
          |||||||||||||:|||||||||||||||||:|||:|||||||::|
Db   2249 LRRRAPASDSKDPSASSPLDSTAASPSPKKDAISLSGLSSDPTDLDP 2295
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RESULT 5
Q6PFV8

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Qy    902 CMLLMLFIFISILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKV 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 CMLLMLFIFISILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKV 928

Qy    962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE----------- 1003
          ||||||||||||||||||||||||||||||||||||||||||
Db    929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEEIGKREDTSGQLSCIQLP 988

Qy   1004 ----GDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1058
               |||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db    989 VNSQGGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHSELRKSLLPPLIIHTAATPM 1048

Qy   1059 SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPFSARSSPHSPWSAASSWTSRR 1118
          ||:||||||||||||||||||||||||||||:||:||||||||:|||||||||||||||
Db   1049 SLPKSSSTGVGEALGSGSRRTSSSGSAEPGTAHHEMKSPPSARSSPHSPWSAASSWTSRR 1108

Qy   1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLERE 1178
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLERE 1168

Qy   1179 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDE 1238
          ||||||||||||||||||||||||||||||:|||||||||||||||:|| ::|
Db   1169 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRADDPPLDGDGDDE 1228

Qy   1239 GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1298
          ||||||||||:||::|||||||||||||||||||||||||||||||||||||||||||||
Db   1229 GNLSKGERLRAWVRARLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1288

Qy   1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1348

Qy   1359 VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1418
          ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349 VLSVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1408

Qy   1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKY 1478
          |||||||||||||||||||||||||||||||||||||||||||||||||:||||:||||
Db   1409 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCABASYRWVRHKY 1468

Qy   1479 NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF 1528

Qy   1539 VLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRRSKEKQMA----------- 1586
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 VLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRKLEKKRRSKEKQMADLMLDDVIASGS 1588

Qy   1587 ------EAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILD 1640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 SASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILD 1648

Qy   1641 EALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLS 1700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   1649 EALKICNYIFTVIFVFLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNAS 1708

Qy   1701 LPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAAL 1760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 LPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAAL 1768

Qy   1761 GVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQRST 1820
          |||||||||||||||||||||||||||||||||||||||||||||||:|:|||:||||||
Db   1769 GVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQEST 1828

Qy   1821 CYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAEELEAELELEMKTLSP 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 CYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAEELEAELELEMKTLSP 1888

Qy   1881 QPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAA-SGFSLEHPTMVPHPEEVPVPL 1939
          |||||||||||||||||||||| |||||||||||||||  ||||||||:|||:|| |||
Db   1889 QPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAASSGFSLEHPTMVPHTEEGPVPL 1948
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DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   2248 AA;  248888 MW;  332C5A8D9115A64F CRC64;

Query Match             93.6%;  Score 11263;  DB 2;  Length 2248;
Best Local Similarity   96.3%;  Pred. No. 0;
Matches 2155;  Conservative 12;  Mismatches 40;  Indels 30;  Gaps 4;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
         ||||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   30 GRQGPGSTEKDPGSADSEAEGLPYPA.APVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy  122 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 VILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy  182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy  242 MLGNVLLLCFFVFPIFGIVGVQLMAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  210 MLGNVLLLCFFVFPIFGIVGVQLMAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy  302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 361
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCGLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy  362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLII---------- 380

Qy  422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVIYILRKAAR 481
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381 -------FSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVIYILRKAAR 432

Qy  482 RLAQVSRAIGVRAGLLSSPVARSQOEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN 541
         ||||||| |||||||||||| || ||||||||| ||||||||||||||||||||||||
Db  433 RLAQVSRAVGVRAGLLSSPVVRGGQEPQPSGSCSRSHRRLSVHHLVHHHHHHHYHLGN 492

Qy  542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
         |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  493 GTLRVPRASPEIQDRDANGSRWLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 552

Qy  602 APPPRCPSEASGRITVGSGKVYPTVTHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
         |||| |||||||| |||||||||||||||||| |||||||| ||||||||||||||||||
Db  553 APPPSPSEASGRTVGSGKVYPTVTHTSPPPEMLKDKALVBVAPSPGPPTLTSFNIPPGPF 612

Qy  662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
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Db  613 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHEMPDSD 672

Qy  722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
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Db  673 SEAVYEFTQDAQHSDLRDPH.RRRRPSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 731

Qy  782 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  732 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 791

Qy  842 IFDGVIVIISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
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Db  792 IFDGVIVIISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 851

Qy  902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
         |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  852 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIITVFQILTQEDWNKV 911

Qy  962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  912 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 971

Qy 1022 GDGDRKKRIALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSSGRRTSS 1081
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Db  972 GDGDRKKRIALVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSSGRRTSS 1031

Qy 1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
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Db 1032 SGSAEPGTAHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1091

Qy 1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
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Db 1092 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1151

Qy 1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
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Db 1152 SSASEHQDCNGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLRAWVRARLPACCRE 1211

Qy 1262 RDSWSAYIFPPQSRFRLLCHRIIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
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Db 1212 RDSWSAYIFPPQSRFRLLCHRIIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1271

Qy 1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSG 1381
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Db 1272 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSG 1331

Qy 1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKIVVETLMSSLKPIGNIVVICCAFFIFGILG 1441
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Db 1332 TKILGMLRVLRLLRTLRPLRVISRAQGLKIVVETLMSSLKPIGNIVVICCAFFIFGILG 1391

Qy 1442 VQLFKGKFFVCQGEDTRNINKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1501
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Db 1392 VQLFKGKFFVCQGEDTRNINKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVD 1451

Qy 1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
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Db 1452 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1511

Qy 1562 EARRREEKRLRRLEKKR----------SKEKQMAEAAQCKPYYSDYSRRFLLVHHLCTS 1610
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Db 1512 EARRREEKRLRKRRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRRFLLVHHLCTS 1571

Qy 1611 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVESVFKIVAFAFRRF 1670
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Db 1572 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVLESVFKIVAFGFRRF 1631

Qy 1671 FQDRWNQLDIAIVLLSIMGTLEEIEVNLSLPINPTIIRMVLRIARVLKLLKMAVGMR 1730
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Db 1632 FQDRWNQLDIAIVLLSIMGITLEEIEVNASLPINPTIIRMVLRIARVLKLLKMAVGMR 1691

Qy 1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1790
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Db 1692 ALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1751

Qy 1791 AFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1850
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Db 1752 AFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1811

Qy 1851 MKHLEESNKEAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPH 1910
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Db 1812 MKHLEESNKEAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGVNSPDSPKPGAPH 1871

Qy 1911 TTAHIGAA---SGFSLEHPTMVPHPEEVPVLPGPDLLTVRKSGYSRTHLPNDSYMCRNGST 1969
         ||||||||   |||||||||||| ||  ||||||||||||||||||||||||||||||||
Db 1872 TTAHIGAASSGFSLEHPTMVPHTEEGPVLPGPDLLTVRKSGYSRTHLPNDSYMCRNGST 1931

Qy 1970 AERSLGHRGWGLPKAQGSSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPP 2029
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 1932 AERSLGHRGWGLPKAQGSSILSVHSQPADTSCIIQLPKDAHYLLQPHGAPTWGAIPKLPP 1991

Qy 2030 PGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQ 2089
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1992 PGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQ 2051
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Qy   2090 RSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPIFP 2149
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Db   2052 RSGSQSKVSKHIRLPAPCPGLEPSWAKDPQETRSSLELDTELSWISGDLLPSSQEEPISP 2111

Qy   2150 RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGS 2209
          ||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||||
Db   2112 RDLKKCYSVEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGS 2171

Qy   2210 RPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKK 2269
          |||||||||||||||||||||||||||||||||||||||||||| :|||||||||||||
Db   2172 RPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSAASPLDSTAASPSPKK 2231

Qy   2270 DTLSLSGLSSDPTDMDP 2286
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Db   2232 DALSLSGLSSDPTDLDP 2248
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RESULT 6
AAH57399
ID   AAH57399   PRELIMINARY;   PRT;   2248 AA.
AC   AAH57399;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cacna1g protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;

RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Matsusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC057399; AAH57399.1; -.
SQ   SEQUENCE 2248 AA; 248888 MW; 332CSA8D9115A64F CRC64;

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Query Match         93.6%;  Score 11263;  DB 2;  Length 2248;
Best Local Similarity   96.3%;  Pred. No. 0;
Matches 2155;  Conservative 12;  Mismatches 40;  Indels 30;  Gaps 4;

Qy     62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
          |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy    122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
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Db     90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy    182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
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Db    150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy    242 MLGNVLLLCFFVFFIFGIVGVQLMAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
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Db    210 MLGNVLLLCFFVFFIFGIVGVQLMAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy    302 ICSQPRENGMRSCRSVPTLRGEGGGPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
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Db    270 ICSQPRENGMRSCRSVPTLRGEGGGPCSLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy    362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFIFILLIIVGSFFMINL 421
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Db    330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFIFILLII---------- 380

Qy    422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
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Db    381 -------FSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 432

Qy    482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHYHLGN 541
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Db    433 RLAQVSRAVGVRAGLLSSPVVRGGQEPQPSGSCSRSHRRLSVHHLVHHHHHHYHLGN 492

Qy    542 GTLRVPRASPEIODRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
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Db    493 GTLRVPRASPEIQDRDANGSRWLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 552

Qy    602 APPPRCPSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
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Db    553 APPPRSPEASGRTVGSGKVYPTVHTSPPEMLKDKALVEVAPSPGPPTLTSFNIPPGPF 612

Qy    662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
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Db    613 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHEMPDSD 672

Qy    722 SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFPGRG 781
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Db    673 SEAVYEFTQDAQHSDLRDPH-RRRPSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFPGRG 731

Qy    782 IMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLKLLIVYGPFGYIKNPYN 841
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Qy    842 IFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
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Db    792 IFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 851

Qy    902 CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
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Db    852 CMLLMLFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 911

Qy    962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
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Db    912 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESESPDFFSPSVD 971

Qy   1022 GGDRKKRLAIVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
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Db    972 GGDRKKRLAIVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSS 1031

Qy   1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
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Qy   1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
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Db   1092 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1151

Qy   1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
          |||||||||||||||||||||| |||| ||||| ||||||||||| ||| |||||||||
Db   1152 SSASEHQDCNGKSASGRLARTLRADDPPLDGDDGDEGNLSKGERLRAWVRARLPACCRE 1211

Qy   1262 RDSWSAYIFPPQSRRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
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CCAG_HUMAN
ID   CCAG_HUMAN     STANDARD;     PRT;   2377 AA.
AC   O43497; O43498; O94770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;
AC   Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;
AC   Q9Y5T3;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).
GN   Name=CACNA1G; Synonyms=KIAA1123;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
RC   TISSUE=Brain;
RX   MEDLINE=20014446; PubMed=1548410;
RA   Mittman S., Guo J., Agnew W.S.;
RT   "Structure and alternative splicing of the gene encoding alpha1G, a
RT   human brain T calcium channel alpha1 subunit.";
RL   Neurosci. Lett. 274:143-146(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=20115462; PubMed=10648811;
RA   Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;
RT   "Molecular cloning and functional expression of ca(v)3.1c, a T-type
RT   calcium channel from human brain.";
RL   FEBS Lett. 466:54-58(2000).
RN   [3]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
RC   TISSUE=Brain;
RX   MEDLINE=20158909; PubMed=10692398;
RA   Monteil A., Chemin J., Bourinet E., Mennessier G., Lory P.,
RA   Nargeot J.;
RT   "Molecular and functional properties of the human alpha1G subunit that
RT   forms T-type calcium channels.";
RL   J. Biol. Chem. 275:6090-6100(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 14).
RA   Kishi F.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).
RC   TISSUE=Brain;
RX   MEDLINE=22158633; PubMed=12168954;
RA   Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT   "Construction of expression-ready cDNA clones for KIAA genes: manual
RT   curation of 330 KIAA cDNA clones.";
RL   DNA Res. 9:99-106(2002).
RN   [6]
RP   SEQUENCE OF 750-2377 FROM N.A. (ISOFORM 13).
RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA   Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 3), AND GENE STRUCTURE.
RC   TISSUE=Prostatic carcinoma;
RX   MEDLINE=99421245; PubMed=10493502;
RA   Toyota M., Ho C., Ohe-Toyota M., Baylin S.B., Issa J.-P.J.;
RT   "Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant
RT   methylation of its 5' CpG island in human tumors.";
RL   Cancer Res. 59:4535-4541(1999).
RN   [8]
RP   SEQUENCE OF 1126-1444; 1778-1927 AND 2021-2312 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98154730; PubMed=9495342;
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Qy   1212  RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLIVIIFLNCITIAMERPKIDPHSAERIFL  1271
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Qy   1272  TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDIILVSMVSDSG  1331
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Qy   1332  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLG  1391
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLG  1441

Qy   1392  VQLFKGKFFVCCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442  VQLFKGKFFVCCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1501

Qy   1452  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE  1511
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE  1561

Qy   1512  EARRREEKRLKRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTS  1571
            |||||||||:|:|||||                    ||||||||||||:|:||||||||
Db   1562  EARRREEKRIRRLEKKR--------SKEKQMAFAQCKPYYSDYSRFRLLVHHLCTS  1610

Qy   1572  HYLDLFITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVPFESVFKLVAFGFRRF  1631
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1611  HYLDLFITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVPFESVFKLVAFGFRRF  1670

Qy   1632  FQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMR  1691
            |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db   1671  FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR  1730

Qy   1692  ALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM  1751
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1731  ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM  1790

Qy   1752  AFLTLFRVSTGDNWNGIMKDTLRCDCDQESTCYNTVISPIYFVSFVSFVLTAQFVLNVVIAVL  1811
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1791  AFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVSFVLTAQFVLNVVIAVL  1850

Qy   1812  MKHLEESNKEAKEAELEAELEAELEMKTLSPQHSPLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQ  1871
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1851  MKHLEESNKEAKEAELEAELEAELEMKTLSPQHSPLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQ  1910

Qy   1872  TTAHIGAASSGFSLEHPTMVPHTEEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST  1931
            ||||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||||
Db   1911  TTAHIGAA-SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST  1969

Qy   1932  AERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTWGAIPKLPP  1991
            |||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   1970  AERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPP  2029

Qy   1992  PGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQ  2051
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2030  PGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQ  2089

Qy   2052  RSGSQSKVSKHIRLPAPCPGLEPSWAKDPQFTRSSLELDTELSWISGDLLPSSQEEPLSP  2111
            |||:||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   2090  RSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFP  2149

Qy   2112  RDLKKCYSVEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGS  2171
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2150  RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGS  2209

Qy   2232  DALSLSGLSSDPTDLDP  2248
            | |||||||||||:||
Db   2270  DTLSLSGLSSDPTDMDP  2286
```

RA   Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
RA   Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT   "Molecular characterization of a neuronal low-voltage-activated T-type
RT   calcium channel.";
RL   Nature 391:896-900(1998).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC   entry of calcium ions into excitable cells and are also involved
CC   in a variety of calcium-dependent processes, including muscle
CC   contraction, hormone or neurotransmitter release, gene expression,
CC   cell motility, cell division and cell death. The isoform alpha-1G
CC   gives rise to T-type calcium currents. T-type calcium channels
CC   belong to the "low-voltage activated (LVA)" group and are strongly
CC   blocked by mibefradil. A particularity of this type of channels is
CC   an opening at quite negative potentials and a voltage-dependent
CC   inactivation. T-type channels serve pacemaking functions in both
CC   central neurons and cardiac nodal cells and support calcium
CC   signaling in secretory cells and vascular smooth muscle. They may
CC   also be involved in the modulation of firing patterns of neurons
CC   which is important for information processing as well as in cell
CC   growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=14;
CC   Comment=Additional isoforms seem to exist;
CC   Name=5;
CC   IsoId=O43497-1; Sequence=Displayed;
CC   Name=1;
CC   IsoId=O43497-2; Sequence=VSP_000940, VSP_000943, VSP_000946;
CC   Name=2;
CC   IsoId=O43497-3; Sequence=VSP_000940, VSP_000944, VSP_000946;
CC   Name=3;
CC   IsoId=O43497-4; Sequence=VSP_000940;
CC   Name=4;
CC   IsoId=O43497-5; Sequence=VSP_000940, VSP_000943, VSP_000946,
CC   VSP_000948;
CC   Name=6;
CC   IsoId=O43497-6; Sequence=VSP_000943, VSP_000946;
CC   Name=7;
CC   IsoId=O43497-7; Sequence=VSP_000943, VSP_000947;
CC   Name=8;
CC   IsoId=O43497-8; Sequence=VSP_000940, VSP_000943, VSP_000947;
CC   Name=9;
CC   IsoId=O43497-9; Sequence=VSP_000940, VSP_000946;
CC   Name=10;
CC   IsoId=O43497-10; Sequence=VSP_000940, VSP_000945;
CC   Name=11;
CC   IsoId=O43497-11; Sequence=VSP_000946;
CC   Name=12;
CC   IsoId=O43497-12; Sequence=VSP_000947;
CC   Name=13;
CC   IsoId=O43497-13; Sequence=VSP_000944, VSP_000946;
CC   Name=14;
CC   IsoId=O43497-14; Sequence=VSP_000941, VSP_000942;
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain, in particular in
CC   the amygdala, subthalamic nuclei, cerebellum and thalamus.
CC   Moderate expression in heart; low expression in placenta, kidney
CC   and lung. Also expressed in colon and bone marrow and in tumoral
CC   cells to a lesser extent. Highly expressed in fetal brain, but
CC   also in peripheral fetal tissues as heart, kidney and lung,
CC   suggesting a developmentally regulated expression.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC   hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC   positively charged transmembrane segment (S4). S4 segments
CC   probably represent the voltage-sensor and are characterized by a
CC   series of positively charged amino acids at every third position.
CC   -!- DOMAIN: The linker region between repeat III and IV probably play
CC   a role in the inactivation of the channel. The C-terminal part may
CC   be implicated in the anchoring of the protein to the membrane,
CC   this by interfering/restricting its lateral diffusion.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC   channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC   family.

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).

DR   EMBL; AF134986; AAF19347.1; -.
DR   EMBL; AF134985; AAF19346.1; -.
DR   EMBL; AF227744; AAF37689.1; -.
DR   EMBL; AF227745; AAF37690.1; -.
DR   EMBL; AF227746; AAF37691.1; -.
DR   EMBL; AF227747; AAF37692.1; -.
DR   EMBL; AF227748; AAF37693.1; -.
DR   EMBL; AF227749; AAF37694.1; -.
DR   EMBL; AF227750; AAF37695.1; -.
DR   EMBL; AF227751; AAF37696.1; -.
DR   EMBL; AF124351; AAD34352.1; -.
DR   EMBL; AB032949; BAA86437.2; -.
DR   EMBL; AB012043; BAA36409.1; -.
DR   EMBL; AF126965; AAD29400.1; -.
DR   EMBL; AF126966; AAD29401.1; -.
DR   EMBL; AF190860; AAF35287.1; -.
DR   EMBL; AF029228; AAD12731.1; -.
DR   EMBL; AF029229; AAD12732.1; -.
DR   Genew; HGNC:1394; CACNA1G.
DR   MIM; 604065; -.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.
DR   GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.
DR   GO; GO:0006810; P:transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Repeat; Transmembrane; Voltage-gated channel.
FT   REPEAT   68   398   I.
FT   REPEAT   729   967   II.
FT   REPEAT   1263   1540   III.
FT   REPEAT   1596   1854   IV.
FT   DOMAIN   1   80   Cytoplasmic (Potential).
FT   TRANSMEM   81   101   S1 of repeat I (Potential).
FT   DOMAIN   102   119   Extracellular (Potential).
FT   TRANSMEM   120   141   S2 of repeat I (Potential).
FT   DOMAIN   142   150   Cytoplasmic (Potential).
FT   TRANSMEM   151   170   S3 of repeat I (Potential).
FT   DOMAIN   171   175   Extracellular (Potential).

Query Match   89.2%; Score 10732.5; DB 1; Length 2377;
Best Local Similarity   88.3%;
Matches 2078; Conservative 33; Mismatches 109; Indels 133; Gaps   7;

Qy   62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVPVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||:|||
Db   30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVPVFFYLSQDSRPRSWCLRTVCNPWFERISML 89

Qy   122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy   182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy   242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301

Right-hand column (continuation), reading top to bottom:

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Db   1288  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN   1347
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1359  VLDGLLVLISVIDILVSVSVSDSGTKILGMRLVLRLLRTLRPLRVISRAQGLKLVVETLMS   1418
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1348  VLDGLLVLISVIDILVSMVSDSGTKILGMRLVLRLLRTLRPLRVISRAQGLKLVVETLMS    1407

Qy   1419  SLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKY     1478
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1408  SLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCABASYRWVRHKY     1467

Qy   1479  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF    1538
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFF    1527

Qy   1539  VLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRR------SKEKQMAE          1587
           ||||||||||||||||||||||||||||||||||||||
Db   1528  VLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRNLMDDVIASGSSASAASE       1587

Qy   1588  AQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN   1647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1588  AQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICN   1647

Qy   1648  YIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTI   1707
           ||||||||| ||||||||| ||||||||||||||||||||||||||||||||  |||||||
Db   1648  YIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTI   1707

Qy   1708  IRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD   1767
           |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db   1708  IRIMRVLRIARVLKLLKMAVCMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGD   1767

Qy   1768  LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVIS   1827
           ||||||||||||||||||||||||||||||||||||||||||||   |||||||||||||
Db   1768  LECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVIS   1827

Qy   1828  PIYFVSFVLIAQFVLNVVIAVLMKHLEESNKEAKEAELEAELEMKTLSPQPHSPLG       1887
           ||||||||| ||||||||||||||||||||||||| |||||||||||||||||||||
Db   1828  PIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAEAELEAELEMKTLSPQPHSPLG      1887

Qy   1888  SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPT---------             1927
           |||||||||| |  |||||||  | |||   | |||||||
Db   1888  SPFLWPGVEGPSPDSPKPGALHPAAHARSASHFSLEHPTDRQLFDTISLLIQGSLEWEL    1947

Qy   1928  ---------------------------------------                       1927
Db   1948  KLMDELAGPGGQPSAFPSAPSLGGSDPQIPLAEMEALSLTSEIVSEPSCSLALTDDSLPD   2007

Qy   1928  ---------MVEHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL        1974
                    ||||||||||||||||||||||||||||||||
Db   2008  DMHTLLLSALESNMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPL   2064

Qy   1975  GHRGWGLPKAQGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSP    2034
           |||||||||||| |||||||||||| |||||||  |||||| ||||| ||||||||||||
Db   2065  GHRGWGLPKAQGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSP    2124

Qy   2035  LAQRPLRRQAAIRTDSLDVQLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQ    2094
           |||||||||||||||||||||||||||| |||||  ||  |  |||| ||  ||  |
Db   2125  LAQRPLRRQAAIRTDSLDVQLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAAQQHSRSH   2184

Qy   2095  SKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLK   2153
           ||  || ||| || || ||  | ||||||||||||||||||||| | ||  |||| ||||
Db   2185  SKISKHMTPPAPCCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLK   2244

Qy   2154  KCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKK   2213
           ||||||  ||  ||   ||||||||||||||||||| || |  | | ||||||||||||
Db   2245  KCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKK   2304

Qy   2214  KLSPPSISIDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLS  2273
           |||||||  |||||| || ||  ||||||||| |||  |||  |     ||||||||| ||
Db   2305  KLSPPSITIDPPESQGPRRTPPSPGICLRRRAPSDSDSKDPLASGPPDSMAASPSPKKDVLS  2364

Qy   2274  LSGLSSDPTDMDP                                                 2286
           ||||||||  |||
Db   2365  LSGLSSDPADLDP                                                 2377
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Left-hand column, reading top to bottom:

```
Db    210  MGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF     269

Qy    302  ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNMNQYYYNCSAGEHN    361
           |||||||||||||||||||| ||  ||||| ||| ||||||||||||||||||||||||||
Db    270  ICSQPRENGMRSCRSVPTLRGDGDGGGPPCGLDYEAYNSSSNTTCVNMNQYYYNCSAGEHN   329

Qy    362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL    421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    330  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL    389

Qy    422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVVILRKAAR    481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVVILRKAAR    449

Qy    482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN      541
           |||||||| || |||| |||  |  |||| | | |||||||||||||||||||||||||
Db    450  RLAQVSRAAGVRVGLLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHYHLGN     509

Qy    542  GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSGGPPRGAEVHSFYHADCHLEPVRCQ      601
           |||| ||||||||||||||||||||||||| | |  ||||||||||||||||||||||
Db    510  GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAEVHSFYHADCHLEPVRCQ     569

Qy    602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAEPSPGPPTLTSFNIPPGPF   661
           ||||| ||||||||||||||||||||||||| | |||||||| ||||||||||| |||||
Db    570  APPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY    629

Qy    662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD   721
           ||||||||||||||| ||||||||| ||||||||||||||||| ||||   ||  |||||
Db    630  SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD   689

Qy    722  SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   781
           |||||||||||||||||||| || |||||||||||||||||||||||||||||||||||
Db    690  SEAVYEFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   748

Qy    782  IMIAILVNTLSMGIEYHEQPEELINALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN   841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749  IMIAILVNTLSMGIEYHEQPEELINALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN   808

Qy    842  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF    901
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809  IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF    868

Qy    902  CMLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKV    961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869  CMLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKV    928

Qy    962  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE----------         1003
           ||||||||||||||||||||||||||||||||||||||||||
Db    929  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEEISKREDASGQLSCIQLP   988

Qy   1004  ----GDATKSESEPDFFSPSVDGDGDRKKRLALAVALGEHAELRKSLLPPLIHTAATPM   1058
               |||| |||||:||||| ||||||||:|||| | |||| ||||||||||||||||||
Db    989  VDSQGGDANKSESEDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPLIHTAATPM    1048

Qy   1059  SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPFSARSSPHSPWSAASWTSRR   1118
           | ||| ||| |||| |:|||||||||||||||  :||||| ||||||||||||||||||||
Db   1049  SLPKSTSTGLGEALGPASRRTSSSGSAEPGAA-HEMKSPFSARSSPHSPWSAASWTSRR   1107

Qy   1119  SSRNSLGRAPSLKRRSPSGERRSLLSGEGQGSDEEESSEEDRASPAGSDHRHRGSLERE   1178
           |||||||||||||||||||||||||||||| ||||||||||||:|||||||||||||||||
Db   1108  SSRNSLGRAPSLKRRSPSGERRSLLSGEGQBSGDEEESSEEERASPAGSDHRHRGSLERE   1167

Qy   1179  AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDE   1238
           ||||||||||||||||||||||||:|||||||||||||||||||:||:|||:|||||:|:
Db   1168  AKSSFDLPDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPLDGDDADDE   1227

Qy   1239  GNLSKGERIQAWVRSRLPACCRERDGWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIF   1298
           |||||||| :||:|:|||||| ||| ||||||||||||||||||||||||||||||||||
Db   1228  GNLSKGERVRAWTRARLPACCLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIF   1287

Qy   1299  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN  1358
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RESULT 8

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Q6ZPX4
ID   Q6ZPX4      PRELIMINARY;      PRT; 1389 AA.
AC   Q6ZPX4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA1123 protein (Fragment).
GN   Name=mKIAA1123;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=14621295;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:167-180(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
DR   EMBL; AK129294; BAC98104.1; -.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 2.
DR   PRINTS; PR00167; CACHANNEL.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
FT   NON_TER       1        1
SQ   SEQUENCE   1389 AA;  153067 MW;  DA31535CA3C03B10 CRC64;
```

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Query Match             56.6%;  Score 6809.5;  DB 2;  Length 1389;
Best Local Similarity   94.8%;  Pred. No. 0;
Matches 1317;  Conservative  8;  Mismatches  29;  Indels  35;  Gaps  3;

Qy    933  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL   992
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL   60

Qy    993  VAILVVEGFQAE----------------------------GDATKSESEPDFFSPSVDGDGDRKKR  1029
           ||||||||||||                            :||||||||||||||||||||||||
Db     61  VAILVVEGFQAEEIGKREDTSGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGDRKKR  120

Qy   1030  LALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGA  1089
           ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LALVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGT  180

Qy   1090  AHHEMKCPPSARSSPHSPWSAAASWTSRSSRRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1149
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  AHHEMKSPPSARSSPHSPWSAAASWTSRSSRRNSLGRAPSLKRRSPSGERRSLLSGEGQE  240

Qy   1150  SQDEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD  1209
           ||||||||||||||||||||||||||||||||||||||||::||||||||||||||||
Db    241  SQDEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD  300

Qy   1210  CNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVSRLPACCRERDSWSAYI  1269
           |||||||||||||||:|||||||||:|:|||||||||||||:||||||||||||||||
Db    301  CNGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLRAWTVARLPACCRERDSWSAYI  360

Qy   1270  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1329
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    361  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  420

Qy   1330  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  480

Qy   1390  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKF  1449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKF  540

Qy   1450  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1509
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  600

Qy   1510  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK  1569
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK  660

Qy   1570  RLRRLEKKRR-------------SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1618
           |:|||||||:|            :|||||||||||||||||||||||||||||||||||||
Db    661  RLKRLEKKRRNLMLDDVIASGSSASAAESEAQCKPYYSDYSRFRLLVHHLCTSHYIDLFIT  720

Qy   1619  GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFARRFFQDRWNQL  1678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFLESVFKLVAFGFRRFFQDRWNQL  780

Qy   1679  DLAIVLLSIMGITLEEIENLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQ  1738
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ  840

Qy   1739  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  900

Qy   1799  STGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  1858
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  960

Qy   1859  KEAKEEAEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAA  1918
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  KEAKEEAEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAA  1020

Qy   1919  -SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR  1977
            ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db   1021  SSGFSLEHPTMVPHTEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR  1080

Qy   1978  GWGLPKAQSGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQ  2037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GWGLPKAQSGSILSVHSQPADTSCIIQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPLAQ  1140

Qy   2038  RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKV  2097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGSQSKV  1200

Qy   2098  SKHIRLPAPCGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYS  2157
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  SKHIRLPAPCGLEPSWAKDPQETRSSLELDTELSWISGDLLPSSQEEPLSPRDLKKCYS  1260

Qy   2158  VETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP  2217
           :|||:|||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  VEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGGPLGGPGSRPKKKLSP  1320

Qy   2218  PSISIDPPESQGSRRPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGL  2277
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  PSISIDPPESQGPRRPCSPGVCLRRRAPASDSKDPSAASSPLDSTAASPSPKKDALSLSGL  1380

Qy   2278  SSDPTDMDP  2286
           ||||:|:|
Db   1381  SSDPTDLDP  1389
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RESULT 9

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Qy  1570 RLRRLEKKRR--------SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT 1618
         ||||||||||        ||||||||||||||||||||||||||||||||||||||
Db   661 RLKRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT 720

Qy  1619 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQL 1678
         |||||||||||||||||||||||||||||||||||||| ||||||||   |||||||||
Db   721 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVLESVFKLVAFGFRRFFQDRWNQL 780

Qy  1679 DLAIVLLSIMGITLEEIEVNLSLPINPTIRIMRVLRIARVLKLLKMAVGMRALLHTVMQ 1738
         |||||||||||||||||||| ||||||||||||||||||||||||||||||||| ||||
Db   781 DLAIVLLSIMGITLEEIEVNASLPINPTIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ 840

Qy  1739 ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1798
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 900

Qy  1799 STGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESN 1858
         ||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db   901 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESN 960

Qy  1859 KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAA 1918
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   961 KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAA 1020

Qy  1919 -SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR 1977
          |||||||||||| ||| |||||||||||||||||||||||||||||||||||||||||
Db  1021 SSGFSLEHPTMVPHTEEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR 1080

Qy  1978 GWGLPKAQSGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQ 2037
         ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  1081 GWGLPKAQSGSILSVHSQPADTSCIIQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPLAQ 1140

Qy  2038 RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKV 2097
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  1141 RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGQSKV 1200

Qy  2098 SKHIRLPAPCGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLPRDLKKCYS 2157
         ||||||||||||||||||| |||||||||||||||||||||||||||||| ||||||
Db  1201 SKHIRLPAPCGLEPSWAKDPQETRSSLELDTELSWISGDLLPSSQEEPLSPRDLKKCYS 1260

Qy  2158 VETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP 2217
         || ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 VEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP 1320

Qy  2218 PSISIDPPESQGSRRPCPSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGL 2277
         ||||||||||| ||||||||||||||||||||||||||||||| ||||||||||| |||||
Db  1321 PSISIDPPESQGPRPCSPGVCLRRRAPASDSKDPSASSPLDSTAASPSPKKDALSLSGL 1380

Qy  2278 SSDPTDMDP 2286
         |||||| |||
Db  1381 SSDPTDLDP 1389
```

RESULT 10
CCAH_RAT

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ID   CCAH_RAT    STANDARD;    PRT;   2359 AA.
AC   Q9EQ60;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.2).
GN   Name=Cacna1h;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA   McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
```

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BAC98104
ID   BAC98104    PRELIMINARY;    PRT;   1389 AA.
AC   BAC98104;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA1123 protein (Fragment).
GN   MKIAA1123;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT   III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous
RT   cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT   Randomly Sampled from Size-fractionated Libraries.";
RL   DNA Res. 10:167-180(2003).
DR   EMBL; AK129294; BAC98104.1; -.
FT   NON_TER     1      1
SQ   SEQUENCE   1389 AA;   153067 MW;   DA31535CA3C03B10 CRC64;

Query Match             56.6%;
Best Local Similarity   94.8%;
Matches 1317;  Conservative 8;  Mismatches 29;  Indels 35;  Gaps 3;
```

```
Qy   933 LPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 992
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 LPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 60

Qy   993 VAILVEGFQAE------------------------GDATKSESEEPDFFSPSVDGDGDRKKR 1029
         |||||||||||                        ||||||||||||||||||||||||||
Db    61 VAILVEGFQAEEIGKREDTSGQLSCIQLPVNSQGGDATKSESEEPDFFSPSVDGDGDRKKR 120

Qy  1030 LALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVEALGSGSRRTSSSGSAEPGA 1089
         |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Db   121 LALVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVEALGSGSRRTSSSGSAEPGT 180

Qy  1090 AHHEMKCPPSGARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1149
         ||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AHHEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 240

Qy  1150 SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASAEHQD 1209
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASAEHQD 300

Qy  1210 CNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1269
         |||||||||||||| |||| ||||| :::|||||||| ||| ||||||||||||||||
Db   301 CNGKSASGRLARTLRADDPPLDGDDGDDGGDDEGNLSKGERLRAWVRARLPACCRERDSWSAYI 360

Qy  1270 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 420

Qy  1330 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKIIGMLR 1389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   421 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSTKIIGMLR 480

Qy  1390 VIRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGIIGVQLFKGKF 1449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 VIRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGIIGVQLFKGKF 540

Qy  1450 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 600

Qy  1510 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK 1569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK 660
```

RA   Baillie D.L., Stea A., Snutch T.P.;
RT   "Molecular and functional characterization of a family of rat brain T-
RT   type calcium channels.";
RL   J. Biol. Chem. 276:3999-4011(2001).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC   entry of calcium ions into excitable cells and are also involved
CC   in a variety of calcium-dependent processes, including muscle
CC   contraction, hormone or neurotransmitter release, gene expression,
CC   cell motility, cell division and cell death. The isoform alpha-1H
CC   gives rise to T-type calcium currents. T-type calcium channels
CC   belong to the "low-voltage activated (LVA)" group and are strongly
CC   blocked by nickel and mibefradil. A particularity of this type of
CC   channels is an opening at quite negative potentials, and a
CC   voltage-dependent inactivation. T-type channels serve pacemaking
CC   functions in both central neurons and cardiac nodal cells and
CC   support calcium signaling in secretory cells and vascular smooth
CC   muscle. They may also be involved in the modulation of firing
CC   patterns of neurons which is important for information processing
CC   as well as in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in brain.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC   hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC   positively charged transmembrane segment (S4). S4 segments
CC   probably represent the voltage-sensor and are characterized by a
CC   series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC   channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC   family.
DR   EMBL; AF290213, AAG35187.1; -.
DR   RGD; 68943; Cacna1h.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M-channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Phosphorylation; Repeat; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT   87   422   I.
FT   REPEAT   776   1015   II.
FT   REPEAT   1292   1569   III.
FT   REPEAT   1607   1868   IV.
FT   DOMAIN   1   100   Cytoplasmic (Potential).
FT   TRANSMEM   101   119   S1 of repeat I (Potential).
FT   DOMAIN   120   139   Extracellular (Potential).
FT   TRANSMEM   140   160   S2 of repeat I (Potential).
FT   DOMAIN   161   169   Cytoplasmic (Potential).
FT   DOMAIN   170   184   S3 of repeat I (Potential).
FT   DOMAIN   185   193   Extracellular (Potential).
FT   TRANSMEM   194   212   S4 of repeat I (Potential).
FT   DOMAIN   213   232   Cytoplasmic (Potential).
FT   TRANSMEM   233   253   S5 of repeat I (Potential).
FT   DOMAIN   254   394   Extracellular (Potential).
FT   TRANSMEM   395   419   S6 of repeat I (Potential).
FT   DOMAIN   420   790   Cytoplasmic (Potential).
FT   TRANSMEM   791   811   S1 of repeat II (Potential).
FT   DOMAIN   812   824   Extracellular (Potential).
FT   TRANSMEM   825   846   S2 of repeat II (Potential).
FT   DOMAIN   847   852   Cytoplasmic (Potential).
FT   TRANSMEM   853   871   S3 of repeat II (Potential).

FT   DOMAIN   872   879   Extracellular (Potential).
FT   TRANSMEM   880   903   S4 of repeat II (Potential).
FT   DOMAIN   904   914   Cytoplasmic (Potential).
FT   TRANSMEM   915   935   S5 of repeat II (Potential).
FT   DOMAIN   936   987   Extracellular (Potential).
FT   TRANSMEM   988   1012   S6 of repeat II (Potential).
FT   DOMAIN   1013   1301   Cytoplasmic (Potential).
FT   TRANSMEM   1302   1324   S1 of repeat III (Potential).
FT   DOMAIN   1325   1342   Extracellular (Potential).
FT   TRANSMEM   1343   1363   S2 of repeat III (Potential).
FT   DOMAIN   1364   1373   Cytoplasmic (Potential).
FT   DOMAIN   1374   1393   S3 of repeat III (Potential).
FT   DOMAIN   1394   1407   Extracellular (Potential).
FT   TRANSMEM   1408   1429   S4 of repeat III (Potential).
FT   DOMAIN   1430   1439   Cytoplasmic (Potential).
FT   TRANSMEM   1440   1463   S5 of repeat III (Potential).
FT   DOMAIN   1464   1540   Extracellular (Potential).
FT   TRANSMEM   1541   1566   S6 of repeat III (Potential).
FT   DOMAIN   1567   1621   Cytoplasmic (Potential).
FT   TRANSMEM   1622   1642   S1 of repeat IV (Potential).
FT   DOMAIN   1643   1656   Extracellular (Potential).
FT   TRANSMEM   1657   1678   S2 of repeat IV (Potential).
FT   DOMAIN   1679   1685   Cytoplasmic (Potential).
FT   DOMAIN   1686   1704   S3 of repeat IV (Potential).
FT   DOMAIN   1705   1718   Extracellular (Potential).
FT   TRANSMEM   1719   1742   S4 of repeat IV (Potential).
FT   DOMAIN   1743   1756   Cytoplasmic (Potential).
FT   TRANSMEM   1757   1777   S5 of repeat IV (Potential).
FT   DOMAIN   1778   1840   Extracellular (Potential).
FT   TRANSMEM   1841   1868   S6 of repeat IV (Potential).
FT   DOMAIN   1869   2359   Cytoplasmic (Potential).
FT   DOMAIN   521   531   Poly-His.
FT   DOMAIN   1594   1597   Poly-Arg.
FT   SITE   378   378   Calcium ion selectivity and permeability
FT   (By similarity).
FT   SITE   971   971   Calcium ion selectivity and permeability
FT   (By similarity).
FT   SITE   1515   1515   Calcium ion selectivity and permeability
FT   (By similarity).
FT   CARBOHYD   192   192   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   271   271   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   1477   1477   N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   2359 AA; 261138 MW; F738083B94180081 CRC64;

Query Match   51.8%; Score 6226; DB 1; Length 2359;
Best Local Similarity   56.3%; Pred. No. 4.5e-303;
Matches 1356; Conservative 248; Mismatches 518; Indels 286; Gaps 58;

Qy   30 LARGWTRRRMERAPRSRDSPV-ASRSSTTCPG---PGAAGAG-STEKDPGS---AD---S   78
                || : |: | : : | : |:: |:.| |
Db   6 LAADEVRVPLGASPPAPAAPVRASPASPGAPGREEQGSGSGVLAPESPGTECGADLGAD   65

Qy   79 EAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERVSMLIVILLNCVTLGMFRPCED 138
                :.:|||||||||| :|||| | .| |||::|||||: |||||||.||||||||||||
Db   66 EEQPVPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCED 125

Qy   139 IACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLE 198
                ||| .||:|||||:|||||||||||||||:|||||||.|||||||||||||||:|||:|
Db   126 VECRSERCSILEAFDDFIFAFFAVEMVVKMVALGLFGQKCYLGDTWNRLDFFIVAGMME 185

Qy   199 YSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFFVFFIFG 258
                ||||| |||:||||||||||||||||||||||||||||||||||||||||||||||
Db   186 YSLDGHNVSLsSAIRTVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFFVFFIFG 245

Qy   259 IVGVQLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENEDESPFICSQPRENGMRSCRSV 317
                |||||||||||||||||||||||||||| :| || ::| |:::|
Db   246 IVGVQLWAGLLRNRCFLDSAFVRNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHI 305

Qy   318 PT--LRGEGGGPCSLLDYETY------NSSSNTTCVWNNQYTNCSAGEHPFKGAI   367
                || ::.| | | |:.||||||||||||||||||||||||||
Db   306 PSRRELRVQ-----CTILGWEAYGQPQAEDGGAGRNACINWNQYYNVCRSGEFNPHNGAI   359

```
1392 Qy RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKFFV 1451
1410 Db RLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFIIFGIIGVQLFKGKFYY 1469

1452 Qy CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1511
1470 Db CEGTDTRNITTKAECHAAHYRWVRRKYNFDNLGQALMSLFVLSLSKDGWVNIMYDGLDAVG 1529

1512 Qy VDQQPIMNHPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1571
1530 Db IDQQPVQNHPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREEKRL 1589

1572 Qy RRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1631
1590 Db RRLERRRR----------KAQRRPYYADYSHTRRSIHSLCTSHYLDLFTTFICLNVVITMSME 1642

1632 Qy HYQQPQILDEALKICNYIFTVIFVFESVKIVAFAFRRFFQDRWNQLDLAIVLLSIMGIT 1691
1643 Db HYNQPKSLDEALKYCNYVFTIVFVFEAALKLVAFGFRRFFKDRWNQLDLAIVLLSIMGIA 1702

1692 Qy LEEIVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFM 1751
1703 Db LEEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFM 1762

1752 Qy LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDP 1811
1763 Db LLFFIYAALGVELFGGLECSDNPCEGLSRHATFTNFGMAFLTLFRVSTGDNWNGIMKDT 1822

1812 Qy SRDC---DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEREALE 1868
1823 Db LRECTREDKHCLSLYLPALSPVYFVFTFMLVAQFVLVNVVAVLMKHLEESNKEAREDAEMD 1882

1869 Qy AELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTM 1928
1883 Db AEIELEM---------------------------------AQSTAQPPPTAQES---- 1904

1929 Qy VPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLP-------- 1982
1905 Db --------QGTQPDTPNLLVVRKVSVSRMLSLPNDSYMFRPVAPAAAPHSH------PLQEVEM 1954

1983 Qy KAQSGSIILSVHSQPADTSCILQLP-------------KDVHYLLQPHGAPTWGAIPKLPPPGRS 2033
1955 Db ETYTGPVTSAHSPPLEPRASFQVPSAASSPARVSDPLCALSPRGTP--------------------RS 2002

2034 Qy PLAQRPLRRQAAIRTDSLD--VQGLGSREDLLSEVSGPSCPLTRSSSFWGG----------- 2082
2003 Db LSLSRILCRQEAMHSESLEGKVDDVGG--DSIPDYTEPAENMSTSQASTGAPRSPPCSPR 2060

2083 Qy -SSIQVQQRGSIQSKVSKHIRLPAPCPGLEPSWAKDPETRSSLELDTELSWISGDLLPS 2141
2061 Db PASVRTRKHTFGQRCISSR-----PPTLGGDEABAADP------------------------- 2108

2142 Qy SQEEPLFP------------------RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAV--- 2181
2109 Db PATEPHSPEASPTASPVKGTMGSGRDPRRFCSVDAQSFLDKPG-RPDAQRWSSVELDNGE 2167

2182 Qy SCLDSGS--------QPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPP--ESQGSR 2231
2168 Db SHLESGEVGRASELEPAL-----------------GSRRRKKQMSPPCISIEPPTKDEGSSR 2212

2232 Qy PPCSPG--VCLRRRAPASDS---KDPSVSSPLDSTAASP-------------SPKKDTLSLSG 2276
2213 Db PPAAEGGNTTLRRRTPSCEAALHRDCPEPTEGPGTGGDPVAKGERWGQASCRAEHLTVPN 2272

2277 Qy LSSDPTDM 2284
2273 Db FAFEPLDM 2280
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RESULT 11
CCAH_HUMAN
ID   CCAH_HUMAN   STANDARD;   PRT; 2353 AA.
AC   O95180; O95802; Q8WWI6; Q96QI6; Q96RZ9; Q9NYY4; Q9NYY5;

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 368 Qy NFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIA 427
 360 Db NFDNIGYAWIAIFQVITLEGWVDIMYYVMDAHSFYNFIYFILLIIMGSFFMINLCLVVIA 419

 428 Qy TQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVLYLRKAARRLAQVS 487
 420 Db TQFSETKQRENQLMREQRARYLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLY 479

 488 Qy RAIGVRAGLLSSPVAR-----SGQEPQPSGSCTRSHRRLSVHHLV-HHHHHHHYHLGN 541
 480 Db ARWQSRWRKKKVDPSSTVHGQGPGRRPRRAG------RRTASVHHLVYHHHHHHHYHFSH 534

 542 Qy GTLRVPRRASPEIQDRDANGSRRIM--LPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVR 599
 535 Db GGPR--RPSPE---PGAGDNRLVRACAPPSPSPGHGPP-DSESVHSIYHADCHVEGPQ 587

 600 Qy CQAPPPRCPSEASGRTVGSG---KVYPIV------HTSPPPEILKDKALVEVAPSP 646
 588 Db ERARVAHSIATAASLKLASGLGTMNYPTTLPSGTVNSKGGTSSRPKGLRG------AGAP 641

 647 Qy GPPTLTSFNI-PPCPFSSMHKLLETQSTGACHSSCK-ISSPC----SKADSGACGPDSCP 700
 642 Db GAAVHSPLSLGSPRPYEKIQDVVGEQGLGRASSHLSGLSVPCPLPSPQAGTLTCELKSCP 701

 701 Qy YCARTGAGEP--ESADHVMPDSDSEAVYEFTQDAQHSDLRDP---------HSRRRQR 747
 702 Db YCA-SALEDPEPEFSGSESGDSDAHGVYEFTQDVRHGDCRDPVQQPHEVGTPGHSNERRR 760

 748 Qy S-LGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTN 806
 761 Db TPLRKASQPGIGHLWASFSGKLRRRIVDSKYFNRGIMAAILVNTLSMGVEYHEQPEELTN 820

 807 Qy ALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVL 866
 821 Db ALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIVVVISVWEIVGQADGGQSVL 880

 867 Qy RTFRLMRVLKLKVRFLPALQRQLVLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS 926
 868 Db RTFRLLRVLKLVKLVRFLPALRRQLVVLMRTMDNVATFCMLLMLFIFIFSILGMHLFGCKFSL 940

 927 Qy ERD-GDTLPDRKNFDSLLWAIVTTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN 985
 941 Db KTDSGDTVPDRKNFDSLLWAITTVFVQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGN 1000

 986 Qy YVLFNLLVAIIIVEGFQAEGDATKSESEPDFFSPSVDGDRKKRL----------ALVALG 1036
1001 Db YVLFNLLVAILIVEGFQAEGDATRSDTDEDKTSTQLEGDFDKLRDLRATEMKMYSLAVTPN 1060

1037 Qy EHAELRKSLLPPLIIHTAATPMSHPKSS-STCVGEALGSGSRRTSSSGSAAPGAAAHEMK 1095
1061 Db GHLEGRGSLPPPLLITHTAATPMPTPKSSPNLDVAHAL-LDSRR-SSSGSVDPQLG-DQK 1116

1096 Qy CPPSARSSPHGPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEE- 1154
1117 Db SLASLRRSSPCTPWGPNSAGSSRRRSSWNSLGRAPSLKRRNQCGERESLLSGEGKGSTDDEA 1176

1155 Qy ESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSA--SEHQDCN 1211
1177 Db EDSRPSTGTHPGASPGPRATPLRRAE-SLDHRSTLDL----------CPPPRAALLPTKFHDCN 1229

1212 Qy GKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFP 1271
1230 Db GQMVALPSEFFLRIDSHKEDAAEFDDDIEDSCCFRLHKVLEPYAPQWCRSRESWALYLFP 1289

1272 Qy PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1331
1290 Db PQNRLRVSCQKVIAHKMPDHVVLVFIFLNCITIALERPDIDPGSTERAFLSVSNYIFTAI 1349

1332 Qy FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKIIGMLRVL 1391
1350 Db FVVEMMVKVVALGLLWGEHAYLQSSWNVLDGLLVLVIVAMASAGGAKILGVLRVV 1409
```

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DT   15-JUL-1999 (Rel. 38, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated
DE   calcium channel alpha1 3.2 subunit).
GN   Name=CACNA1H;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Heart;
RX   MEDLINE=98333998; PubMed=9670923;
RA   Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N.,
RA   Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.;
RT   "Cloning and characterization of alpha1H from human heart, a member of
RT   the T-type Ca2+ channel gene family.";
RL   Circ. Res. 83:103-109(1998).
RN   [2]
RP   REVISIONS.
RA   Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Thyroid carcinoma;
RX   MEDLINE=9912795; PubMed=9930755;
RA   Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F.,
RA   Prodanovich P., Harpold M.M., Stauderman K.A.;
RT   "Structure and functional characterization of a novel human low-
RT   voltage activated calcium channel.";
RL   J. Neurochem. 72:791-799(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=21096910; PubMed=11157797;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Testis;
RX   MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200;
RA   Jagannathan S., Punt E.L., Gu Y., Arnoult C., Sakkas D., Barratt C.L.,
RA   Publicover S.J.;
RT   "Identification and localization of T-type voltage-operated calcium
RT   channel subunits in human male germ cells. Expression of multiple
RT   isoforms.";
RL   J. Biol. Chem. 277:8449-8456(2002).
RN   [6]
RP   SEQUENCE OF 86-817 FROM N.A.
RA   Cobley V.E.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).
RA   Mittman S., Agnew W.S.;
RT   "Organization and alternative splicing of CACNA1H.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1H
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=AlH-a;
CC         IsoId=O95180-1; Sequence=Displayed;
CC       Name=2; Synonyms=AlH-b;
CC         IsoId=O95180-2; Sequence=VSP_000949;
CC   -!- TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.
CC       Isoform 2 seems to be testis-specific.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown
CC       in this entry. The additional 20 amino acids found in the Ref.4
CC       and Ref.6 sequences are due to a misunderstanding of the real type
CC       of splicing mechanism involved.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF051946; AAC67239.3; -.
DR   EMBL; AF073931; AAD17668.1; -.
DR   EMBL; AE006466; AAK61268.1; ALT_SEQ.
DR   EMBL; AJ420779; CAD12646.1; -.
DR   EMBL; AL031703; CAC42094.1; ALT_SEQ.
DR   EMBL; AF223562; AAF60162.1; -.
DR   EMBL; AF223563; AAF60163.1; -.
DR   Genew; HGNC:1395; CACNA1H.
DR   MIM; 607904; -.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.
DR   GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.
DR   GO; GO:0006936; P:muscle contraction; TAS.
DR   GO; GO:0007520; P:myoblast fusion; TAS.
DR   GO; GO:0008016; P:regulation of heart rate; TAS.
DR   GO; GO:0006810; P:transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Repeat; Transmembrane; Voltage-gated channel.
FT   REPEAT         87    422       I.
FT   REPEAT        779   1018       II.
FT   REPEAT       1281   1558       III.
FT   REPEAT       1602   1863       IV.
FT   DOMAIN          1    100       Cytoplasmic (Potential).
FT   TRANSMEM      101    119       S1 of repeat I (Potential).
FT   DOMAIN        120    139       Extracellular (Potential).
FT   TRANSMEM      140    160       S2 of repeat I (Potential).
FT   DOMAIN        161    169       Cytoplasmic (Potential).
FT   TRANSMEM      170    184       S3 of repeat I (Potential).
FT   DOMAIN        185    193       Extracellular (Potential).
FT   TRANSMEM      194    212       S4 of repeat I (Potential).
FT   DOMAIN        213    232       Cytoplasmic (Potential).
FT   TRANSMEM      233    253       S5 of repeat I (Potential).
```

```
FT   DOMAIN      254    394    Extracellular (Potential).
FT   TRANSMEM    395    419    S6 of repeat I (Potential).
FT   DOMAIN      420    793    Cytoplasmic (Potential).
FT   TRANSMEM    794    814    S1 of repeat II (Potential).
FT   DOMAIN      815    827    Extracellular (Potential).
FT   TRANSMEM    828    849    S2 of repeat II (Potential).
FT   DOMAIN      850    855    Cytoplasmic (Potential).
FT   TRANSMEM    856    874    S3 of repeat II (Potential).
FT   DOMAIN      875    882    Extracellular (Potential).
FT   TRANSMEM    883    906    S4 of repeat II (Potential).
FT   DOMAIN      907    917    Cytoplasmic (Potential).
FT   TRANSMEM    918    938    S5 of repeat II (Potential).
FT   DOMAIN      939    990    Extracellular (Potential).
FT   TRANSMEM    991   1015    S6 of repeat II (Potential).
FT   DOMAIN     1016   1290    Cytoplasmic (Potential).
FT   TRANSMEM   1291   1313    S1 of repeat III (Potential).
FT   DOMAIN     1314   1331    Extracellular (Potential).
FT   TRANSMEM   1332   1352    S2 of repeat III (Potential).
FT   DOMAIN     1353   1362    Cytoplasmic (Potential).
FT   TRANSMEM   1363   1382    S3 of repeat III (Potential).
FT   DOMAIN     1383   1396    Extracellular (Potential).
FT   TRANSMEM   1397   1418    S4 of repeat III (Potential).
FT   DOMAIN     1419   1428    Cytoplasmic (Potential).
FT   TRANSMEM   1429   1452    S5 of repeat III (Potential).
FT   DOMAIN     1453   1529    Extracellular (Potential).
FT   TRANSMEM   1530   1555    S6 of repeat III (Potential).
FT   DOMAIN     1556   1616    Cytoplasmic (Potential).
FT   TRANSMEM   1617   1637    S1 of repeat IV (Potential).
FT   DOMAIN     1638   1651    Extracellular (Potential).
FT   TRANSMEM   1652   1673    S2 of repeat IV (Potential).
FT   DOMAIN     1674   1680    Cytoplasmic (Potential).
FT   TRANSMEM   1681   1699    S3 of repeat IV (Potential).
FT   DOMAIN     1700   1713    Extracellular (Potential).
FT   TRANSMEM   1714   1737    S4 of repeat IV (Potential).
FT   DOMAIN     1738   1751    Cytoplasmic (Potential).
FT   TRANSMEM   1752   1772    S5 of repeat IV (Potential).
FT   DOMAIN     1773   1835    Extracellular (Potential).
FT   TRANSMEM   1836   1863    S6 of repeat IV (Potential).
FT   DOMAIN     1864   2353    Cytoplasmic (Potential).
FT   DOMAIN      520    530    Poly-His.
FT   DOMAIN     1107   1110    Poly-Ser.
FT   DOMAIN     1583   1586    Poly-Arg.
FT   SITE        378    378    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE        974    974    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE       1504   1504    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE       1808   1808    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   CARBOHYD    192    192    N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    271    271    N-linked (GlcNAc. . .) (Potential).

Query Match          51.7%;    Score 6222;  DB 1;  Length 2353;
Best Local Similarity 56.7%;   Pred. No. 7.1e-303;
Matches 1370;  Conservative 208;  Mismatches 529;  Indels 310;  Gaps 62;
```

```
Qy    25  PPGPRLARGWTRRMERAPRSRDSP--VASRSTTCPGPGAAGAGSTEKDPGSADSEAEG   82
Db    19  PPGPAALVG------ASPESPGAPGREAERGSELGVSPSESPAAERGAELGA--DEEQR   69

Qy    83  LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLLNCVTLGMFRPCEDIACD  142
Db    70  VPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVECG  129

Qy   143  SQRCRIIQAFDDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLD  202
Db   130  SERCNILEAFDAFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVVAGMMEYSLD  189

Qy   203  LQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGV  262
Db   190  GHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGV  249
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Qy   263  QLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENBDESPFICSQPRENGMRSCRSVPTLR  321
Db   250  QLWAGLLRNRCFLDSAFVRNNNLTFLRPYYQTEGEENPFICSSRRDNGMQKCSHIP--   306

Qy   322  GEGGGPPCSLDYETYN--------SSSNTTCVWNQYYTNCSAGEHNPPKGAINFDNIGY   374
Db   307  GRRELRMPCTLGWEAYTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGY  366

Qy   375  AWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETK  434
Db   367  AWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETK  426

Qy   435  QRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRA  494
Db   427  QRESQLMREQRARHLSNDSTLASFSEPGSCYEELLKKYVGHIFRKVKRRSLRLYARWQSRW  486

Qy   495  GLLSSPVARSGQEFQPSGSGCTRSHRR------LSVHHLV-HHHHHHHYHLGNGTLRV   546
Db   487  RKKVDPSAVQGQGP-------GHRQRAAGRHTASVHHLVYHHHHHHHYHFSHGSPRR   538

Qy   547  PRASPEIQDRDANGSRRLML--PPPSTPTPSGGPPRGAESVHSFYHADCHLE--PVRCQA  602
Db   539  PGPEPGACD-----TRLVRAGAPPSPPSPGRGPP-DAESVHSIYHADCHIEGPQERARV  591

Qy   603  PPPRCPSEASGR-TVGSGKV-YPTV------HTSPPPEILKDKALVEVAPSP----   646
Db   592  AHAAATAAASLRLATGLGTMNYPTILPSGVGSGKGSTSPGPK------GKWAGGPPGTG  644

Qy   647  --GPPTLTSFNIPPGPFSSMHKLLETQSTGAC--HSS-----CKISSPCSKADSGACGPD  697
Db   645  GHGPLSLNS-----PDPYEKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP--PAGTLTCELK  698

Qy   698  SCPYCART-GAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDP-----   740
Db   699  SCPYCTRALEDPEGELSGSESGDSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGS  758

Qy   741  HSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ  800
Db   759  PQRRAQQRAAP-GEPGWMGRLWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGVEYHEQ  817

Qy   801  PEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVVVISVWEIVQQG   860
Db   818  PEELTNALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIIVVISVWEIVGQAD  877

Qy   861  GGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLF  920
Db   878  GGLSVLRTFRLLRVLKLVRFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLF  937

Qy   921  GCKFASERD-GDTLPDRKNFDSLLWAIVTVFQLTQEDWNKVLYNGMASTSSWAALYFIA  979
Db   938  GCKFSLKTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVA  997

Qy   980  LMTFGNYVLFNLLVALLVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVAL----  1035
Db   998  LMTFGNYVLFNLLVAILVEGFQAEGDANRSDTTDEDKTSVHFEEDFHKLRELQTTELKMCS  1057

Qy  1036  ----GEHAELRKSLLPPLIIHTAATPMSHPKSSS-TGVGEALGSGSRRTSSSGSAEPGA  1089
Db  1058  LAVTPNGHLEGRGSLSPPLIMCTAATPMTPKSSPFLDAAPSLPDSRGGSSSGDPPLG-  1116

Qy  1090  AHHEMKCCPSARSSPHSPWSAASSWTSRRSSRNSIGRAPSLKRRSPSGERRSLLSGEGQE  1149
Db  1117  --DQKPPASLRSSPCAPWGPSGAWSSRRSSWSSLGRAPSLKRRGQCGERESLLSGEGKG  1173

Qy  1150  SQDEEESSEEDRASPA--GSDHRHRGSLEREAKSSFDLPDTL---------QVPGLH--R  1196
Db  1174  STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDGQVALPSDFFLR  1231

Qy  1197  TASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLP  1256
Db  1232  IDSHREDAAELDDDSEDSCCLRLHKVLEPYKPQ------------------W--------  1265

Qy  1257  ACCRERDWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPKIDPHSA  1316
```

Db   2264 PSFAFEPLDLGVPSGDP 2280

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RESULT 12
CCAH_MOUSE
ID   CCAH_MOUSE      STANDARD;      PRT;   2365 AA.
AC   O88427; Q9JKU5;
DT   15-JUL-1999 (Rel. 38, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.2).
GN   Name=Cacna1h;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Mittman S.;
RT   "Exon organization of mouse Cacna1h.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1823-1952 FROM N.A.
RC   STRAIN=C57BL/6J;
RA   Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1H
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF226868; AAK21607.2; -.
DR   EMBL; AY026385; AAK21607.2; JOINED.
DR   EMBL; AF051947; AAC67240.1; -.
DR   MGD; MGI:1928842; Cacna1h.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M-channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
```

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Db   1266 --CRSREAWALYLFSPQNRFRVSCCQKVITHKMFDHVVLVFIFLNCVTIALERPDIDPGST 1323
             ||  |:||:  ||:| ||:|  ||||| ||||||| :||||  ::||||:|||| ||||||
Qy   1317 ERIFITLSNYIFTAVFLAEMTVKVVALGWCFGEQAXLRSSWNVLDGLLVLISVIDILVSM 1376
             ||||:|::||:|||:||::|||| ||||| :|||| :|||||||||||:||:|||||||||
Db   1324 ERVFLSVSNYIFTAIFVAEMVKVVALGLLSGEHAYLQSSWNLLDGLLVLVSLVDIVVAM 1383

Qy   1377 VSDSGTKILGMLRVLRLLRTLRPLVRLVISRAQGLKLVVETIMSSLKPIGNIVVICCAFFII 1436
             ||| | |||:|||||||||||||||:||||||| ||||||| |::||||||||:||||||||
Db   1384 ASAGAKILGVLRVLRLLRTLRPLVRLVISRAPGLKLVVETILSSLRPIGNIVLICCAFFII 1443

Qy   1437 FGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASK 1496
             |||||||||||||: :||||||||::|||  |||||| ||:|||||||||||||||||||
Db   1444 FGILGVQLFKGKFYYCEGPDTRNISTKAQCRAAHYRWVRRKYNFDNLGQALMSLFVLSSK 1503

Qy   1497 DGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQ 1556
             |||:|||:||||||||||||: ||||:||||||:|||:|||||||||| ||:||||||:|
Db   1504 DGWVNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQ 1563

Qy   1557 HQEEEEARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLF 1616
             ||| ||||||||||||||||||||: |||||| |||||:||||:|||:|||||||| ||:
Db   1564 HQAEEEARRREEKRLRRLERRRSTFPS-PEAQRRPYIADYSPTRRSIHSLCTSHYLDLF 1622

Qy   1617 ITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWN 1676
             || :| :|| ||:|||| ||||:|||:||||||||:|||| |||| | |||||||||||||
Db   1623 ITFIICVNVITMSMEHYNQPKSIDEALKYCNYVFTIVFVFEAALKLVAFGFRRFFKDRWN 1682

Qy   1677 QLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTV 1736
             |||||||| ||||||||||:  ||:||||||||||||||||||||||||| |||||||||
Db   1683 QLDLAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTV 1742

Qy   1737 MQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLF 1796
             : |||||||||||||||||||||||||||| |: :|:||||::||||||||||||||||||
Db   1743 VQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLTLF 1802

Qy   1797 RVSTGDNWNGIMKDPSRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKH 1853
             ||||||||||||||| |:   :  :|  :|:: ||||:|:||||||||||||||||||||
Db   1803 RVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPVVFVTFVLVAQFVLVNVVVAVLMKH 1862

Qy   1854 LEESNKEAKEEAELAELELEMKTLSPQHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTA 1913
             |||||||| || ||:|| |||:  :  |   |
Db   1863 LEESNKEAREDAELDAEIELEMA----------------QGPGSARRVDADRP-------- 1899

Qy   1914 HIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA---- 1970
Db   1900 ----------------------PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP 1943

Qy   1971 -----ERSLGHRGWGLPKAQSGSIISVHSQPADTSCILQLPKDVH---------YLLQP 2015
             :||| :|:: :  : : |                       :
Db   1944 HPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIPLAVSSPARSGEPLHALSP 2000

Qy   2016 HGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEV----SGPSC 2071
             || :  :| |  || |    :  :  : ||
Db   2001 RGT------------ARSPSLSRLLCRQEAVHTDSLEGK-IDSPRDTLDPAEPGEKTPVR 2047

Qy   2072 PLTRSSSFWGGSSIQVQQRSGIQSKV--SKH------IRLPAPCPGLEPSWAKDPPETRS 2123
             | :||                  |:|  |||
Db   2048 PVTQ-------GGSLQSPPRSPRASVRTRKHTFGQRCVSSRPAAPGGEEAEASDP----- 2096

Qy   2124 SLELDTELSWISGDLLP-SSQEEPLFP---------RDLKKCYSVETQSCRRRPGFWLDE 2173
             || |:|| :|                  |:           |  |   :||||||||:||
Db   2097 ---ADEEVSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGFLDKPG-RADE 2152

Qy   2174 QRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGP--GSRPKKKLSPPSISIDPP-ESQGS 2230
             | :||                 :| |  ||      |::
Db   2153 QWRPSAE---LGSGE-----PGEAKAWG-PEAEFALGARRKKKMSPPCISVEPPAEDEGS 2203

Qy   2231 -RPPCSPG--VCLRRRAPA------SDSKDPSVSSPLDSTAAS-----PSPKKDTLSL 2274
             :||            ||          :  |    |:  |:            ::|:|:
Db   2204 ARPSAAEGGSTTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWQQASCRAEHLTV 2263

Qy   2275 SGLSSDPTDM-----DP 2286
             :  |:         ||
Db   2275 ---------------DP 2286
```

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KW   Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Phosphorylation; Repeat; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT        87    422       I.
FT   REPEAT       776   1015       II.
FT   REPEAT      1292   1569       III.
FT   REPEAT      1613   1874       IV.
FT   DOMAIN         1    100       Cytoplasmic (Potential).
FT   DOMAIN       101    119       S1 of repeat I (Potential).
FT   TRANSMEM     120    139       Extracellular (Potential).
FT   DOMAIN       140    160       S2 of repeat I (Potential).
FT   TRANSMEM     161    169       Cytoplasmic (Potential).
FT   DOMAIN       170    184       S3 of repeat I (Potential).
FT   TRANSMEM     185    193       Extracellular (Potential).
FT   DOMAIN       194    212       S4 of repeat I (Potential).
FT   TRANSMEM     213    232       Cytoplasmic (Potential).
FT   DOMAIN       233    253       S5 of repeat I (Potential).
FT   TRANSMEM     254    394       Extracellular (Potential).
FT   DOMAIN       395    419       S6 of repeat I (Potential).
FT   TRANSMEM     420    790       Cytoplasmic (Potential).
FT   DOMAIN       791    811       S1 of repeat II (Potential).
FT   TRANSMEM     812    824       Extracellular (Potential).
FT   DOMAIN       825    846       S2 of repeat II (Potential).
FT   TRANSMEM     847    852       Cytoplasmic (Potential).
FT   DOMAIN       853    871       S3 of repeat II (Potential).
FT   TRANSMEM     872    879       Extracellular (Potential).
FT   DOMAIN       880    903       S4 of repeat II (Potential).
FT   TRANSMEM     904    914       Cytoplasmic (Potential).
FT   DOMAIN       915    935       S5 of repeat II (Potential).
FT   TRANSMEM     936    987       Extracellular (Potential).
FT   DOMAIN       988   1012       S6 of repeat II (Potential).
FT   TRANSMEM    1013   1301       Cytoplasmic (Potential).
FT   DOMAIN      1302   1324       S1 of repeat III (Potential).
FT   TRANSMEM    1325   1342       Extracellular (Potential).
FT   DOMAIN      1343   1363       S2 of repeat III (Potential).
FT   TRANSMEM    1364   1373       Cytoplasmic (Potential).
FT   DOMAIN      1374   1393       S3 of repeat III (Potential).
FT   TRANSMEM    1394   1407       Extracellular (Potential).
FT   DOMAIN      1408   1429       S4 of repeat III (Potential).
FT   TRANSMEM    1430   1439       Cytoplasmic (Potential).
FT   DOMAIN      1440   1463       S5 of repeat III (Potential).
FT   TRANSMEM    1464   1540       Extracellular (Potential).
FT   DOMAIN      1541   1566       S6 of repeat III (Potential).
FT   TRANSMEM    1567   1627       Cytoplasmic (Potential).
FT   DOMAIN      1628   1648       S1 of repeat IV (Potential).
FT   TRANSMEM    1649   1662       Extracellular (Potential).
FT   DOMAIN      1663   1684       S2 of repeat IV (Potential).
FT   TRANSMEM    1685   1691       Cytoplasmic (Potential).
FT   DOMAIN      1692   1710       S3 of repeat IV (Potential).
FT   TRANSMEM    1711   1724       Extracellular (Potential).
FT   DOMAIN      1725   1748       S4 of repeat IV (Potential).
FT   TRANSMEM    1749   1762       Cytoplasmic (Potential).
FT   DOMAIN      1763   1783       S5 of repeat IV (Potential).
FT   TRANSMEM    1784   1846       Extracellular (Potential).
FT   DOMAIN      1847   1874       S6 of repeat IV (Potential).
FT   TRANSMEM    1875   2365       Cytoplasmic (Potential).
FT   DOMAIN       521    531       Poly-His.
FT   DOMAIN      1594   1597       Poly-Arg.
FT   SITE         378    378       Calcium ion selectivity and permeability
FT                                 (By similarity).
FT   SITE         971    971       Calcium ion selectivity and permeability
FT                                 (By similarity).
FT   SITE        1515   1515       Calcium ion selectivity and permeability
FT                                 (By similarity).
FT   SITE        1819   1819       Calcium ion selectivity and permeability
FT                                 (By similarity).
FT   CARBOHYD     192    192       N-linked (GlcNAc. . .)    (Potential).
FT   CARBOHYD     271    271       N-linked (GlcNAc. . .)    (Potential).
FT   CARBOHYD    1477   1477       N-linked (GlcNAc. . .)    (Potential).
FT   CONFLICT    1823   1825       GIM -> ARG (in Ref. 2).
FT   CONFLICT    1914   1914       D -> E (in Ref. 2).
FT   CONFLICT    1945   1947       APA -> LLQ (in Ref. 2).
FT   CONFLICT    1952   1952       S -> A (in Ref. 2).
```

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FT   CONFLICT    1953   2351       Missing (in Ref. 2).
SQ   SEQUENCE    2365 AA;  261944 MW;  9A8AI7570C210596 CRC64;

Query Match
Best Local Similarity 51.5%;  Score 6190; DB 1;  Length 2365;
              Conservative 56.0%;  Pred. No. 2.9e-301;
Matches 1356;  Conservative 249;  Mismatches 511;  Indels 304;  Gaps 61;

Qy    30 LARGWTRRRMERAPRSRDSPVASRSSTTCPG-PG---AAGAGST---EKDPGS---AD--  77
Db     6 LAADEVRVPLGASPSAPAAPV--RASPASPGVPGREEQRGSGSSVLAPESPGTECGADLG  63

Qy    78 -SEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPC 136
Db    64 ADEQPVPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHISMLVIMLNCVTLGMFRPC  123

Qy   137 EDIACDSQRCRILQAFDDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGM  196
Db   124 EDVECRSERCSILEAFDDFIFAFFAVEMVKMVALGFGQKCYLGDTWNRLDFFIVAGM   183

Qy   197 LEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFVFFI  256
Db   184 MEYSLDGHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFVFFI  243

Qy   257 FGIVGVQLWAGLLRNCFLPENFSLPLSVD-LEPYYQTENEDESPFICSQPRENGMRSCR  315
Db   244 FGIVGVQLWAGLLRNCFLDSAFVRNNNLIFLRPYYQTEBGEENPFICSSRRDNGMQKCS  303

Qy   316 SVPT-----LRGEGGGGPPCSLDYETY----------NSSSNTTCVNWNQYYTNCSAGEHNPFKG 365
Db   304 HIPSRRELRVQ------CTLGWEAYGQPQAEDGAGRNACINWNQYNVCRSGEFNPHNG   357

Qy   366 AINFDNIGYAWIAIFQVITLBGWVDIMYFVMDAHSFYNFIYFILLIIVGSFMINLCLVV  425
Db   358 AINFDNIGYAWIAIFQVITLBGWVDIMYYVMDAHSFYNFIYFILLIIVGSFMINLCLVV  417

Qy   426 IATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQ 485
Db   418 IATQFSETKQRENQLMREQRARYLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLR  477

Qy   486 VSRAIGVRAGLLSSPVARSGQEPQPSGSC---------TRSHRR-LSVHHLV-HHHHHHH 534
Db   478 --------LYARWQSWRKKVDPSSTLHGQGPRRRPRRAGRRTASVHHLVVHHHHHHH     527

Qy   535 HHYHLGNGTLRVPRASPEIQDRDANGSRRLM-LPPPSTTPSGGPPRGAEBVHSFYHAD   592
Db   528 HHYHFSHGGPR--RPSPE----PGAGDTRLVRACVPFSPPSPGHGPP-DSESVHSIYHAD 580

Qy   593 CHLEPVRCQAPPPRCPSEASGRTVGSG---KVYPTV---------HTSPPPEILKDKAL  639
Db   581 CHVEGPQERARVAHTIATAASLKLASGLGTMNYPTILPSGAVNSKGSTSRPKGLRS---- 637

Qy   640 VEVAPSPGPPTLTSFNI-PPGPFSSMHKLLETQSTGACHSSCK-ISSPC---SKADSGA  693
Db   638 --AGTPGATAHSPLSLGSPSPYEKIQHVVGEQGLGRASSHLSGLSVPCPLPSPQAGTLT  694

Qy   694 CGPDSCPYCARTGAGEP--ESADHVMPDSDSEAVYEFTODAQHSDLRDP---------- 740
Db   695 CELKSCPYCA-SALEDPEFFSGSESGDSDAHGVVEFTQDVRHGDCRDPVQQPHEGGTPG  753

Qy   741 HSRRRQR-SLGPDAEPSSVLAFWRLICDTFRKIVDSKYPGRGIMIAILVNTLSMGIEYHE 799
Db   754 HGNERWRPPLRTASQPGGLGRLWASFSSKLRRIVDSKYFNRGIMAAILVNTLSMGVEYHE 813

Qy   800 QPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGVIKPYNIFDGVIVVISVWEIVGQQ  859
Db   814 QPDELTNALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIVVVISVWEIVGQA 873

Qy   860 GGGLSVLRTFRLMRVLKLVRFLPALQRQLVVIMKTMDNVATFCMLLMLFIFSIIGMHL  919
Db   874 DGGLSVLRTFRLLRVLKLVKLVRFLPALRRQLVVLMRTMDNVATFCMLLMLFIFSIIGMHL 933

Qy   920 FGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILLTQEDWNKVLYNGMASTSSSWAALYFI 978
```

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Db   934  FGCKFSLKTDSGDTVPDRKNFDSLLWAIVTVPQILTQEDWNVVLYNGMASTSSWAALYFV  993

Qy   979  ALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKK--------  1028
         |||||||||||||||||||||:||||||||||:::||  :: :  :::
Db   994  ALMTFGNYVLFNLLVAILVAIIVEGFQAEGDATRSDTDEDKTSTHLEEDFDKLRDVRATEMKMY  1053

Qy  1029  RLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSS-STGVGEALGSGSRRTSSSGSAEP  1087
         .:|| ||:| ||:||| |||||||||||||||:.:::  :||| :|:||:|||::||| |
Db  1054  SLAVTPNG-HLEGRGSLPPPLITHTAATPMPTPKSSPHLDMAHTL-LDSRR-SSSGSVDP  1110

Qy  1088  GAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEG  1147
         .   .  :  ||| ||| .| ||.||||||||||||||||||||||| .|||||||||||
Db  1111  QLG--DQKSLASLRSSPCAPWGPNSAGSSRRSSWNSLGRAPSLKRRSQCGERRSLLSGEG  1168

Qy  1148  QESQDEE-ESSEEDRASPAGSDHRHRGSLRERA-----KSSFDL---PDTLQVPGLHRT  1197
         : |.:|  |||.||:.|..||.| :||| |:.|     |||.||   | |:::  :|
Db  1169  KGSTDDEAEDSRPNSGTHPGASPGPRATPLRRAESLGHRSTMDLCPPRPATL-LP-----  1222

Qy  1198  ASGRSSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPA  1257
                     .:|.||. :. .:|:|||| :|::| :::  ||:|||||:::|| :||||
Db  1223  ------TKFRDCNGQMVALPSEFFLRIDSHKEDAAEFDDDIEDSCCFRLHKVLEPYAPQ  1275

Qy  1258  CCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLIVIIFLNCITIAMERPKIDPHSAE  1317
          |..:.||:||:|||| .|:|| | ::|||||||||||:|||||||::|:|||.|||.|:|
Db  1276  WCSSRESWALYLFPPQNRLRVSCQKVIAHKMFDHVVLVFIIFLNCITTIALERPDIDPGSTE  1335

Qy  1318  RIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLVISVIDILVSMV  1377
         | ||::||||||::|:.||.|||||:|   ||||||.|||||||||||||:|||::|:||.
Db  1336  RAFLSVSNYIFTAIFVVEMMVKVVAIGLLWGEHAYLQSSWNVLDGLLVLVLSVDIIVAVA  1395

Qy  1378  SDSGTKILGMLVRLVRLLRTLRPLRVISRAQGLKIVVETLMSSLKPIGNIVVICCAFFIIF  1437
          . | |||| ||||||||||||||||||||.||:::|||::||:|||||||:|||||||||
Db  1396  SAGGAKILGVLVRLVRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFIIF  1455

Qy  1438  GILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKD  1497
         ||||||||||||::|:| ||||||.|::| .|.|||||.|||||||||||||||||:|||
Db  1456  GILGVQLFKGKFYYCEGTDTRNITTKAECHAAHYRWVRRKYNFDNLGQALMSLFVLSSKD  1515

Qy  1498  GWVDIMYDGLDAVGVDQQPIMNHNPWMLIYFISFLLIVAFFVLNMFVGVVVENFHKCRQH  1557
         ||| ||||||||||:||||: |||||||:||||||||:||||:||||||||||||||||||
Db  1516  GWVNIMYDGLDAVGIDQQPVQNHNPWMLLYFISFLLIVSFFVVLNMFVGVVVENFHKCRQH  1575

Qy  1558  QEEEEARRREEKRLRLEKKRRSKEKQMAEAAQCKPYYSDYISRFRLLVHHLCTSHYLDLFI  1617
         || :|||||||||||||::||||.  | .   |:| .||||.:.:  | :||||||||||||
Db  1576  QEAEEARRREEKRLRLERRRRSTFPN-PEAQRPYYADYSHTRRSIHSLCTSHYLDLFI  1634

Qy  1618  TGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVPESVFKIVAFAFRRFFQDRWNQ  1677
         | :  ||||||:|||:.:||:|||||:|||::||::|| |::||||||.|||||:|||||
Db  1635  TFIICLNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVFEAALKIVAFGFRRFFKDRWNQ  1694

Qy  1678  LDLAIVLLSIMGITLEEIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRALLHTVM  1737
         ||||||||||||:|||||| |.:|||||||||||||||||||||||||.||||||.||:
Db  1695  LDLAIVLLSIMGIALEEIEMNAALPINPTIIRMRVLRIARVLKLLKMATGMRALLDTVV  1754

Qy  1738  QALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFR  1797
         |||||||||||||||||||:|||||||||.|||.|::|||||.|||||:||||||||||||
Db  1755  QALPQVGNIGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFTNFGMAFLTLFR  1814

Qy  1798  VSTGDNWNGIMKDPSRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHL  1854
         ||||||||||||||.|:|  |||||||||:|||||||:|||:||||||||||:|||||||
Db  1815  VSTGDNWNGIMKDTLRECTREDKHCLSYLPALSPVYFVTFVLVAQFVLVNVVAVLMKHL  1874

Qy  1855  EESNKEAKEAEELEAEELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAH  1914
         |||||||:|:||:.||:  |||
Db  1875  EESNKEAREDAEMDAEITLEI-------------------  1895

Qy  1915  IGAASGFSLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL  1974
           .||   :  :  ::|.||:: :|. ||:|||.|||||:|||||||||| | ||.   :
Db  1896  --AQGSTAQPPSTAQESQGTD--PDTPNLLVRKVSVSRMLSLPNDSYMFRRVAPAAPH  1951

Qy  1975  GHRGWGLP------KAQSGSIILSVHSQPADTSCILQLP-------KDVHYLLQPHGAP  2019
          .   .:|        ::: :  ||:|| ::  ::|.|        :  :|:| |.|.|
Db  1952  SH-----PLQEVEMETYTGPVTSAHSPSLEPRTSFQVPSAASSPARASDPLCALSPRDTP  2006
```

```
Qy  2020  TWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSF  2079
                                  ||::   ::  |  :.::  |:||||:::|:||  :||
Db  2007  -----RSLSLSRILYRQEAMHAESLEGQIDDAGEDGIPDYTEPAENISMSQAP  2054

Qy  2080  WG----GSSIQVQQRSGIQSKVSKGHIRLPAPCPGLEPSWAKDPPETRSSLELDT  2129
         ||     .::   :|..|. .: :  ||  | | :.  .  .::: . ::: ::
Db  2055  LGTILRSPPCSPRPASVRTRKHTFGQHCISSR---PPTLGGDDARAADP-----ADE  2102

Qy  2130  ELSWISGDLLPSSQEEPLFP-----------RDLKKCYSVETQSCRRRPGFWLDE  2173
         | ..:|   ||..:|||. |           | |:| ||  |.| | |.  :.|
Db  2103  EVSHITSSAHPWPATEPHSPEASPTASPAKGTVGSGRDPHRFCSVDAQSFLDKPG-RPDA  2161

Qy  2174  QRRHSIAV----SCLDSGS-----------QPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS  2221
         || .|        | |.||            . |||| ||||.|||| ||||  || ||| ||
Db  2162  QRWSSVELDNGDGHLESGEVRARASELEPAL------------GARRKKKMSPPCIS  2206

Qy  2222  IDPP-ESQG-SRPPCSPG--VCLRRRAPASDS---KDPSVSSPLDSTAASP-------  2265
         |||| |..| |||| ..|    |||| | ::     : ::.   | : |||
Db  2207  IDPPTEDEGSSRPPAAEGGNTTLRRRTPSCEAALHRDCPESTEGPGTGDPVAKGERWGQ  2266

Qy  2266  -SPKKDTLSLSLGLSSDPTDM  2284
          : ::| | || | ||||.||
Db  2267  ASCRAEHLTVPNFAFEPLDM  2286
```

RESULT 13

CCAI_HUMAN

```
RA   Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA   Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA   Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA   Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA   Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA   Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA   Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA   Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA   Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA   Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA   Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA   Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA   Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA   Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA   Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA   Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA   Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA   Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA   Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA   Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA   Roe B.A., Chen F., Fang L., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA   Dorman A., Fang F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA   Lewis J., Lewis J., Lin S.-P., Loh P., Hua A., Malaj E., Nguyen T., Pan H.,
RA   Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan S., Song L.,
RA   Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA   Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA   Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA   Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA   Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohling T.,
RA   Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA   Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA   Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA   Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA   Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA   Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA   O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA   Ohara O.;
RT   "The DNA sequence of human chromosome 22.";
RL   Nature 402:489-495(1999).
RN   [5]
RP   SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA   Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. Isoform alpha-1I
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes. Gates in voltage ranges
CC       similar to, but higher than alpha 1G or alpha 1H (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=Delta35b;
CC         IsoId=Q9P0X4-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9P0X4-2; Sequence=VSP_000951;
CC       Name=3; Synonyms=Alpha1I-a;
CC         IsoId=Q9P0X4-3; Sequence=VSP_000950, VSP_000951;
CC       Name=4;
CC         IsoId=Q9P0X4-4; Sequence=VSP_000950;
CC   -!- TISSUE SPECIFICITY: Brain specific.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   -!- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to
CC       erroneous gene model prediction.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF129133; AAD45251.1; -.
DR   EMBL; AF142567; AAF25722.1; -.
DR   EMBL; AF211189; AAF44626.1; -.
DR   EMBL; AF393329; AAM67414.1; -.
DR   EMBL; AL008716; CAA15494.1; -.
DR   EMBL; AL022312; CAB62988.1; ALT_SEQ.
DR   EMBL; AL022319; CAB62996.1; ALT_SEQ.
DR   EMBL; AL022319; CAD92536.1; -.
DR   EMBL; AB032946; BAA86434.1; -.
DR   Genew; HGNC:1396; CACNA1I.
DR   MIM; 608230; -.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.
DR   GO; GO:0008332; F:low voltage-gated calcium channel activity; NAS.
DR   GO; GO:0006816; P:calcium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Alternative splicing; Calcium; Calcium channel; Calcium-binding; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Polymorphism; Repeat; Transmembrane; Voltage-gated channel.
FT   REPEAT        66    401       I.
FT   REPEAT       626    865       II.
FT   REPEAT      1157   1434       III.
FT   REPEAT      1472   1733       IV.
FT   DOMAIN         1     78       Cytoplasmic (Potential).
FT   TRANSMEM      79     99       S1 of repeat I (Potential).
FT   DOMAIN       100    120       Extracellular (Potential).
FT   TRANSMEM     121    141       S2 of repeat I (Potential).
FT   DOMAIN       142    148       Cytoplasmic (Potential).
FT   TRANSMEM     149    168       S3 of repeat I (Potential).
FT   DOMAIN       169    173       Extracellular (Potential).
FT   TRANSMEM     174    191       S4 of repeat I (Potential).
FT   DOMAIN       192    211       Cytoplasmic (Potential).
FT   TRANSMEM     212    232       S5 of repeat I (Potential).
FT   DOMAIN       233    377       Extracellular (Potential).
FT   TRANSMEM     378    398       S6 of repeat I (Potential).
FT   DOMAIN       399    640       Cytoplasmic (Potential).
FT   TRANSMEM     641    661       S1 of repeat II (Potential).
FT   DOMAIN       662    676       Extracellular (Potential).
FT   TRANSMEM     677    697       S2 of repeat II (Potential).
FT   DOMAIN       698    702       Cytoplasmic (Potential).
FT   TRANSMEM     703    721       S3 of repeat II (Potential).
FT   DOMAIN       722    729       Extracellular (Potential).
FT   TRANSMEM     730    753       S4 of repeat II (Potential).
```

```
FT   DOMAIN      754    764          Cytoplasmic (Potential).
FT   TRANSMEM    765    785          S5 of repeat II (Potential).
FT   DOMAIN      786    841          Extracellular (Potential).
FT   TRANSMEM    842    862          S6 of repeat II (Potential).
FT   DOMAIN      863   1166          Cytoplasmic (Potential).
FT   TRANSMEM   1167   1187          S1 of repeat III (Potential).
FT   DOMAIN     1188   1209          Extracellular (Potential).
FT   TRANSMEM   1210   1230          S2 of repeat III (Potential).
FT   DOMAIN     1231   1244          Cytoplasmic (Potential).
```

```
Query Match      45.0%;   Score 5418;  DB 1;  Length 2223;
Best Local Similarity   49.9%;  Pred. No. 1.3e-262;
Matches 1235;  Conservative  243;  Mismatches 533;  Indels  462;  Gaps  68;
```

```
Qy     12  TPPLRGSARPSSDP------PGPRLARGWTRRRMERAPRSRDSPVASRSSTTCPGPGAAG   65
                          |:|:::|                     ||||
Db      6  SPPSSAAAPAAEPGVTTEQPGPR------------------SPPSSPPGLEEPLDGA--   45
```

```
Qy     66  AGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSMLVILL  125
                          ||||  ::|:| :|:  ||:|:|||||||||||||||
Db     46  DP----------HVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECVSMLVILL     91
```

```
Qy    126  NCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWN  185
           ||||||:|| :||: ::|||::||:|:|| ||:|||||||||||||||||||||||||||
Db     92  NCVTLGMYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKCYLGDTWN  151
```

```
Qy    186  RLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGN  245
           ||||||:|||:||||||||||||:||||||||||||||||||:||||:|||||||||||||
Db    152  RLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRIIVNLLLDTLPMLGN  211
```

```
Qy    246  VLLLCPFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPFICSQ  305
           ||||| ||||||||||||||||||||||:| ::|:     : :|:||:::::|::||||:|
Db    212  VLLLCFFVFFIFGIIGVQLWAGLLRNRCFLENFTIQGDVALPYYQPEEDDEMPFICSL    271
```

```
Qy    306  PRENGMRSCRSVPTLRGEGGGGPPCSL---------DYETYNSSSNTT--CVNWNQYYNCSA  357
                  ||: ::::|                        ::: :: |: :||:||:|:|
Db    272  SGDNGIMGCHEIPPLKEQ---GRECCLSKDDVDYFGGAGRQDLNASGLCVNWNRYYNVCRT  328
```

```
Qy    358  GEHNPKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFF   417
           ||:| |||||||||||:| :|||:|||||||||||||:|||||||||||||||||||||||
Db    329  GSANPHKGAINFDNIGYAWIVIFQVTTLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFF   388
```

```
Qy    418  MINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILR  477
           ||||||||||||||||||||||||::|||||      : ::|| ||||:||||| ::|::|
Db    389  MINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEELFQYVCHILR  447
```

```
Qy    478  KAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHY  537
                || | ||  |:|     ::::                          |:|
Db    448  KAKRRALGLYQALQSRRQAL-GPEAPAPAKPGP----------------------HAKEPRHY  487
```

```
Qy    538  H---LGNGTLRVPRASPEIQDRDAN-GSRRLLM-LPPPSTPTPSGGPPRGAESVHSFYHAD  592
                  :| : ::                             |:|:|     : :
Db    488  HGKTKGQG------------DEGRHLGSRHCQTLHGPASP----GNDHSGRE------    523
```

```
Qy    593  CHLEPVRCQAPPRCPSRASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLT   652
           ||:  ::                       : :||::::    || :||::
Db    524  ---LC----PQHSPLDA-----------------TPHT---------LVQ----PIPATLA   547
```

```
Qy    653  SFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSKADSGACGPDSCPYCARTGAGEPE   711
                  | ||:|  :|  :: ::| ::|:|        ||| || |   ::||
Db    548  S------------DPASCPCCOHEDGRRPSGLGSTDSGQESGGS---GSSAGGEDE    588
```

```
Qy    712  SADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLA--FWRLICDTF  769
           || :  :|                : ::|: :|:| |           :|     :||
Db    589  A-----DGDGA--RSSEDGASSELGKEEEEEQ------ADGAVWLCGDVWRETRAKL    633
```

```
Qy    770  RKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLIV  829
           | |||||:|||:||||:|||:| |||||| |||||||:| |:|||||:|||| ||::||:
Db    634  RGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAA   693
```

```
Qy    830  YGPFGYIKNPYNIFDGVIVVISVWEIVQQGQGGGLSVLRTFRLMRVLKLVRFLPALQRQLV   889
           ||:|||:|||||||| ||:|::|:||||| |  :|| | |:|::|:|:|::| :|||::||
Db    694  FGLFDYLRNPYNIFDSIIVIISIWEIVGQADGLGSVLRIFRLLRVLKLVRFMPALRRQLV   753
```

```
Qy    890  VLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVT   948
           |||||||||||||||||||||||||||||||||||||:|: ||||| ||||||||||||||
Db    754  VLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFSLRTDTGDTVPDRKNFDSLLWAIVT   813
```

```
Qy    949  VFQILTQEDWNKVLYNGMASTSSWAALYFIALMTGNYVLFNLLVAILVEGFQAEGDATK  1008
           |||||||||||||||||||||| ::|||||:||||||||||||||:|||||||||||::
Db    814  VFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAILVEGFQAEGDANR   873
```

```
Qy   1009  SESEPDFFSPSV----------DGDGDRKKRLALVALGEHAELRKSLLPLIIHT----A  1054
           ::|  : : |:             |::||:::|
Db    874  SYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPMTPNGHLDPSL--PLGGHLGPAGA  929
```

```
Qy   1055  ATPMSHPKSSSTGVGEALGSGSRRTSSSGGAEPGAAHHEMKCPFSARSSPHSPWSAASSW  1114
               ::::     |  :|| |:|: :| :  :                 |: : :::
Db    930  AGPA--PRLSLQPDPMLVALGSRKSSVMSL--GRMSYDQRSLSSSRSSYYGPWGRSAAW    984
```

```
Qy   1115  TSRRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQESQDEEESEE--DRASPAGSDH--  1169
              ::: :: |||                |::||   : ::: : :      | :
Db    985  ASRRSSWN----------SLKHKPPSAEHESLLSAERGGGARVCEVAADEGPPRAAPLHTPHAH 1038
```

```
Qy   1170  ------------RHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSS--ASEHQDCNGKS  1214
                            : :|::     :: :|        : :|:
Db   1039  HIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRM  1098
```

```
Qy   1215  ASGRLARTLRTD-DPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQ  1273
                : | |:      ::|  :  :::: |  :  : ::::   :   :: :| :: ||
Db   1099  PS--IAKDVFTKMGDRGDRGEDEEIDYTLCFRVRKMIDVYKPDWCEVREDWSVVLFSPE  1156
```

```
Qy   1274  SRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFL  1333
             | |||||:::| :|| |:||| :|: :||   :||: |: |::|||:| |||||||||:
Db   1157  NRFRVLCQTIIAHKLFDVVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFV  1216
```

```
Qy   1334  AEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRL  1393
           ||| |:|| ||| ||||||||||||||||| ||:: : |||| |: :: |: | ||||||
Db   1217  GEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSLASAGGAKILGVRVLRL  1276
```

```
Qy   1394  LRTLRPLRVISRAQGLKVVETLMSSLGKPIGNIVIVICCAFFIFGILGVQLFKGKFYVCQ  1453
           ||||||||||:||| |||||| ::||:|||||:|| :|||||||||||||||||||||:
Db   1277  LRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLICCAFFIFGILGVQLFKGKFYHCL  1336
```

```
Qy   1454  GEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVD  1513
           | |||||| :|| |||: ||| |||||||||||||||||||||||||||:| ::| |: |
Db   1337  GVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVD  1396
```

```
Qy   1514  QQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRR  1573
           |||: ||||||||||||||| ||||||||| ||||||||||||||:|   |||||:|||
Db   1397  QQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEEAARRREEKRLRR  1456
```

```
Qy   1574  LEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHY  1633
           ||||:|              :|:||||| :: :|::|||||:|||: ||: |:::|:|:
Db   1457  LEKKR-------KAQRLPYYATYCHTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHY  1509
```

```
Qy   1634  QQPILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLE  1693
           |||:|:|| |||| ||::||| |||: ::::|:|||| ||||||||||||||||:||||||
Db   1510  NQPTSLETALKYCNYMFTTVFVLEAVLKVIAFGLRFFKDRWNQLDLLAIVLLSVMGITLE  1569
```

```
Qy   1694  EIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLL  1753
           ||| | | |||||||||||||||||:|||||||| ||||::||::||||| ||||||||
Db   1570  EIEINAALPINPTIIRMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLL  1629
```

```
Qy   1754  FFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDWNGIMKDPSR  1813
           |||:|||||||||| |:  ||| ||:|:|| ||||||| |||||||||||||||||| |
Db   1630  FFIYAALGVELFGKLVCNDENPCEGMSRHATFENFGMAFLTLFQVSTGDWNGIMKDTLR  1689
```

```
Qy   1814  DC-DQESTCYNTV--ISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAE  1870
           || |  |:|:: :   :  :||||:|||||:|:|||||:||||| ::||| ||: ::||
Db   1690  DCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLVNVVAVLMKHLDDSNKEAQEDAEMDAE   1749
```

```
Qy   1871  LELEM-KTLSPQPHSPLGSP-------------------------------FLW         1892
           ||||| | ||:||||||:|                               | |
Db   1750  LELEMAHGLGPGPRLPTGSPGAPGRGPGAGGGDTEGGLCRRCYSPAQENLWLLDSVSLI  1809
```

```
Qy   1893  --PGVEG-VNSTDSPKPGAPHTAHIGAASG------------------------  1920
                 : ||:  |:
Db   1810  IKDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHHDKQEVQLAETEAFSLNSDRSSSI  1866

Qy   1921  --FSLEHPTMVP---------HPEEVPV-PLGPDLLTVRKSGVSRTHSLPN-DSY       1962
                |||||                 |: ||  :  |:    ||  :  :::
Db   1867  LLIGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGECFFPLSSTAVS-----PDPENF  1921

Qy   1963  MCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQOPADTSCIIQLPKDVHY------LLQPH  2016
             |:|       |: ||     |  :|:   ||   | ::     ::|::
Db   1922  LCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSPDASSPLLPMPAEFFHPAVSASQKGPE   1977

Qy   2017  GAPTWGAIPKLPPPG-----RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSC   2071
               |     ||  ||     ||          ||
Db   1978  KGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS---------------    2020

Qy   2072  PLTRSSFWGGSSIQVQORSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTEL    2131
                 :   :            :  :  ||:: ||
Db   2021  ----PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAPG------------------     2054

Qy   2132  SWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLLDSGSQPR  2191
                                      |  ||: :||   ::|:
Db   2055  ------PRAGLSPAARRRL------SLRCRGLFSLRGLRAHQRSHS--SGGSTSP       2095

Qy   2192  LCPSPSSL---------GGQPLGGSRPKKKLSPPSIS---IDDPESQGSRPPCSPGVCL   2240
              | |:||          || || :|      |::|:        |:    ||
Db   2096  GCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSLSLNTSLLFCPPP-----PPPAPGLTP  2149

Qy   2241  RR---------RAP--ASDSKDPSVSSPLDSTAASPSPKKDTLS                 2273
             |:                |: |||  |||
Db   2150  ARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKDPPGRAPLPMGLGPLAPPPQPL-  2208

Qy   2274  LSGLSSDPTDMDP                                                2286
                :::|
Db   2209  ------PGELEP                                                 2214
```

CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC   entry of calcium ions into excitable cells and are also involved
CC   in a variety of calcium-dependent processes, including muscle
CC   contraction, hormone or neurotransmitter release, gene expression,
CC   cell motility, cell division and cell death. Isoform alpha-1I
CC   gives rise to T-type calcium currents. T-type calcium channels
CC   belong to the "low-voltage activated (LVA)" group and are strongly
CC   blocked by nickel and mibefradil. A particularity of this type of
CC   channels is an opening at quite negative potentials, and a
CC   voltage-dependent inactivation. T-type channels serve pacemaking
CC   functions in both central neurons and cardiac nodal cells and
CC   support calcium signaling in secretory cells and vascular smooth
CC   muscle. They may also be involved in the modulation of firing
CC   patterns of neurons which is important for information processing
CC   as well as in cell growth processes. Gates in voltage ranges
CC   similar to, but higher than alpha 1G or alpha 1H.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC   hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC   positively charged transmembrane segment (S4). S4 segments
CC   probably represent the voltage-sensor and are characterized by a
CC   series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC   channels are activated by CaM-kinase II (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC   family.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF086827; AAD17796.2; -.
DR   EMBL; AF290214; AAG35188.1; -.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW   Ionic channel; Multigene family; Phosphorylation; Repeat;
KW   Transmembrane; Voltage-gated channel.
FT   REPEAT   64   399   I.
FT   REPEAT   584   823   II.
FT   REPEAT   1116   1393   III.
FT   REPEAT   1431   1692   IV.
FT   DOMAIN   1   76   Cytoplasmic (Potential).
FT   TRANSMEM   77   97   S1 of repeat I (Potential).
FT   DOMAIN   98   115   Extracellular (Potential).
FT   TRANSMEM   116   137   S2 of repeat I (Potential).
FT   DOMAIN   138   146   Cytoplasmic (Potential).
FT   TRANSMEM   147   166   S3 of repeat I (Potential).
FT   DOMAIN   167   171   Extracellular (Potential).
FT   TRANSMEM   172   189   S4 of repeat I (Potential).
FT   DOMAIN   190   209   Cytoplasmic (Potential).
FT   TRANSMEM   210   230   S5 of repeat I (Potential).
FT   DOMAIN   231   371   Extracellular (Potential).
FT   TRANSMEM   372   396   S6 of repeat I (Potential).
FT   DOMAIN   397   598   Cytoplasmic (Potential).
FT   TRANSMEM   599   619   S1 of repeat II (Potential).
FT   DOMAIN   620   632   Extracellular (Potential).
FT   TRANSMEM   633   654   S2 of repeat II (Potential).
FT   DOMAIN   655   660   Cytoplasmic (Potential).
FT   TRANSMEM   661   679   S3 of repeat II (Potential).
FT   DOMAIN   680   687   Extracellular (Potential).

RESULT 14
CCAI_RAT
ID   CCAI_RAT   STANDARD;   PRT;   1835 AA.
AC   Q9Z0Y8; Q9EQ59;
DT   30-MAY-2000 (Rel. 39, Created)
DT   10-OCT-2003 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.3) (CaV3.3).
GN   Name=Cacna1i;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=99165796; PubMed=10066244;
RA   Lee J.-H., Daud A.N., Cribbs L.L., Lacerda A.E., Pereverzev A.,
RA   Kloeckner U., Schneider T., Perez-Reyes E.;
RT   "Cloning and expression of a novel member of the low voltage-activated
RT   T-type calcium channel family.";
RL   J. Neurosci. 19:1912-1921(1999).
RN   [2]
RP   REVISIONS TO 345; 1656 AND 1737.
RA   Perez-Reyes E.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA   McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA   Baillie D.L., Stea A., Snutch T.P.;
RT   "Molecular and functional characterization of a family of rat brain T-
RT   type calcium channels.";
RL   J. Biol. Chem. 276:3999-4011(2001).

```
FT   TRANSMEM    688    711       S4 of repeat II (Potential).
FT   DOMAIN      712    722       Cytoplasmic (Potential).
FT   TRANSMEM    723    743       S5 of repeat II (Potential).
FT   DOMAIN      744    795       Extracellular (Potential).
FT   TRANSMEM    796    820       S6 of repeat II (Potential).
FT   DOMAIN      821   1125       Cytoplasmic (Potential).
FT   TRANSMEM   1126   1148       S1 of repeat III (Potential).
FT   DOMAIN     1149   1166       Extracellular (Potential).
FT   TRANSMEM   1167   1187       S2 of repeat III (Potential).
FT   DOMAIN     1188   1197       Cytoplasmic (Potential).
FT   TRANSMEM   1198   1217       S3 of repeat III (Potential).
FT   DOMAIN     1218   1231       Extracellular (Potential).
FT   TRANSMEM   1232   1253       S4 of repeat III (Potential).
FT   DOMAIN     1254   1263       Cytoplasmic (Potential).
FT   TRANSMEM   1264   1287       S5 of repeat III (Potential).
FT   DOMAIN     1288   1364       Extracellular (Potential).
FT   TRANSMEM   1365   1390       S6 of repeat III (Potential).
FT   DOMAIN     1391   1445       Cytoplasmic (Potential).
FT   TRANSMEM   1446   1466       S1 of repeat IV (Potential).
FT   DOMAIN     1467   1480       Extracellular (Potential).
FT   TRANSMEM   1481   1502       S2 of repeat IV (Potential).
FT   DOMAIN     1503   1509       Cytoplasmic (Potential).
FT   TRANSMEM   1510   1528       S3 of repeat IV (Potential).
FT   DOMAIN     1529   1542       Extracellular (Potential).
FT   TRANSMEM   1543   1566       S4 of repeat IV (Potential).
FT   DOMAIN     1567   1580       Cytoplasmic (Potential).
FT   TRANSMEM   1581   1601       S5 of repeat IV (Potential).
FT   DOMAIN     1602   1664       Extracellular (Potential).
FT   TRANSMEM   1665   1692       S6 of repeat IV (Potential).
FT   DOMAIN     1693   1835       Cytoplasmic (Potential).
FT   SITE        355    355       Calcium ion selectivity and permeability
FT                                (By similarity).
FT   SITE        779    779       Calcium ion selectivity and permeability
FT                                (By similarity).
FT   SITE       1339   1339       Calcium ion selectivity and permeability
FT                                (By similarity).
FT   SITE       1637   1637       Calcium ion selectivity and permeability
FT                                (By similarity).
FT   CARBOHYD    171    171       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    242    242       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD   1301   1301       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD   1304   1304       N-linked (GlcNAc...)  (Potential).
FT   CONFLICT    193    193       M -> L (in Ref. 3).
FT   CONFLICT    291    291       C -> V (in Ref. 3).
FT   CONFLICT    394    394       V -> L (in Ref. 3).
FT   CONFLICT    406    406       E -> N (in Ref. 3).
FT   CONFLICT    485    485       C -> S (in Ref. 3).
FT   CONFLICT    512    512       D -> Y (in Ref. 3).
FT   CONFLICT    558    558       G -> R (in Ref. 3).
FT   CONFLICT    683    683       G -> S (in Ref. 3).
FT   CONFLICT    691    691       F -> S (in Ref. 3).
FT   CONFLICT    739    740       MH -> ID (in Ref. 3).
FT   CONFLICT    833    833       C -> Y (in Ref. 3).
FT   CONFLICT    846    846       F -> L (in Ref. 3).
FT   CONFLICT    856    856       S -> R (in Ref. 3).
FT   CONFLICT    905    905       L -> R (in Ref. 3).
FT   CONFLICT    913    913       M -> YW (in Ref. 3).
FT   CONFLICT    936    936       W -> G (in Ref. 3).
FT   CONFLICT    996    996       A -> R (in Ref. 3).
FT   CONFLICT   1060   1060       I -> M (in Ref. 3).
FT   CONFLICT   1094   1094       D -> CC (in Ref. 3).
FT   CONFLICT   1197   1198       SS -> TD (in Ref. 3).
FT   CONFLICT   1229   1231       Missing (in Ref. 3).
FT   CONFLICT   1422   1422       K -> Y (in Ref. 3).
FT   CONFLICT   1623   1625       FGM -> SAR (in Ref. 3).
FT   CONFLICT   1656   1656       S -> T (in Ref. 3).
FT   CONFLICT   1737   1737       P -> A (in Ref. 3).
SQ   SEQUENCE   1835 AA;  205348 MW;  B6025E0F1BE80CCA CRC64;
```

```
Qy    43  PRSRDSPVASRSSTTCPGPGAAGAGSTEKDPGSADSEAEG----LPYPALAPVVFFYLSQ    98
              :   :       :     :          ::   |: |||::|||||
Db     8  PSSAAAPAPEPGITEQPGP-----RSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQ    62

Qy    99  DSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAPDDFIPA   158
          ||||  |:|::|| |||| |||||:|||||||||:|::|:|:: ||:|:|||||:||||
Db    63  TTSPRNWCIKMVCNPWFECVSMLVILLNCVTLGMYQPCDDMECLSDRCKLLQVFDDFIFI   122

Qy   159  FFAVEMVVKMVALGFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLR   218
          |||  ||| |:|||||||||||||||||||||||:||:||||||||:|:||:|||||
Db   123  FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLR   182

Qy   219  PLRAINRVPSMRILVTLLLDTLPMLGNVLLCFVFFIFGIVGVQLWAGLLRNRCFLPEN   278
          ||||||||||||| :|||||||||||||||||||||||||||||||||||||||||||
Db   183  PLKAINRVPSMRIIVNLLLDTLPMLGNVLLCFVFFIFGIIGVQLWAGLLRNRCFLEEN   242

Qy   279  FSILPLSVDLEPYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPCSL------   332
          |: |:|       :    :   |  :   | |:|   :|:   |         :|
Db   243  FTIQGDVALPPYYQPEEDDEMPFICSLTGDNGIMGCHEIPPLKEQ---GRECCLSKDDVY   299

Qy   333  DYETYNSSSNT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD   390
          | | |  |:|   ||| |:   ||  |:|| |||||||||||||:|:|||||||||| :
Db   300  DFGAGRQDLNASGLCVNWNRYYNVCRTGNANPHKGAINFDNIGYAWIVIFQVITLEGWVE   359

Qy   391  IMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESOLMREQRVRFLS   450
          ||| ||||||||||||||||||||||||||||||||||||||||:||||:|||:|: |
Db   360  IMYYVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS   419

Qy   451  NASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQP   510
               |:     : :||:||    |:         ||   : |       :||
Db   420  -SSTVASYAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQAL-                458

Qy   511  SGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPS   570
                              ||  |
Db   459  ------------------QNRRQA-------MGPGT------------PAPA          473

Qy   571  TPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPP   630
                 ||  |  :   |||  :
Db   474  KPGP------------------------HAK--EPSHCKLCPRHSPLD--PTPHT----   500

Qy   631  PEILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKAD   690
Db   501  ----------LVQ---------------------------------PISAIL-          509

Qy   691  SGACGPDSCPYC-------------------------ARTGAGEPESADHVMPDSDEAVYEFTQDAQH   734
          |  ::|
Db   510  --ASDPSSCPHCQHEAGRRPSGLGSTDSGQEGSGSGSAE---AEANGDGL-QSSEDGVS   563

Qy   735  SDLRDPHSRRRQRSLGPDAEPSSVLA----------FWRLICDTERKIVDSKYFGRGIMIAILVN   789
          ||                                  |||||| |||:||||||||||||
Db   564  SD------------LGKEEEQEDGAARLCGDVWRETRKKLRGIVDSKYFNRGIMMAILVN   611

Qy   790  TLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPEYNIFDGVIVV   849
          |:||||||:|||||:||:|| ||:|||:|||||||||| :|| |:||||||||||:|||:
Db   612  TVSMGIEHHQPEELJTNILEICNVVFTSMFALEMLIKLAAFGLFDYLRNPYNIFDSIIVI   671

Qy   850  ISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFI   909
          ||:|||||||  |||||||||||||||||||||||:|||||||||||||||||||||||
Db   672  ISIWEIVGQADGGGLSVLRTFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFI   731

Qy   910  FIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTFQIITQEDWNKVLYNGMAS   968
          |||||||||:|||||::  |  |||:||||||||||||||| ||||||||||:|||||||
Db   732  FIFSILGMHIFGCKFSLRTDTDGDTVPDRKNFDSLLWAIVTFVFQIITQEDWNVVLYNGMAS   791

Qy   969  TSSWAALYFIALMTFGNYVLFNLLVAIILVEGFQAEGDATKSESEPDFFSPSVDG------   1022
          |: ||:|||:|||||||||||||||||||||||||||||:| || :       ::
Db   792  TTPWASLYFVALMTFGNYVLFNLLVAIILVEGFQAEGDANRSCSDEDQSSNLEEFDKLPE   851

Qy  1023  --DGDRKKRLALVALGEHAELRKSLLPLLIH--TAATPMSHPKSSTGVGEALGSGSRR   1078
               :               : :  :::        | |  ::      :    | |
Db   852  GLDNSRDLKLCPIPMTPNGHLDPSL--PLGAHLGPAGTMGTAPRLSLQDPVLJVALDSRK   909
```

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DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   DJ172B20.1 (Calcium channel, voltage-dependent, alpha 1I subunit)
DE   (Fragment).
GN   Name=CACNA1I;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Phillips S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL022319; CAD92537.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M-channel_nlg.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER    1       1
SQ   SEQUENCE    1994 AA;    220004 MW;    A5EFAE5FA32DCF76 CRC64;

Query Match             39.5%;  Score 4750.5;  DB 2;  Length 1994;
Best Local Similarity   49.0%;  Pred. No. 3e-229;
Matches 1099;  Conservative 214;  Mismatches 485;  Indels 447;  Gaps 61;
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Qy          1 MRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLE    288
              |||||||||||||||||||||||| |||||||||||||||||||||||| :
Db          1 MRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALP    60

Qy        289 PYYQTFNEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPCSL------DYETYNSSSN    342
              |||||       :::  :::|||   ::|    |  ||| :
Db         61 PYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVDYFGAGRQDLN    117

Qy        343 TT--CVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHS    400
              ||  :|       ||  ||| |||||||||||||||| ||:||||||||| | :| ||||
Db        118 ASGLCVNWNRYNYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHS    177

Qy        401 FYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSE    460
              ||||||||||||||||||||||||||||||||||||:   | |||  || || ::
Db        178 FYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAE    236

Qy        461 PGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQRPQPSGGSCTRSHRR    520
              |     ||  |||| | |||     |  :|  ||||||||| |    |  |  |::    :
Db        237 PGDCYEIFQYVCHILRKAKR-----RALGLYQALQS--------------------RR    270

Qy        521 LSVHHLVIHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPR    580
              :::|    |||:                |  |      |        |:||
Db        271 QAL--------------------------------------------APAPAKPGP---    285

Qy        581 GAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALV    640
              |  ||||| ||  ||    |        |||  :|  |     :       : |  : |
Db        286 --AHGLGPCPGPCPG----------------PCPCPCPCPGPRLPTSSPGAPG----TPHT    310

Qy        641 EVAPSPGPTLTSFNIPGPFSSMHKLLETQSTGAC-HSSCKISSPCSKADSGACGPDSC    699
              :    | | :     |  |  |  |  ||       |  |  :|    |  ::  |  :  |
Db        311 Q---PIPATLAS-----------------DPASCPCCQHEDGRRPSGLGSTDSGQEGSGS-    350

Qy        700 PYCARTGAGPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVL    759
              :::                                  :  :    | ::
Db        351 ---GSSAGGEDEA--------DGDGA----RSSEDGASSELGKEEEEQ-----ADGAVWL    392

Qy        760 A--FWRLICDTFRKIVDSKYFGRGIMIALIVNTLSMGIEYHEQPELTNALEISNIVFTS    817
              |   | | |||  ||||||| | :||| |||||:||||||||||||||||| |:| ||||
Db        393 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPELTNILEICNVVFTS    452
```

```
Qy       1079 TSSSGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRSSRNSLGRAPSLKRRSPSGE    1138
              : :  :: |          |:::::  |: |  :   :   : :             :
Db        910 SSVMSL---GRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWN-----SLKHKPPSAE    960

Qy       1139 RRSLLSGEGQES--QDEEESSEE--DRASPAGSDH-------------RHRGSLEREA    1179
                :|||:|:|  :   |:::|::     ||  |:               |  || | |
Db        961 HESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAHHAHHGPHLAHRHRHRRRTLSLDT    1020

Qy       1180 KSSFDLPDTLQVPGLHRTAS--GRSSASEHQDCNGKSASGRLARTLRTD-DPQLDGDDDN    1236
              |:||:|  |     | :: |    || :||::    ::: |:     :|  :  ::  :
Db       1021 RDSVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDDRRDRGEDE    1078

Qy       1237 DEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVI    1296
              :|  |  |||  :  |  | ::  :  |   |:|| :|:| ||| |:  ||:|||:|:
Db       1079 EEIDYTLCFRVRKMIDVVYKPDWCEVREDWSVVLFSPENKFRILCQTIIAHKLFDYVVLAF    1138

Qy       1297 IFLNCITTAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSS    1356
              |||||||| |||||:||||:||||:||||||:|:|| |||||||||:|| || ||||||||
Db       1139 IFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSS    1198

Qy       1357 WNVLDGLLVLVLISVIDIILVSMVGSDGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETL    1416
              |||||| ||||  ||  ||:|:|   |:||: || ||||||||||| |||||||| |||||||
Db       1199 WNVLDGFLVFVSIIDIVVSVASAGGAKIIGVLRVLRLLRTLRPLRVISRAPGLKLVVETL    1258

Qy       1417 MSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRH    1476
              :||||||||||:|||||||||||||||||| || ||:| |||||:|||| ||:|| | ||
Db       1259 ISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCVAANYRWVHH    1318

Qy       1477 KYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVA    1536
              ||||||||||||||||||||||||||:|  ||| ||||||:|:|||||||||||||||:
Db       1319 KYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVS    1378

Qy       1537 FFVLNMFVGVVVENFHKCRQHQEBEEARRREEKLRRLEKKRRSKEKQMAEAAQCKPYYSD    1596
              ||||||||||||||||||| |||:|||||||||||||||||        |   |   |
Db       1379 FFVLNMFVGVVVENFHKCRQHQEAEARRREEKLRRLEKKRR------KAQRLPYYAT    1431

Qy       1597 YSRFPRLLIVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVF    1656
              |:|  |||:| |  ||||| :| |||||| |:|  |||:| || :|| | | |||||:| ||
Db       1432 YCPTRLLIHSMCTSHYLDIFITFICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVL    1491

Qy       1657 ESVFKIVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRMRVLRI    1716
              | |  |||| |   |::||||||||||||||:|||||||::| | | |||||||||||||
Db       1492 EAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRMRVLRI    1551

Qy       1717 ARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPC    1776
              ||||||| :|  |||:  || ||||||||||||||||||||  ||||||||: | ||: ||
Db       1552 ARVLKILKLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPC    1611

Qy       1777 EGLGRHATFRNFGMAPLITLFRVSTGDNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVS    1833
              ||  |||||:|||||||||||| |||||||||||| ||:||  |:|  |||     ||:|:
Db       1612 EGMSRHATFENFGMAPLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVS    1671

Qy       1834 FVLTAQFVLVNVVIAVLMKHLEESNKEAKEAKEALEAELEEMKTLSPQHSPLGSPFLWP    1893
              |||||||||:|||:|||||||::|:|:| |  |: | :|:::
Db       1672 FVLTAQFVLINVVAVLMKGHLDDSNKEAQEDAEMDARIELEM----------------    1713

Qy       1894 GVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPL-GPDLLTV------    1946
              : :  : | |  || |  |    |:
Db       1714 -AHGLGPCPGPCPG--------------------PCPCPCPCPGPRLPTSSPGAPG    1750

Qy       1947 RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHRGWGLPKAQGSIILSVHSQPADTSCIQL    2005
              | ::            :  |    |
Db       1751 RGSGGAGAGG-DTESHLCRHCYSPAQEFL----W----LDSVSLIIKDSLEGELTIIDNL    1801

Qy       2006 PKDV-HYLLQPHG    2017
                 :  :: : | |
Db       1802 SGSVFHYASPDG    1814
```

```
RESULT 15
Q7Z6S8
ID   Q7Z6S8            PRELIMINARY;       PRT;    1994 AA.
AC   Q7Z6S8;
```

```
Qy   818  LFALEMLLKLLVVGPFGVYIKNPYNIFDGVIVVISVWEIVGQOGGGLSVLRTFRLMRVLKL  877
          |||::||:.:||||||
Db   453  MFALBMILKLLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRILRVLKL  512

Qy   878  VRFLPALQRQLVLMKTMDNVATFCMLLMLFIFISILGMHLFGCKFASERD-GDTLPDR     936
Db   513  VRFMPALRRQLVLVLMKTMDNVATFCMLMLFIFISILGMHIFGCKFSLRTDTGDTVPDR    572

Qy   937  KNFDSLLWAIVTVFQILLTQEDWNKVLYNGMASTSWAALYFIALMTFGNYVLFNLLVAIL   996
Db   573  KNFDSLLWAIVTVFQILTQEDWNVLYNGMASTSPWASLYFVAILMTFGNYVLFNLLVAIL   632

Qy   997  VEGFQAEGDATKSESEBPDFFSPSV--------DGDGRKKRLALVALGEHAELRKSLL    1046
Db   633  VEGFQAEGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPK--LCPIPMTPNGHLDPSL-   689

Qy  1047  PPLIIHT---AATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHEMKCPPSARS   1102
Db   690  -PLGGHLGPAGAGPA--PRLSLQPDEMLVALGSRKSSVMSL--GRMSYDQRSLSSSRS    743

Qy  1103  SPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQESQDEEESSE--  1159
Db   744  SYYGPWGRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGARVCEVAADEGP   797

Qy  1160  DRASPAGSDH------------RHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSS-    1203
Db   798  PRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVGAHPRAAWRAAG   857

Qy  1204  -ASEHQDCNGKSASGRLARTLRTD-DPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRE   1261
Db   858  PAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEEIDYTLCFRVRKMIDVYKPDWCEV  915

Qy  1262  RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIVIIFLNCITIAMERPKIDPHSAERIFL 1321
Db   916  REDWSVYLFSPENRFRVLCQTIAHKLFDYVVLAFIFLNCITIALERPQIEAGSTRIFL     975

Qy  1322  TLSNYIFTAVFLAEMTVKVVALGWCFEGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSG 1381
Db   976  TVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFVSIIDIVSVSLASAGG 1035

Qy  1382  TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG  1441
Db  1036  AKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLICCAFFIIFGILG  1095

Qy  1442  VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD  1501
Db  1096  VQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVN  1155

Qy  1502  IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEE   1561
Db  1156  IMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAE  1215

Qy  1562  EAARREEKRLRLEKKRRSKEKQMAEAAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI  1621
Db  1216  EAARREEKRLRRLEKKRR------KAQRLPYATYCHTRLLIHSMCTSHYLDIFITFII    1268

Qy  1622  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVPESVFKLVAFAFRRFFQDRWNQLDLA  1681
Db  1269  CLNVVTMSLEHYNQPTSLETALKYCNYMFTTVVLEAVLKLIVAFGLRRFFKDRWNQLDLA  1328

Qy  1682  IVLLSIMGITLEEIEVNLSLPINPTIRIMRVLRIARVLKLKMAVGMRALLHTVMQALP    1741
Db  1329  IVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALP  1388

Qy  1742  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTG  1801
Db  1389  QVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEGMSRHATTENFGMAFLTLFQVSTG  1448

Qy  1802  DNWNGIMKDPSRDC-DQESTCYNTV--ISPIYFVSFVLTAQFLVNVVIAVLMKHLEESN  1858
Db  1449  DNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFVLTAQFVLINVVAVLMKHLDDSN  1508

Qy  1859  KEAKEEAELEAELELEM-KTLSPQPHSPLGSP---------                    1889
```

```
Db  1509  KEAQEDAEMDAELELEMAHGIGPGPRLPTGSPGAPGRGPGGAGGGDTEGGLCRRCYSPA  1568

Qy  1890  --FLW----PGVEG-VNSTDSPKPGAPHTAHIGAASG------------           1920
Db  1569  QENLWLDSVSLIIKDSLEGELTIIDNLSGGIFH--HYSSPAGCKKCHHDKQEVQLAETE  1625

Qy  1921  --------------FSLEHPTMVP------HPEVPV-PLGPDLLTVRKSGV          1951
Db  1626  AFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGECFFPLSSTAV 1685

Qy  1952  SRTHSLPN-DSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVH 2010
Db  1686  S------PDPENFLCEMEEIPFNPV--RSW-LKHDSSQAPPSPFSPDASSPLLPMPAEFF 1736

Qy  2011  Y----LLQPHGAPTWGAIPKLPPPG----RSPLAQRPLRRQAAIRTDSLDVQGLGSR    2059
Db  1737  HPAVSASQKGPEKGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS------  1791

Qy  2060  EDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP 2119
Db  1792  ------PSSSAGSLQTTLEDSLTLSDSPRRALGPPAPAPG---                 1825

Qy  2120  ETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSI 2179
Db  1826  --------PRAGLSPAARRRL--------SLRGRGLFSLRGLRAHQR             1856

Qy  2180  AVSCLDSGSQPRLCPSPSSL------GGQPLGGPGSRPKKKLSPPSIS---IDPPESQ   2228
Db  1857  SHS--SGGSTSPGCTHHDSMDPSDEEERGGAGGGAGSEHSETLSSLSTSLFCPPP---  1911

Qy  2229  GSRPPCSPGVCLRR-----RAP-----ASDSKDPSVSSPLDST                2261
Db  1912  ---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKDPPGRAPLPMG 1968

Qy  2262  AASPSPPKDTLSLSGLSSDPTDMDP                                   2286
Db  1969  LGPLAPPPQPL-------PGELEP                                    1985
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Search completed: November 18, 2004, 13:32:21
Job time : 270.167 secs

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               GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    November 18, 2004, 13:06:00 ; Search time 186.635 Seconds
                                          (without alignments)
                                          4355.452 Million cell updates/sec

Title:            US-09-611-257A-37
Perfect score:    11904
Sequence:      1 MDEEEDGAGAEBSGQPRSFM.........PKKDVLSLSGLSSDPADLDP 2266

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:      2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_23Sep04:*
             1: geneseqp19808:*
             2: geneseqp1990s:*
             3: geneseqp2000s:*
             4: geneseqp2001s:*
             5: geneseqp2002s:*
             6: geneseqp2003as:*
             7: geneseqp2003bs:*
             8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11862.5	99.7	2273	4	AAE01019	Aae01019 Human T-t
2	11758.5	98.8	2243	4	AAY14589	Aay14589 Human T-t
3	11758.5	98.8	2243	7	ADJ68819	Adj68819 Human hea
4	11741	98.6	2250	2	AAY14586	Aay14586 Human T-t
5	11735.5	98.5	2261	2	AAY14587	Aay14587 Human T-t
6	11727	98.5	2268	2	AAY14588	Aay14588 Human T-t
7	11653	97.9	2266	4	AAB66481	Aab66481 Human alp
8	11111	93.3	2428	3	AAY70720	Aay70720 Rat pancr
9	10962.5	92.1	2247	2	AAY15593	Aay15593 Rat T-typ
10	10945	91.9	2254	2	AAY14590	Aay14590 Rat T-typ
11	10939.5	91.9	2265	2	AAY14591	Aay14591 Rat T-typ
12	10925	91.8	2272	2	AAY14592	Aay14592 Rat T-typ
13	10774	90.5	2287	4	AAB66475	Aab66475 Rat alpha
14	6315.5	53.1	1207	4	AAU00474	Aau00474 Human T-t
15	6218	52.2	2359	4	AAB66476	Aab66476 Rat alpha
16	6212	52.2	2353	2	AAY06299	Aay06299 Human act
17	6212	52.2	2353	6	ABP72254	Abp72254 Human T-t
18	6212	52.2	2353	2	ADJ69322	Adj69322 Human hea
19	6211	52.2	2353	2	AAY06298	Aay06298 Human act
20	6178	51.9	2353	5	ABG30840	Abg30840 Human vol
21	5855.5	49.2	2038	2	AAY14595	Aay14595 Human T-t
22	5845.5	49.1	2044	2	AAY14594	Aay14594 Human T-t
23	5709.5	48.0	2034	2	AAY06300	Aay06300 Human act
24	5492.5	46.1	2175	5	AAU10535	Aau10535 Human T-t
25	5492.5	46.1	2175	6	ABU08511	Abu08511 Human T-t
26	5492.5	46.1	2175	8	ADH69265	Adh69265 Human TCC
27	5484	46.1	2188	5	AAU10536	Aau10536 Human T-t
28	5484	46.1	2188	6	ABU08512	Abu08512 Human T-t
29	5484	46.1	2188	8	ADH69267	Adh69267 Human TCC
30	5366	45.1	1835	2	AAY14597	Aay14597 Rat T-typ
31	5366	45.1	1835	8	ADH69268	Adh69268 Rat T-typ
32	5361.5	45.0	1823	2	AAY14596	Aay14596 Human T-t
33	5198.5	43.7	1792	4	AAB66477	Aab66477 Rat brain
34	5043.5	42.4	982	4	AAM23743	Aam23743 Human EST
35	3959.5	33.3	1854	2	AAW79161	Aaw79161 Human cal
36	3959.5	33.3	1854	4	AAB66472	Aab66472 Protein e
37	3442	28.9	2435	4	ABB60448	Abb60448 Drosophil
38	3427	28.8	644	4	AAB66478	Aab66478 Human alp
39	3020.5	25.4	1859	4	ABG10954	Abg10954 Novel hum
40	1960	16.5	853	4	AAM93437	Aam93437 Human pol
41	1960	16.5	853	8	ADL31041	Adl31041 Human pro
42	1753	14.7	2264	8	ADM31026	Adm31026 Human cal
43	1752.5	14.7	2339	4	AAR33549	Aar33549 Sequence
44	1750.5	14.7	2343	2	AAY31809	Aay31809 N-type ca
45	1749	14.7	2337	2	AAW37878	Aaw37878 Human cal

ALIGNMENTS

```
RESULT 1
AAE01019
ID   AAE01019 standard; protein; 2273 AA.
XX
AC   AAE01019;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Human T-type low voltage activated calcium channel alpha1G-c protein.
XX
KW   Human T-type low voltage activated calcium channel alpha1G-c; stress;
KW   epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
KW   endocrine disorder; respiratory disorder; peripheral muscle disorder;
KW   muscle excitability; fertilisation; contraception; hypertension;
KW   neuronal firing regulation; cardiovascular disorder; gene therapy;
KW   forensic analysis; epidemiological study; neuroleptic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1138
FT                   /note= "Encoded by GAG"
FT   Misc-difference 1142
FT                   /note= "Encoded by GAA"
FT   Misc-difference 1680
FT                   /note= "Encoded by ACG"
FT   Misc-difference 1683
FT                   /note= "Encoded by GAA"
XX
PN   WO200130844-A1.
XX
PD   03-MAY-2001.
XX
PF   06-OCT-2000; 2000WO-US027761.
XX
PR   26-OCT-1999;  99US-00426998.
XX
PA   (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI   Dubin AE,  Galindo JE,  Pyati J,  Zhu JY,  Erlander MG;
XX
PN   WPI; 2001-300486/31.
DR   N-PSDB; AAD04756.
XX
PT   New nucleic acid encoding human calcium channel protein, useful for
PT   identifying specific modulators and potential pharmaceuticals for
PT   treating e.g. epilepsy.
XX
```

PS   Claim 11; Page 81-99; 115pp; English.
XX
CC   The invention relates to isoform of human T-type low voltage activated
CC   calcium channel (alpha1G-c) cDNA and protein. Cells transformed with
CC   calcium channel DNA to express calcium alpha1G-c channel protein are used
CC   to identify specific modulators (antagonists or agonists). These
CC   modulators are useful as therapeutic agents and are used for treating
CC   wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress
CC   epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
CC   endocrine disorders, respiratory disorder, peripheral muscle disorder,
CC   muscle excitability, fertilisation, contraception, disorders involving
CC   hypertension, neuronal firing regulation, potentiation of synaptic
CC   signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
CC   hypertrophy, angina pectoris). Calcium alpha1G-c channel DNA is useful
CC   for isolating and identifying related molecule mutations. It is also
CC   optionally used as antisense sequences, in gene therapy. Calcium channel
CC   alpha1G-c DNA, protein and antibodies are useful for forensic analysis,
CC   diagnosis and epidemiological studies, by standard hybridisation or
CC   immunological assays. The present sequence is T-type low voltage
CC   activated calcium channel alpha1G-c protein
XX
SQ   Sequence 2273 AA;

Query Match   99.7%; Score 11862.5; DB 4; Length 2273;
Best Local Similarity   99.4%;
Matches 2260; Conservative   4; Mismatches   4; Indels   7; Gaps   1;

```
Qy        1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy       61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Db      121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVR 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVR 180

Db      181 TVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      181 TVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy      241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Db      301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Db      361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy      421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480

Db      481 SCSRSHRRLSVHHLVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      481 SCSRSHRRLSVHHLVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy      541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy      601 TLKEKALVEVAASSGPPTLTSLNIPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TLKEKALVEVAASSGPPTLTSLNIPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

Qy      661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy      721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNI 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNI 780

Qy      781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISWEIVGQQGGGLSVLRTFRLMR 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISWEIVGQQGGGLSVLRTFRLMR 840

Qy      841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900

Qy      901 PDRKNFDSLLWAIVTVFQLITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 PDRKNFDSLLWAIVTVFQLITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960

Qy      961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020

Qy     1021 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080

Qy     1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQQSQ 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||:
Db     1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQQSQ 1140

Db     1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
            :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1141 DQEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200

Db     1201 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||.|||||||||||
Qy     1201 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP 1260

Db     1261 PQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1261 PQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320

Qy     1321 FLAEMTVKVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRVL 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 FLAEMTVKVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRVL 1380

Db     1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILGVQLFKGKFFV 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILGVQLFKGKFFV 1440

Db     1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500

Db     1501 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1501 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1560

Qy     1561 RRLEKKR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1613
            |||||||      :||||||||||||||||||||||||||||||||||||||||||||
Db     1561 RRLEKKRRSKEKKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1620

Qy     1614 HYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGIT 1673
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 HYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGIP 1680

Db     1674 LEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLLFM 1733
            ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1681 LEQIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLLFM 1740

Qy     1734 LLFFIFAALGVELFGDLECDETHPCEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 LLFFIFAALGVELFGDLECDETHPCEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1800
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Qy 1794 LRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKERAELRAEL 1853
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||
Db 1801 LRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEL 1860

Qy 1854 ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH 1913
        |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db 1861 ELEMKTLSPQPHSPLGSFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH 1920

Qy 1914 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1973
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1980

Qy 1974 QPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLLDVQ 2033
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 QPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLLDVQ 2040

Qy 2034 GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNW 2093
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNW 2100

Qy 2094 GKGPPETRSSLELDTELSWISGDLLPPGGQOEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2153
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 GKGPPETRSSLELDTELSWISGDLLPPGGQOEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2160

Qy 2154 QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP 2213
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP 2220

Qy 2214 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2273
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RESULT 2
AAY14589
ID   AAY14589 standard; protein; 2243 AA.
XX
AC   AAY14589;
XX
DT   07-DEC-1999 (first entry)
XX
DE   Human T-type voltage-gated Ca channel alpha-1-G (hCavT1d).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO992847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998; 98WO-US023161.
PR   05-DEC-1997; 97US-00985809.
XX
PA   (LOYO) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83484.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 58-67; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCavT1d. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2243 AA;

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Query Match             98.8%;  Score 11758.5;  DB 2;  Length 2243;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches 2242;  Conservative   0;  Mismatches  1;  Indels  23;  Gaps  1;

Qy   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEARGLPYPALAPVV 60
        |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy  61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy 181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy 241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Qy 301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy 361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy 421 STLASFSEPGSCYEELLKYLVYIILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 STLASFSEPGSCYEELLKYLVYIILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480

Qy 481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQQSSCKISSPCLKADSG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQQSSCKISSPCLKADSG 660

Qy 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAIIVNTLSMGIEYHEQPELTNALEISNI 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNI 780

Qy 781 VFTSLFALEMLKLLVGPFGYIKNPYNIFDGVIVISVWEIVGQQGGGLSVLRTFRLMR 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    781 VFTSLFALEMLLKLLVYGPGYIKNPYNIFDGVIVVVISWEIVGQGGLSVLRTFRLMR      840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 VLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSLLGMHLFGCKFASERDGDTL     900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSLLGMHLFGCKFASERDGDTL     900

Qy    901 PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV    960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV    960

Qy    961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL   1020
             ||||||||||                -------GDANKSESEPDFFSPSLDGDDRKKCL
Db    961 AILVEGFQAE---------GDANKSESEPDFFSPSLDGDDRKKCL                  997

Qy   1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA   1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA   1057

Qy   1081 HEMKSPPSARSSPHSPWSAAASWTSRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ    1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 HEMKSPPSARSSPHSPWSAAASWTSRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ    1117

Qy   1141 DEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN    1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 DEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN    1177

Qy   1201 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP   1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP   1237

Qy   1261 PQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV   1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 PQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV   1297

Qy   1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL   1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL   1357

Qy   1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV   1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV   1417

Qy   1441 CQGEDTRNITNKSDCAEASYRWRHKYNPDNLGQALMSLFVLASKDGWVDIMYDGLDAVG   1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 CQGEDTRNITNKSDCAEASYRWRHKYNPDNLGQALMSLFVLASKDGWVDIMYDGLDAVG   1477

Qy   1501 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEBEARRREEKRL   1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEBEARRREEKRL   1537

Qy   1561 RRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTTGVIGLNVVTMAMEHYQQPQI   1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1538 RRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTTGVIGLNVVTMAMEHYQQPQI   1597

Qy   1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN   1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN   1657

Qy   1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA   1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA   1717

Qy   1741 ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE   1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1718 ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE   1777

Qy   1801 STCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEBAEBLEAELELEMKTL   1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778 STCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEBAEBLEAELELEMKTL   1837

Qy   1861 SPQHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAAHARSASHFSLEHPTMQPHPTELPGP   1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1838 SPQHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAAHARSASHFSLEHPTMQPHPTELPGP   1897

Qy   1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY   1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1898 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY   1957

Qy   1981 IIQLPKDAPHLLQPHSAPTWGTIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED   2040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1958 IIQLPKDAPHLLQPHSAPTWGTIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED   2017

Qy   2041 LLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET  2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2018 LLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET  2077

Qy   2101 RSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA   2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2078 RSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA   2137

Qy   2161 VSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPPSPGICL  2220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2138 VSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPPSPGICL  2197

Qy   2221 RRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLLDP                2266
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   2198 RRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLLDP                2243
```

RESULT 3
ADJ68819

```
ID   ADJ68819 standard; protein; 2243 AA.
XX
AC   ADJ68819;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID625.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 625; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
```

CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
XX   mitochondrial protein of the invention.
SQ   Sequence 2243 AA;

Query Match   98.8%; Score 11758.5; DB 7; Length 2243;
Best Local Similarity   98.9%; Pred. No. 0;
Matches 2242; Conservative   0; Mismatches   0; Indels   23; Gaps   1;

Qy   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
Db   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120

Qy   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
Db   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240
Db   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy   241 CFLPENFSLEPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
Db   241 CFLPENFSLEPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300

Qy   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWTIAIFQVITLEGWVDIM 360
Db   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWTIAIFQVITLEGWVDIM 360

Qy   361 YFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
Db   361 YFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
Db   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480

Qy   481 SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db   481 SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

Qy   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
Db   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDDAQHSDLRDPHSRRQRSLGPDA 720
Db   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDDAQHSDLRDPHSRRQRSLGPDA 720

Qy   721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db   721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780

Qy   781 VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISWNEIVGQQGGGLSVLRTFRLMR 840
Db   781 VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISWNEIVGQQGGGLSVLRTFRLMR 840

Qy   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
Db   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900

Qy   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
Db   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960

Qy   961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGDRKKCL 1020
Db   961 ----------------------------GDANKSESEPDFFSPSLDGDGDRKKCL 997

Qy   1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db   998 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057

Qy   1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGEERRSLLSGEGQESQ 1140
Db   1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGEERRSLLSGEGQESQ 1117

Qy   1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
Db   1118 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1177

Qy   1201 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYYFP 1260
Db   1178 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYYFP 1237

Qy   1261 PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
Db   1238 PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297

Qy   1321 FLAEMTVKVAVLGWCFGEQAYLRSSWNVLDGLLVLIFLSSWNVLDGLLVLISVDSGTKILGMLRVL 1380
Db   1298 FLAEMTVKVAVLGWCFGEQAYLRSSWNVLDGLLVLISVDILIVSMVSDSGTKILGMLRVL 1357

Qy   1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIFGILGVQLFKGKFFV 1440
Db   1358 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIFGILGVQLFKGKFFV 1417

Qy   1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
Db   1418 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1477

Qy   1501 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1560
Db   1478 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1537

Qy   1561 RRLEKKRRKAQCKPYYSSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQI 1620
Db   1538 RRLEKKRRKAQCKPYYSSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQI 1597

Qy   1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1680
Db   1598 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1657

Qy   1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA 1740
Db   1658 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA 1717

Qy   1741 ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1800
Db   1718 ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1777

Qy   1801 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMKTL 1860
Db   1778 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMKTL 1837

Qy   1861 SPQHSPLGSPFLWPGVEGPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP 1920

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Db    1838  SPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP  1897

Qy    1921  DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGVLSVHSQPADTSY  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1898  DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGVLSVHSQPADTSY  1957

Qy    1981  ILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1958  ILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED  2017

Qy    2041  LLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2018  LLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET  2077

Qy    2101  RSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2078  RSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA  2137

Qy    2161  VSCLDSGSSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPPSPGICL  2220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2138  VSCLDSGSSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPPSPGICL  2197

Qy    2221  RRRAPSSDSKDPLASGPPDSMAASPPKKDVLSLGLSSDPADLDP  2266
            |||||||||||||||||||||||||||||||||||||||||||
Db    2198  RRRAPSSDSKDPLASGPPDSMAASPPKKDVLSLGLSSDPADLDP  2243
```

RESULT 4
AAY14586
ID   AAY14586 standard; protein; 2250 AA.
XX
AC   AAY14586;
XX
DT   07-DEC-1999   (first entry)
XX
DE   Human T-type voltage-gated Ca channel alpha-1-G (hCaVT1a).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83481.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 31-40; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCaVT1a. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid

CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2250 AA;

Query Match   98.6%; Score 11741; DB 2; Length 2250;
Best Local Similarity   98.6%; Pred. No. 0;
Matches 2241; Conservative 1; Mismatches 1; Indels 30; Gaps 2;

```
Qy      1  MDEEEDGAGAEBGSQPRSFMRLNDLSGAGGRPGPGSASAEKDPGSADSEAEGLPYPALAPVV    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV    60

Qy     61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF   120

Qy    121  DDFIPAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVR   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  DDFIPAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLLDLQNVSFSAVR   180

Qy    181  TVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFVFFIFGIVGVLWAGLLRNR    240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFVFFIFGIVGVLWAGLLRNR    240

Qy    241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL   300

Qy    301  DYEAYNSSSNTTCVNWNQYYNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  DYEAYNSSSNTTCVNWNQYYNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM   360

Qy    361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA   420

Qy    421  STLASFSEPGSCYEELLKYLVYLIRKAARRLAQVSRAAGVRGLLSSPAPLGGQETQPSS   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  STLASFSEPGSCYEELLKYLVYLIRKAARRLAQVSRAAGVRGLLSSPAPLGGQETQPSS   480

Qy    481  SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP   540

Qy    541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE   600

Qy    601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG   660

Qy    661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA   720

Qy    721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI   780

Qy    781  VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVSVLRTFRLMR  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVSVLRTFRLMR  840

Qy    841  VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGGCKFASERDGDTL   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  VLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGGCKFASERDGDTL   900

Qy    901  PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV   960
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Db    901  PDRKNFDSLLWAIVTVFQIITQEDMNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLIV  960
Qy    961  AIIVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL  1020
Db    961  AIIVEGFQAE----------GDANKSESEPDFFSPSLDGDGDRKKCL               997
Qy   1021  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPASRTSSSGSAEPGAA    1080
Db    998  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPASRTSSSGSAEPGAA    1057
Qy   1081  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ  1140
Db   1058  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ  1117
Qy   1141  DEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN   1200
Db   1118  DEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN   1177
Qy   1201  GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP  1260
Db   1178  GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP  1237
Qy   1261  PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV  1320
Db   1238  PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV  1297
Qy   1321  FLAEMTVKVKVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLRVL  1380
Db   1298  FLAEMTVKVKVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLRVL  1357
Qy   1381  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV  1440
Db   1358  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV  1417
Qy   1441  CQGEDTRNITNKSDCAEAASYRWVRHYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG  1500
Db   1418  CQGEDTRNITNKSDCAEAASYRWVRHYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG  1477
Qy   1501  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRL  1560
Db   1478  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRL  1537
Qy   1561  RRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME   1613
Db   1538  RRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME  1597
Qy   1614  HYQQPQILDEALKICNYIFTVIFVLESVFKIVAFGFRRFFQDRWNQLDLAIVLLSIMGIT  1673
Db   1598  HYQQPQILDEALKICNYIFTVIFVLESVFKIVAFGFRRFFQDRWNQLDLAIVLLSIMGIT  1657
Qy   1674  LEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFM  1733
Db   1658  LEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFM  1717
Qy   1734  LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT  1793
Db   1718  LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT  1777
Qy   1794  LRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEL  1853
Db   1778  LRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEL  1837
Qy   1854  ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH  1913
Db   1838  ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH  1897
Qy   1914  PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS  1973
Db   1898  PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS  1957
Qy   1974  QPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQ   2033

Db   1958  QPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPGRSPLAQRPLRRQAAIRTDSLDVQ   2017
Qy   2034  GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNW  2093
Db   2018  GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNW  2077
Qy   2094  GKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYSVEAQSCQRRPTSWLDE   2153
Db   2078  GKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYSVEAQSCQRRPTSWLDE   2137
Qy   2154  QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP  2213
Db   2138  QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP  2197
Qy   2214  PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP         2266
Db   2198  PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP         2250
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RESULT 5
AAY14587
```
ID   AAY14587 standard; protein; 2261 AA.
XX
AC   AAY14587;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human T-type voltage-gated Cc channel alpha-1-G (hCavT1b).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;    98WO-US023161.
XX
PR   05-DEC-1997;    97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83482.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 40-49; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCavT1b. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2261 AA;
```

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Query Match      98.6%;   Score  11735.5;   DB  2;   Length  2261;
Best Local Similarity  98.1%;   Pred. No.  0;
Matches  2241;   Conservative  1;   Mismatches  1;   Indels  1;   Gaps  41;   2;


Qy      1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60

Qy     61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF  120

Qy    121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180

Qy    181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240

Qy    241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300

Qy    301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLBGWVDIM  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLBGWVDIM  360

Qy    361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420

Qy    421  STLASFSEPGSCYEELLKYLVYIILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  STLASFSEPGSCYEELLKYLVYIILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480

Qy    481  SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP  540

Qy    541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600

Qy    601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660

Qy    661  ACGPDSCPYCARAGAGEVELADAREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ACGPDSCPYCARAGAGEVELADAREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720

Qy    721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780

Qy    781  VFTSLFALEMLLKLLVGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMR  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  VFTSLFALEMLLKLLVGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMR  840

Qy    841  VLKLIVRFLPALQRQLVVMLKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  VLKLIVRFLPALQRQLVVMLKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL  900

Qy    901  PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960

Qy    961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
           |||||||||                --------|||||||||||||||||||||||||||
Db    961  AILVEGFQAE----------------GDANKSESEPDFFSPSLDGDGDRKKCL  997

Qy   1021  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPASRRTSSSGSAEPGAA 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPASRRTSSSGSAEPGAA 1057

Qy   1081  HEMKSPPSARSSPHSPWSAAASWTSRRSRRSNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058  HEMKSPPSARSSPHSPWSAAASWTSRRSRRSNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117

Qy   1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1177

Qy   1201  GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178  GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP 1237

Qy   1261  PQSRRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238  PQSRRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297

Qy   1321  FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSWVSDSGTKILGMLRVL 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298  FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSWVSDSGTKILGMLRVL 1357

Qy   1381  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFV 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFV 1417

Qy   1441  CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418  CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1477

Qy   1501  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHOEEEARRREEKRL 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHOEEEARRREEKRL 1537

Qy   1561  KAQCKPYSDYSRFRLLVHHLCTSHYLDLFITGV 1602
           ||||||||||||||||||||||||||||||||||||
Db   1538  RRLEKKRRNLMLDDVIASGSSASAAAAESEAQCKPYSDYSRFRLLVHHLCTSHYLDLFITGV 1597

Qy   1603  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDL 1662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDL 1657

Qy   1663  AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMOAL 1722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658  AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMOAL 1717

Qy   1723  PQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST 1782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1718  PQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST 1777

Qy   1783  GDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE 1842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778  GDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE 1837

Qy   1843  AKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPSPDSPKPGALHPAAHARSASH 1902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1838  AKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPSPDSPKPGALHPAAHARSASH 1897

Qy   1903  FSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPK 1962
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1898  FSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPK 1957

Qy   1963  AQSGSVLSVHSQPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQ 2022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1958  AQSGSVLSVHSQPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQ 2017

Qy   2023  AAIRTDSLDVQGLGSREDLLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTP 2082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2018  AAIRTDSLDVQGLGSREDLLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTP 2077

Qy   2083  PAPCGPEPNWGKGPPETRSSLELDTELSWISGDILPPGGQOEEPSPRDLKKCCYSVEAQS 2142
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Db  2078 PAPCGPGPENWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYSVEAQS 2137
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2143 CQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITI 2202
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2138 CQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITI 2197

Qy  2203 DPPESQGPRTPPSPGICLRRRAPSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDDPA 2262
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2198 DPPESQGPRTPPSPGICLRRRAPSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDDPA 2257

Qy  2263 DLDP 2266
              ||||
Db  2258 DLDP 2261
```

RESULT 6
AAY14588

```
ID   AAY14588  standard; protein; 2268 AA.
XX
AC   AAY14588;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human T-type voltage-gated Ca channel alpha-1-G (hCavT1c).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Homo sapiens.
XX
PN   WO929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;  98WO-US023161.
XX
PR   05-DEC-1997;  97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83483.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 49-58; 138pp; English.
XX
CC   This sequence represents a human T-type voltage-gated calcium (Ca)
CC   channel alpha-1-G designated hCavT1c. Voltage gated channels are membrane
CC   bound glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2268 AA;
```

```
Qy    1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120

Qy  121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy  181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy  241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Qy  301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy  361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy  421 STLASFSEPGSCYEELLKYLVYLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRR 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 STLASFSEPGSCYEELLKYLVYLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRR 480

Qy  481 SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy  541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy  601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKISSPCLKADSG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKISSPCLKADSG 660

Qy  661 ACGPDSCPYCARAGAGEVELADREMPDSDSRAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy  721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEELTNALEISNI 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEELTNALEISNI 780

Qy  781 VFTSLFALEMLLKLLVYGPGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMR 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 VFTSLFALEMLLKLLVYGPGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMR 840

Qy  841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900

Qy  901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960

Qy  961 AILVBGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDRKKCL 1020
          |||||||||||                          |||||||||||||||||||||
Db  961 AILVBGFQAR--------------------------GDANKSESEPDFFSPSLDGDGDRKKCL 997

Qy 1021 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  998 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057

Qy 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
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Query Match          98.5%;  Score 11727;  DB 2; Length 2268;
Best Local Similarity  97.8%;  Pred. No. 0;
Matches 2240;  Conservative  1;  Mismatches  1;  Indels  48;  Gaps  2;
```

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Db  1058 HEMKSPPSARSPHSPWSAAASWTSRRSSRNSIGRAPSLKRRSPSGERRSLLSGEGQESQ 1117
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1118 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200

Qy  1178 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1237
         ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  1201 GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP 1260

Qy  1238 PQSRFRLLCHRIITHKMFDHVVLIVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297
         |||||||||||||||||||||||| :||||||||||||||||||||||||||||||||||
Db  1261 PQSRFRLLCHRIITHKMFDHVVLIFIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320

Qy  1298 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1357
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380

Qy  1358 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGIIGVQLFKGKFFV 1417
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGIIGVQLFKGKFFV 1440

Qy  1418 CQGEDTRNITNKSDCARASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1477
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500

Qy  1478 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1537
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1560

Qy  1538 RRLEKKRRSKEKQMADLMLDDVIASGSSAAASEAQCKPYYSDYSRFRLLVHHLCTSHYL 1597
         ||||||||                         :||||||||||||||||||||||||||
Db  1561 RRLEKKRR-------------------------KAQCKPYYSDYSRFRLLVHHLCTSHYL 1595

Qy  1598 DLFITGVIGLNVVIMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQD 1657
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1596 DLFITGVIGLNVVIMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQD 1655

Qy  1658 RWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALL 1717
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1656 RWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALL 1715

Qy  1718 DTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFL 1777
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1716 DTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFL 1775

Qy  1778 TLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKH 1837
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1776 TLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKH 1835

Qy  1838 LEESNKEAKEAEAELRAELAELEMKTLSPQPHSPLGSPFLWPGVEGPDSPKPGALHPAA 1897
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1836 LEESNKEAKEAEAELRAELAELEMKTLSPQPHSPLGSPFLWPGVEGPDSPKPGALHPAA 1895

Qy  1898 HARSASHFSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGH 1957
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1896 HARSASHFSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGH 1955

Qy  1958 RGWGLPKAQSGSGVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLA 2017
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1956 RGWGLPKAQSGSGVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLA 2015

Qy  2018 QRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPLARAYSFWGQSTQAQQHSRSHSK 2077
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2016 QRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPLARAYSFWGQSTQAQQHSRSHSK 2075

Qy  2078 ISKHMTPPAPCPGPEPNWGKGPEPTRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKC 2137
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2076 ISKHMTPPAPCPGPEPNWGKGPEPTRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKC 2135

Qy  2136 YSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSGQPHLGTDPSNLGGQPLGGPSRPKKKL 2195
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2138 YSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSGQPHLGTDPSNLGGQPLGGPSRPKKKL 2197

Qy  2196 SPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLS 2255
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2198 SPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLS 2257

Qy  2256 GLSDPADLDP 2266
         ||||||||||
Db  2258 GLSDPADLDP 2268
```

RESULT 7
AAB66481
ID   AAB66481 standard; protein; 2266 AA.
XX
AC   AAB66481;
XX
DT   09-APR-2001 (first entry)
XX
DE   Human alpha-IG T-type calcium channel protein.
XX
KW   Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;
KW   T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
KW   hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.
XX
OS   Homo sapiens.
XX
PN   WO200102561-A2.
XX
PD   11-JAN-2001.
XX
PF   04-JUL-2000; 2000WO-CA000794.
XX
PR   02-JUL-1999; 99US-00346794.
XX
PA   (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI   Snutch TP, Baillie DL;
XX
DR   WPI; 2001-123111/13.
DR   N-PSDB; AAF31684.
XX
PT   Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT   cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT   epilepsy.
XX
PS   Example 3; Fig 6; 103pp; English.
XX
CC   The present sequence is given in a specification providing sequences and
CC   partial sequences for three types of mammalian (human and rat) T-type
CC   calcium channel subunits. An expression cassette has been generated which
CC   comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC   subunit operably linked to control sequences to effect its expression.
CC   The novel calcium channel nucleic acids and proteins are useful for
CC   treating conditions characterised by undesirable levels of T-type calcium
CC   channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC   hypertension, sleep disorder and epilepsy
XX
SQ   Sequence 2266 AA;

Query Match   97.9%;   Score 11653;   DB 4;   Length 2266;
Best Local Similarity 98.8%;   Pred. No. 0;
Matches 2239; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

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Qy    1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy  121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
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Db   121 DDFIFAFFAVEMVVKNVALGIFGKKCYLGDTNRLDFFVIAGMLEYSLDLQNVSFSAVR 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300

Qy   301 DYEAYNSSNNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
         ||||||||: : |||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DYEAYNSSSKTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy   361 YFVMDAHSFYNFYFYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 YFVMDAHSFYNFYFYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy   421 STLASFSEPGSCYEELLSKYLVVILRKAARRLAQVSRAAGVRVGLLLSSPAPLGGQETQPSS 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 STLASFSEPGSCYEELLSKYLVVILRKAARRLAQVSRAAGVRVGLLLSSPAPLGGQETQPSS 480

Qy   481 SCSRSHRRLSVHHLVHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRIMLPPPSTP 540
         |||||||||||:|||||:||:|||||||||||||||||||||||||||||||||||
Db   481 SCSRSHRRLSVNHLVHHHNHMHNHYHLGNGTLRAPRASPEIQDRDANGSRRIMLPPPSTP 540

Qy   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
         |||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||||
Db   541 ALSGAPPGGAESVHSFYHADCMLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVNTSPPPE 600

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy   721 EPSSVLAFWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 EPSSVLAFWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780

Qy   781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVNEIVGQQGGGLSVLRTFRLMR 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVNEIVGQQGGGLSVLRTFRLMR 840

Qy   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMLLFGCKFASERDGDTL 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMLLFGCKFASERDGDTL 900

Qy   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960

Qy   961 AIIVEGFQAEEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDRKKCL 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AIIVEGFQAEEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDRKKCL 1020

Qy  1021 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSSGSAEPGAA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSSGSAEPGAA 1080

Qy  1081 HEMKSPPSARSSPHSPWSAAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 HEMKSPPSARSSPHSPWSAAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140

Qy  1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGASEHQDCN 1200
         |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db  1141 DEEESSEEERASPAGSDHRNRGSLEREAKSSFDLPDTLQVPGLHRTASGRGASEHQDCN 1200

Qy  1201 GKSASGRLARALRPDDPPLLGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1201 GKSASGRLARALRPDDPPLLGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260

Qy  1261 PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
         ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db  1261 PQSRFRLLCHRIITNNKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320

Qy  1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380

Qy  1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440

Qy  1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
         |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db  1441 CQGEDTRNITNKSDCAEASYRWVRMKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500

Qy  1501 VDQQPIMNHPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEKRL 1560
         ||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db  1501 VDQQPIMNHNPNMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEKRL 1560

Qy  1561 RRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQI 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 RRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQI 1620

Qy  1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1680

Qy  1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA 1740

Qy  1741 ALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1800
         ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db  1741 ALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWEGIMKDTLRDCDQE 1800

Qy  1801 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAEALELEMKTL 1860
         ||||:|||||||||||||||||||:|||||||||||||||||||||||||||||
Db  1801 STCYFTVISPIYFVSFVLTAQFVLVMVVIAVLMKHLEESNKEAKEAEALELEMKTL 1860

Qy  1861 SPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP 1920
         ||||||||||||:|||||||||||||||||:|||||||||||||||||||||||||||||
Db  1861 SPQPHSPLGSPFLNPGVEGPDSPDSPKPGALMPAAHARSASHFSLEHPTMQPHPTELPGP 1920

Qy  1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY 1980
         |||||||||||||:||||||||||:|||||||||||||||||||||||||||||||||||
Db  1921 DLLTVRKSGVSRTMSLPNDSYMCRRGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY 1980

Qy  1981 IIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED 2040
         |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 IIQLPKDAPHLLQPMSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED 2040

Qy  2041 LLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET 2100
         ||||||||||||||||||||||||||||||||||||||||||:|||||:||||||||||
Db  2041 LLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHHTPPAPCAGPEPNWGKGPPET 2100

Qy  2101 RSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA 2160
         |||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 RSSLELDTELSNISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA 2160

Qy  2161 VSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPSPGICL 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 VSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDDPPESQGPRTPSPGICL 2220

Qy  2221 RRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2221 RRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266
```

RESULT 8
AAV70720

```
ID   AAY70720 standard; protein; 2428 AA.
XX
AC   AAY70720;
XX
DT   18-JUL-2000 (first entry)
XX
DE   Rat pancreatic T-type calcium channel.
XX
KW   Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;
KW   pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;
KW   antidiabetic; calcium influx; L type calcium channel; NIDDM;
KW   type II diabetes; non-insulin dependent diabetes mellitus.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1..52
FT                   /note= "Region upstream to pancreatic T-type calcium
FT                   channel protein"
FT   Misc-difference 4
FT                   /note= "Encoded by in-frame stop codon TGA"
FT   Protein         53..2428
FT                   /label= Pancreatic_T-type_calcium_channel_alpha1_subunit
FT                   /note= "This region is claimed as SEQ ID NO: 2"
FT   Region          53..86
FT                   /note= "Unique region that differs from amino acid
FT                   sequence of neuronal T-type calcium channel alpha1
FT                   subunit (alpha1G)"
FT   Region          1023..1046
FT                   /note= "Unique region that differs from amino acid
FT                   sequence of neuronal T-type calcium channel alpha1
FT                   subunit (alpha1G)"
FT                   /label= Intracellular loop I(II-III)
FT   Region          1622..1640
FT                   /label= Intracellular loop_L(III-IV)
FT                   /note= "Unique region that differs from amino acid
FT                   sequence of neuronal T-type calcium channel alpha1
FT                   subunit (alpha1G)"
FT   Misc-difference 2341
FT                   /note= "Encoded by in-frame stop codon TGA"
FT   Misc-difference 2371
FT                   /note= "Encoded by in-frame stop codon TAA"
XX
PN   WO200015845-A1.
XX
PD   23-MAR-2000.
XX
PF   26-AUG-1999; 99WO-US019675.
XX
PR   26-AUG-1998; 98US-0098004P;
PR   27-JAN-1999; 99US-0117399P.
XX
PA   (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
PI   Li M;
XX
DR   WPI; 2000-271475/23.
DR   N-PSDB; AAZ52309.
XX
PT   Novel nucleic acids encoding pancreatic T-type calcium channels used for
PT   regulation of T-type calcium channels and treatment of type II diabetes.
XX
PS   Example 1; Page 120; 124pp; English.
XX
CC   The present sequence is a protein that includes pancreatic T-type calcium
CC   channel alpha1 subunit derived from rat insulin secreting beta cell line,
CC   INS-1. The protein shows 96.3 % identity to the neuronal T-type calcium
CC   channel alpha1 subunit (alpha1G). The T-type Ca2+ channel from INS-1
CC   (alpha1G-INS) and neuronal alpha1G are alternative splice isoforms of the
CC   same gene. The INS-1 isoform is also expressed in brain, neonatal heart
CC   and kidney besides pancreatic beta cells. T-type Ca2+ channel belongs to
CC   the family of low voltage activated Ca2+ channels. The present sequence
CC   is used for treating diseases associated with abnormal expression or
```

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CC   function of T-type calcium channels. They are especially used for
CC   treating type II diabetes. Modulators of pancreatic T-type Ca2+ channel
CC   e.g. antisense oligonucleotides, ribozymes and inhibitors are used in
CC   methods for modifying insulin secretion by pancreatic beta cells, basal
CC   calcium levels, potential L type calcium channel activity, pancreatic
CC   cell death, pancreatic beta cell proliferation and calcium influx through
CC   L type calcium channels in cells
XX
SQ   Sequence 2428 AA;

Query Match             93.3%;  Score 11111;  DB 3;  Length 2428;
Best Local Similarity   93.3%;  Pred. No. 0;
Matches 2135;  Conservative   35;  Mismatches   95;  Indels   24;  Gaps  5;

Qy          1 MDEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
              |||||||||||||||||| :|||||||||| |||||||||||||||||||||||||||
Db         53 MDEEDGAGAEESGQPRSFTQLNDLSGAGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 112

Qy         61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
              |||||||||||||||||||||||||| ::|||||||||||||||||||||||||||||||
Db        113 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 172

Qy        121 DDFIPAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 DDFIPAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 232

Qy        181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 292

Qy        241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
              ||||||||||||||| ||||||||||||||||||||||||||||||||||| |||||| |
Db        293 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL 352

Qy        301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 DYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 412

Qy        361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQIMREQRVRFLSNA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQIMREQRVRFLSNA 472

Qy        421 STLASFSEPGSCYEELLKYLVVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
              |||||||||||||||||||||||||||||||||:|||| ||||||||:||||   |:|||
Db        473 STLASFSEPGSCYEELLKYLVVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG 532

Qy        481 SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
              || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        533 SCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 592

Qy        541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
              :|| ||| ||||||||||||||||||||||||| : |||||||||||||||||||||||
Db        593 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPPE 652

Qy        601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
              :||:||||||| : |||||||:|||||| |||||||||||||||: ||||||||| |||||
Db        653 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 712

Qy        661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RQRSLGPD 719
              ||||||||||||:||| ::| : || :|||||||||||||||||||||||  |||||||
Db        713 ACGPDSCPYCARTGAGEPPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 772

Qy        720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIRYEHQPEELTNALEISN 779
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIRYEHQPEELTNALEISN 832

Qy        780 IVFTSLFALEMLLKLLVGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLM 839
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        833 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLM 892

Qy        840 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDT 899
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        893 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 952
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Qy    900  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL   959
           ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db    953  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  1012

Qy    960  VAILVEGFQAEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC   1019
           |:||||||||||:||||||||||||||||||:||||||||| ||||||||||||||||||
Db   1013  VAILVEGFQAEEIGKREDASGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGDRKKR  1072

Qy   1020  LALVSLGEHPELRKSLLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA  1079
           |||||||:|:||||||||:|||||||||||||||||||:||| ||||||||||||||||
Db   1073  LALVALGEHAELRKSLLPPLLIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGA  1132

Qy   1080  A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1138
           | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133  AHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1192

Qy   1139  SQDEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD  1198
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193  SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD  1252

Qy   1199  CNGKSASGRLAARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI  1258
           |||||||||||||:||||| |||||::|||||||||:|||:||:||||||||||||||||
Db   1253  CNGKSASGRLARTIRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI  1312

Qy   1259  FPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313  FPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1372

Qy   1319  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1378
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1432

Qy   1379  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF  1438
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF  1492

Qy   1439  FVCQGEDTRNTNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1498
           |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1552

Qy   1499  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK  1558
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK  1612

Qy   1559  RLRRLEKKR-------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1600
                   :|||            :||||||||||||||||||||||||||||||||
Db   1613  RIRRLEKKRRNLMLDDVIASGSSASAAESEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1672

Qy   1601  GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQL  1660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673  GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFVFESVFKLVAFGFRRFFQDRWNQL  1732

Qy   1661  DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ  1720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1733  DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ  1792

Qy   1721  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1852

Qy   1781  STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  1840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1853  STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  1912

Qy   1841  KEAKEEAELEAELEMKTLSPQHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSA   1900
           ||||||||||||||||||||||||||||||||:||||||||||||||||||||||  :|
Db   1913  KEAKEEAELEAELEMKTLSPQHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAA  1972

Qy   1901  SHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG  1957
           |||||||:||||| :||    |||||||||||||||||||||||||||||||||||||||
Db   1973  SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRG  2032
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Qy   1958  WGLPKAQGSGVLSVHSQPADTSYIILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQR  2017
           |||||||||||:|||||||||||||||||||||||||||||||||:|||||||||||||||
Db   2033  WGLPKAQGSGIILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR  2092

Qy   2018  PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRHSKIS  2077
           |||||||||||||||||||||||||:||||||||||||||||:|||||||||||:||::
Db   2093  PLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVS  2152

Qy   2078  KHMTPPAPCPGPEPNWKGKPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYS  2137
           |||: ||||||||||||||||||||||||||||||||||||:  ||||||||||||||
Db   2153  KHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLSPRDLKKCYS  2211

Qy   2138  VEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP  2197
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2212  VETQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKKLSP  2271

Qy   2198  PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL  2257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2272  PSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDFSVSSPLDSTAASPSPKKDTLSLSGL  2331

Qy   2258  SSDPADLDP  2266
           ||||: |||
Db   2332  SSDPTDMDP  2340
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RESULT 9
AAY14593
ID   AAY14593 standard; protein; 2247 AA.
XX
AC   AAY14593;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCaVT1d).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO992847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;    98WO-US023161.
XX
PR   05-DEC-1997;    97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83488.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 94-103; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCaVT1d. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the T-type voltage
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
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CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2247 AA;

Query Match             92.1%;   Score 10962.5;  DB 2;   Length 2247;
Best Local Similarity   92.8%;   Pred. No. 0;
Matches 2108;  Conservative  33;  Mismatches 101;  Indels  29;  Gaps  5;

Qy      1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      1 MDEEEDGAEESGQPRSFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV   60

Qy     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120

Qy    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180

Qy    181 TVRVLRPLRAINRVPSMRLLVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR  240
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR  240

Qy    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGQGPPCGL  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGEGGPPCSL  300

Qy    301 DYEAVNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DYETVNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360

Qy    361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420

Qy    421 STLASFSEPGSCYEELLKYLVYIHHHHHHYHLVHHLVHHLVHHLVHHLVHHH  480
          |||||||||||||||||||||||||||||||
Db    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG  480

Qy    481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 SCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP  540

Qy    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPPE  600

Qy    601 TLKEKALVEVAASGPPTLTSLNIPPGYSSWHKLLETQSTGACOQSSCKISSPCLKADSG  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ILKDKALVEVAPSPGPPTLTSRNIPPGFSSWHKLLETQSTGACHSSCKISSPCSKADSG  660

Qy    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSLGPD  719
          ||||||||||||| || |||||||||||||||||||||||||||||||||||||||||||
Db    661 ACGPDSCPYCARTGAGEPPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPD  720

Qy    720 AEPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEELTNALRISN  779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AEPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN  780

Qy    780 IVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISWEIVSWEIVGQQGGGLSVLRTFRLM  839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 IVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISWEIVSWEIVGQQGGGLSVLRTFRLM  840

Qy    840 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT  899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT  900

Qy    900 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  960
```

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Qy    960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC 1019
          |||||||||||                                  :||||||||||||||
Db    961 VAILVEGFQAE--------------------------------GDATKSESEPDFFSPSVDGDGDRKKR  997

Qy   1020 LAIVSLGEHPELRKSLLLPLIIHTAATPMSLPKSTGLGEALGPASRRTSSSGSAEPGA 1079
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 LAIVALGEHAELRKSLLLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGA 1057

Qy   1080 A-HEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
          | ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 AHHEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1117

Qy   1139 SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD 1198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD 1177

Qy   1199 CNGKSASGRLARAI.RPDDPPLDGDADDEGNLSKGERVRAWIRARLPACVLERDSWSAYI 1258
          ||||||||||||:::|||::::::|::||::||||||:|:|||||||||||||||||||||
Db   1178 CNGKSASGRLARTLRTDDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCCRERDSWSAYI 1237

Qy   1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 FPPQSRFRLLCHRIITHKMFDHVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297

Qy   1319 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVDILVSMVSDSGTKIIGMLR 1378
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVDILVSMVSDSGTKIIGMLR 1357

Qy   1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKF 1438
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKF 1417

Qy   1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1477

Qy   1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREK 1558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREK 1537

Qy   1559 RLRRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTVMAMEHYQQP 1618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1538 RLRRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTVMAMEHYQQP 1597

Qy   1619 QILDEALKICNYIFTVIFVFLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEBIE 1678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 QILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEBIE 1657

Qy   1679 VNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFI 1738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFMLLFFI 1717

Qy   1739 FAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCD 1798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1718 FAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCD 1777

Qy   1799 QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMK 1858
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778 QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELEMK 1837

Qy   1859 TLSPQPHSPLGSPPLWPGVEGPSDSPSPKPGALHPAAHARSASHFSLEHPTMQPHPTELP 1918
          |||||||||||||||||||||||||||||||||  : ||  :||||||||||||
Db   1838 TLSPQPHSPLGSPPLWPGVEGVNSTDSPSPKPGAPHTTAHIGAASGFSLERPTMVPHPEEVP 1897

Qy   1919 ---GPDLLITVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGSVLVSHSQP 1975
             ||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1898 VPLGPDLLITVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSILVSHSQP 1957

Qy   1976 ADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVGQL 2035
          |||  |||||||| ||| |||| ||||| |||| ||||||||| |||||| ||||||||||
Db   1958 ADTSCILQLPKDVHYILQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVGQL 2017
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Qy  2036  GSREDLLAEVSGPSSPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGK  2095
          |||||||.|||||.|||:.:..|||.|:.||..:.|..:.||.||:.|:.||||||.|..:|||
Db  2018  GSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAK  2077

Qy  2096  GPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQR  2155
          .|||||||||||||||||||||||.:||||.|.|||||||||||:.||.|||.||||||
Db  2078  DPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQR  2136

Qy  2156  RHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTPPS  2215
          |||||||||||||||.|.|.|||.|||||||||||||||||||||:||||||||||.|.||.:
Db  2137  RHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPPESQGSRPPCS  2196

Qy  2216  PGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLLSGLSSDPADLDP       2266
          ||:|||||||:||||||.:.:||||.||||||||||.|||||.||||||:||.|.||
Db  2197  PGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP           2247
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RESULT 10
AAY14590

```
ID   AAY14590 standard; protein; 2254 AA.
XX
AC   AAY14590;
XX
DT   07-DEC-1999 (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCaVT1a).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83485.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 67-76; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCaVT1a. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2254 AA;
```

Query Match   91.9%;   Score 10945;   DB 2;   Length 2254;
Best Local Similarity   92.5%;   Pred. No. 0;

Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;

```
Qy    1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60
         ||||||||||||||||||||:::||||||||||:.||||.|||||||||||||||||||||
Db    1  MDEEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV   60

Qy   61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF  120
         ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db   61  FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF  120

Qy  121  DDFIFAFFAVEMVVKMVVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  DDFIFAFFAVEMVVKMVVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180

Qy  181  TVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240

Qy  241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL  300
         |||||||||||||||.||||||||||||||||||||||||||||||||||||.|||||.||
Db  241  CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL  300

Qy  301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360
         |||.|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  DYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360

Qy  361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420

Qy  421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480
         |||||||||||||||||||||||||||||||||||||:|||.|||||.|..|.||.|||.|
Db  421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG  480

Qy  481  SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP  540
         ||:|||||||||||||||||||||||||||||.|||||||||||||||||||||||||||
Db  481  SCTRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP  540

Qy  541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
         :.||.||.|||||||||||||||||||||||||||.||.||||||.|.:|||||||||||
Db  541  TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSASGRTVGSSGRVYPTVHTSPPPE  600

Qy  601  TLKEKALVEVAASSGPPLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660
         :||:||||||..|.|||.|||:||||||.|||||||||||||||.|||||||||.|||||
Db  601  ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG  660

Qy  661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RQRSLGPD  719
         ||||||||||||.|||||.:.|||.:||||||||||||||||||||||||||.|||||||||
Db  661  ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD  720

Qy  720  AEPSSVLAFWRLICDTFRKIVDSKYPGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN  779
         |||||||||||||||||||||||||.||||||||||||||||||||:||||||||||||||
Db  721  AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHBQPEELTNALEISN  780

Qy  780  IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLM  839
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLM  840

Qy  840  RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT  899
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT  900

Qy  900  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  960

Qy  960  VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDRKKC  1019
         ||||||||||||                          ||:|||||||||||||.|||.|||:
Db  961  VAILVEGFQAE-------------------------GDATKSESEPDFFSPSVDGDGDRKKR  997

Qy 1020  LALVSLGEHPELRKSLLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA  1079
         ||||:|||||:||||||||||||||||||||.||.|||:|||||.:.||||||||||||||
Db  998  LALVALGEHAELRKSLLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGA  1057
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Qy    2149  SWLDEQRRHSIAVSCLDGSGSQPHLGTDPSNLGGQPLGGPLGGSRPKKKLSPPSITIDPPESQ  2208
            ||||||||||||||||||||||  ||||||  |||  |||  |||| |||||||| ||| |||||
Db    2137  FWLDEQRRHSIAVSCLDGSGSQPRLCPSPSLGGQPLGGPGPGSRPKKKLSPPSISIDPPESQ  2196

Qy    2209  GPRTPPSPDGICLRRRAPSDSKDPLASGPPDSMAASPKKDVLSLSGLSSDPADLDP  2266
            |  ||||| |  |||||| ||||  |::|:  || |
Db    2197  GSRPPCSPGVCLRRRAPASDSKDPSVSSFLDSTAASPKKDTLSLSGLSSDPTDMDP  2254
```

RESULT 11

```
AAY14591
ID    AAY14591 standard; protein; 2265 AA.
XX
AC    AAY14591;
XX
DT    07-DEC-1999  (first entry)
XX
DE    Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b).
XX
KW    Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW    activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS    Rattus sp.
XX
XX
PN    WO9929847-A1.
XX
PD    17-JUN-1999.
XX
PF    30-OCT-1998;  98WO-US023161.
XX
PR    05-DEC-1997;  97US-00985809.
XX
PA    (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI    Perez-Reyes E, Cribbs LL;
XX
DR    WPI; 1999-394972/33.
DR    N-PSDB; AAX83486.
XX
PT    New T-type voltage-gated calcium channels.
XX
PS    Disclosure; Page 76-85; 138pp; English.
XX
CC    This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC    alpha-1-G designated rCavT1b. Voltage gated channels are membrane bound
CC    glycosylated proteins formed of several subunits. The large alpha
CC    subunits form a pore in the membrane that is selective for a given ionic
CC    species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC    each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC    -type Ca channels are activated at a lower voltage than L- or N-type
CC    channels. Characteristics of T-type channels include short current time,
CC    slow activation kinetics near threshold, fast inactivation kinetics and
CC    slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC    voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC    -channels contains a putative IVS4 region comprising the amino acid
CC    sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC    channel proteins can be used to screen for drugs which affect calcium
CC    channels. Methods are also disclosed for treating a disease or disorder
CC    associated with a deficiency in a native T-type calcium channel nucleic
CC    acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ    Sequence 2265 AA;

Query Match          91.9%;  Score 10939.5;   DB 2;  Length 2265;
Best Local Similarity  92.0%;  Pred. No. 0;
Matches 2107;  Conservative  34;  Mismatches  47;  Indels  101;  Gaps  6;
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```
Qy       1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSADSEAEGLPYPALAPVV   60
            ||||||||||||||||||||||||||:||||||||||||||| || ||||||||||||||||
Db       1  MDEEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV   60

Qy      61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78  LEPSWAKDPETRSSLEDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVETQSCRRRPG  2136
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```
Qy    1080  A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1138
            |  |||||||||||||||||||||||:|||:||||:||||||||||||||||||||||||||
Db    1058  AHHEMKCPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1117

Qy    1139  SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD  1198
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1118  SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD  1177

Qy    1199  CNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI  1258
            |||||||||||||||:|||:|:||:|  ||::|||||:| ||||||::|:|:|||||||||
Db    1178  CNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI  1237

Qy    1259  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1318
            ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db    1238  FPPQSRFRLLCHRIITHKMFDHVVIVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1297

Qy    1319  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1378
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1298  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1357

Qy    1379  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF  1438
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1358  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF  1417

Qy    1439  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1498
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1418  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1477

Qy    1499  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK  1558
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1478  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK  1537

Qy    1559  RLRRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA  1611
            |||||:||:       :|||||||||||||||||||||||||||||||||||||||||||
Db    1538  RLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA  1597

Qy    1612  MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG  1671
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1598  MEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG  1657

Qy    1672  ITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLL  1731
            ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1658  ITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLL  1717

Qy    1732  FMLLFFIFAAIGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK  1791
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1718  FMLLFFIFAAIGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK  1777

Qy    1792  DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKRAKEEAELEA  1851
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db    1778  DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAELEA  1837

Qy    1852  ELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQ  1911
            |||||||||||||||||||||||||||| |||:|||||||:|||||||||||||||||||
Db    1838  ELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTAHIGAASGFSLEHPTMV  1897

Qy    1912  PHPTELP--GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLLPKAQSGSV  1968
            ||   |  |||||||||||||||||||||||||||||||:|||||||:||||||||||:|
Db    1898  PHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLLPKAQSGSI  1957

Qy    1969  LSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTD  2028
            |||||||||||:|||:||||||||||||||||:|:||||||||||||:|||:|||||||||
Db    1958  LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLLPPPGKSPLAQRPLRRQAAIRTD  2017

Qy    2029  SLDVQGLGSREDLLAEVSGPSSPLLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPG  2088
            |||||||||||||::|:| |||::|||||||||||:::|  |||:|||:||  :|||| |
Db    2018  SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPG  2077

Qy    2089  PEPNWGKGPETRSSLLEDTELSWISGDLLPPGGQEEPSPRDLLKKCYSVEAQSCQRRPT  2148
            |||  ||||||||||||||||||||||||  ||||||||:|||||||||||:||| |||
Db    2078  LEPSWAKDPETRSSLLEDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVETQSCRRRPG  2136
```

```
Db    61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120

Qy   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFTVIAGMLEYSLDLQNVSFSAVR  180
Db   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180

Qy   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR   240
Db   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR   240

Qy   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300
Db   241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL  300

Qy   301 DYEAYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM   360
Db   301 DYETYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM   360

Qy   361 YFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA   420
Db   361 YFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA   420

Qy   421 STLASFSEPGSCYEELLKYLVYLVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480
Db   421 STLASFSEPGSCYEELLKYLVYLVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG  480

Qy   481 SCSRSHRRLSVHHLVHHHHHHHHYHlGNGTLRAPRASPEIQDRDANGSRRIMLPPPSTP   540
Db   481 SCTRSHRRLSVHHLVHHHHHHHHYHlGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP   540

Qy   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
Db   541 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPE  600

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660
Db   601 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG  660

Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSLGPD  719
Db   661 ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPD  720

Qy   720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN  779
Db   721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN  780

Qy   780 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISWEIVGQQGGGLSVLRTFRLM   839
Db   781 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISWEIVGQQGGGLSVLRTFRLM   840

Qy   840 RVLKLVRFLPALQRQLVVLVMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDT  899
Db   841 RVLKLVRFLPALQRQLVVLVMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDT  900

Qy   900 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  959
Db   901 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  960

Qy   960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESRPDFFSPSLDGDRKKC   1019
Db   961 VAILVEGFQAE----------------------------GDATKSESEPDFFSPSVDCGDRKKR   997

Qy  1020 LAIVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPASRRTSSSGSAEPGA   1079
Db   998 LALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGA  1057

Qy  1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGBGQE   1138
Db  1058 AHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1117

Qy  1139 SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD  1198
Db  1118 SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASBHQD  1177


Qy  1199 CNGKSASGRLARALRPDDPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI   1258
Db  1178 CNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI   1237

Qy  1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1318
Db  1238 FPPQSRFRLLCHRIITHKMFDHVVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1297

Qy  1319 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1378
Db  1298 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1357

Qy  1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPGNIVVICCAFFIIFGLLGVQLFKGKF   1438
Db  1358 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPGNIVVICCAFFIIFGLLGVQLFKGKF   1417

Qy  1439 FVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1498
Db  1418 FVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1477

Qy  1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK  1558
Db  1478 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK  1537

Qy  1559 RLRRLEKKR-----------------------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1600
Db  1538 RLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1597

Qy  1601 GVIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQL  1660
Db  1598 GVIGLNVVTMAMEHYQQPOILDEALKICNYIPTVIFVFPESVFKLVAFGFRRFFQDRWNQL  1657

Qy  1661 DLAIVLLSIMGITLEBIEVNASLPINPTIIRIMRVLRIARVLKLKNAVGMRALLDTVMQ  1720
Db  1658 DLAIVLLSIMGITLEBIEVNLSLPINPTIIRIMRVLRIARVLKLKNAVGMRALLHTVMQ  1717

Qy  1721 ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1780
Db  1718 ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1777

Qy  1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  1840
Db  1778 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFYVSFVLTAQFVLVNVVIAVLMKHLEESN  1837

Qy  1841 KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDKPGALHPAAHARSA   1900
Db  1838 KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAA  1897

Qy  1901 SHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG  1957
Db  1898 SGFSLEHPIMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSTAERSLGHRG        1957

Qy  1958 WGLPKAQSGGVLSVHSQPADTSYIILQLPKDAPHLLQPHSGAPTWGTIPKLPPPGRSPLAQR  2017
Db  1958 WGLPKAQSGSILSVHSQPADTSCIILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR  2017

Qy  2018 PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKIS  2077
Db  2018 PLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSGFWGGSSIQVQQRSGIQSKVS  2077

Qy  2078 KHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPRDLKKCYS   2137
Db  2078 KHIRLPAFCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLKKCYS  2136

Qy  2138 VEAQSCQRRPTSWLDEQRRHSIAVSCLLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP  2197
Db  2137 VETQSCRRRPGFWLDEQRRHSIAVSCLLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP  2196

Qy  2198 PSITIDDPESQGRRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL  2257
Db  2197 PSISIDDPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGL  2256
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Qy     2258  SSDPADLDP 2266
             |||  |:|
Db     2257  SSDPTDMDP 2265


RESULT 12
AAY14592
ID    AAY14592 standard; protein; 2272 AA.
XX
AC    AAY14592;
XX
DT    07-DEC-1999  (first entry)
XX
DE    Rat T-type voltage-gated Ca channel alpha-1-G (rCaVT1c).
XX
KW    Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW    activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS    Rattus sp.
XX
PN    WO9929947-A1.
XX
PD    17-JUN-1999.
XX
PF    30-OCT-1998;     98WO-US023161.
PR    05-DEC-1997;     97US-00985809.
XX
PA    (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI    Perez-Reyes E, Cribbs LL;
XX
DR    WPI; 1999-394972/33.
DR    N-PSDB; AAX83487.
XX
PT    New T-type voltage-gated calcium channels.
XX
PS    Disclosure; Page 85-94; 138bp; English.
XX
CC    This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC    alpha-1-G designated rCaVT1c. Voltage gated channels are membrane bound
CC    glycosylated proteins formed of several subunits. The large alpha
CC    subunits form a pore in the membrane that is selective for a given ionic
CC    species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC    each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC    -type Ca channels are activated at a lower voltage than L- or N-type
CC    channels. Characteristics of T-type channels include short current time,
CC    slow activation kinetics near threshold, fast inactivation kinetics and
CC    slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC    voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC    -channels contains a putative IVS4 region comprising the amino acid
CC    sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC    channel proteins can be used to screen for drugs which affect calcium
CC    channels. Methods are also disclosed for treating a disease or disorder
CC    associated with a deficiency in a native T-type calcium channel nucleic
CC    acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ    Sequence 2272 AA;

Query Match             91.8%;  Score 10925;  DB 2;  Length 2272;
Best Local Similarity   91.7%;
Matches 2106;  Conservative 33;  Mismatches 103;  Indels 54;  Gaps 6;

Qy      1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
           ||||||||||||||||||||:|||||||:|||||||||||||||||||||||||||||||
Db      1  MDEEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy     61  FFYLSQDSRPRSWCLRTVCNPWFERISMIVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
           ||||||||||||||||||||||||||:|||:|||||||||||||:|||||||||||||||
Db     61  FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy    121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy    181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy    241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
           ||||||||||||:|||||||||||||||||||||||||||||||||||||||:||||:||
Db    241  CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL 300

Qy    301  DYEAYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  DYETYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy    361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420
           |||||||||||||:||||||||:||||||||||||||||||||||||||||||||||||
Db    361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Qy    421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
           |||||||||||||||||||||:||||||||||||||||||:|||||||||||||||||||
Db    421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG 480

Qy    481  SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
           ||:||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db    481  SCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy    541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
           |||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db    541  TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy    601  TLKEKALVEVAASSGGPPTLTSLNIPPGPYYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
           ||:||:||||||||||||||:||||||||||||||||||||||||||:|||||||||||||
Db    601  ILKDKALVEVAPSGGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 660

Qy    661  ACGPDSCPYCARAGAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSLGPD 719
           ||||||||||||:|||||||||||||||||||||||||||||||||||||||: |||||||
Db    661  ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRRQRSIGPD 720

Qy    720  AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780

Qy    780  IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLM 839
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLM 840

Qy    840  RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDT 899
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDT 900

Qy    900  LPDRKNFDSLLWAIVTVVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  LPDRKNFDSLLWAIVTVVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 960

Qy    960  VAIIVEGFQAEISKREDASGQLSCIQLPVDSQQGDANKSESEPDFFSPLDGGDRKKC 1019
           ||||||||||
Db    961  VAIIVEGFQAE------------------------------------------------GDATKSESEPDFFSPSVDGDGDRKKR 997

Qy   1020  LALVSLGEHPELRKSLLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
           |||:|||||:|||||||||||||||||||:|||||:||||||:||||||||||||||||
Db    998  LALVALGHAELRKSLLPLIIHTAATPMSHPKSSSTGVGEALGSGSGSRRTSSSGSAEPGA 1057

Qy   1080  A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
           |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058  AHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1117

Qy   1139  SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTIQVPGLHRTASGRGSASEHQD 1198
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||:|
Db   1118  SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTIQVPGLHRTASGRGSASEHQD 1177

Qy   1199  CNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACVLERDSWSAYI 1258
           |||||||||||||||||::|||||::|||||||||||||||||||||:||::|||||||||
Db   1178  CNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERRQAWVRSRLPACCRERDSWSAYI 1237
```

```
RESULT 13
AAB66475
ID   AAB66475 standard; protein; 2287 AA.
XX
AC   AAB66475;
XX
DT   09-APR-2001  (first entry)
XX
DE   Rat alpha-IG calcium channel protein.
XX
KW   Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW   hypotensive; cardiant; nootropic; T-type calcium channel subunit;
KW   cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW   epilepsy; alpha-IG calcium channel.
XX
OS   Rattus sp.
XX
PN   WO20102561-A2.
XX
PD   11-JAN-2001.
XX
PF   04-JUL-2000; 2000WO-CA000794.
XX
PR   02-JUL-1999; 99US-00346794.
XX
PA   (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI   Snutch TP, Baillie DL;
XX
DR   WPI; 2001-123111/13.
DR   N-PSDB; AAF31677.
XX
PT   Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT   cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT   epilepsy.
XX
PS   Disclosure; Page 63-72; 103pp; English.
XX
CC   The present sequence is given in a specification providing sequences and
CC   partial sequences for three types of mammalian (human and rat) T-type
CC   calcium channel subunits. An expression cassette has been generated which
CC   comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC   subunit operably linked to control sequences to effect its expression.
CC   The novel calcium channel nucleic acids and proteins are useful for
CC   treating conditions characterised by undesirable levels of T-type calcium
CC   channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC   hypertension, sleep disorder and epilepsy.
XX
SQ   Sequence 2287 AA;

Query Match             90.5%;  Score 10774;  DB 4;  Length 2287;
Best Local Similarity   92.3%;  Pred. No. 0;
Matches 2075;  Conservative 33;  Mismatches 105;  Indels 36;  Gaps 6;
```

```
Qy   1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCTTIAMERPKIDPHSAERIFLTLSNYIFT 1318
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCTTIAMERPKIDPHSAERIFLTLSNYIFT 1297

Qy   1319 AVFLAEMTVKVVALGWCFGEQAYIRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1378
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 AVFLAEMTVKVVALGWCFGEQAYIRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1357

Qy   1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417

Qy   1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1477

Qy   1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK 1558
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK 1537

Qy   1559 RLRRLEKKRR---------------------KAQCKPYYSDYSRFRLLVHHLCTSH 1593
          ||||||||||                     :||||||||||||||||||||||||
Db   1538 RLRRLEKKRRSKEKQMADLMLDDVIASGSSASAAASEAQCKPYYSDYSRFRLLVHHLCTSH 1597

Qy   1594 YLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFF 1653
          |||||||||||||||||||||||||||||||||||||||||:||| :||||||||||||
Db   1598 YLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFEESVFKLVAFGFRRFF 1657

Qy   1654 QDRWNQLDLAIVLLSIMGITILEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRA 1713
          ||||||||||||||||||||||||||||| :||||||||||||||||||||||||||||
Db   1658 QDRWNQLDLAIVLLSIMGITILEEIEVNSLPINPTIIRIMRVLRIARVLKLLKMAVGMRA 1717

Qy   1714 LLDTVMQALPQVGNIGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMA 1773
          ||:|||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db   1718 LLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMA 1777

Qy   1774 FLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM 1833
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778 FLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM 1837

Qy   1834 KHLEESNKEAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGPDSPDSPKPGALHP 1893
          |||||||||||||||||||||||||||||||||||||||||| : ||||:||||||:||
Db   1838 KHLEESNKEAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVNSTDSPKPGAPHT 1897

Qy   1894 AAHARSASHFSLEHPTMQHPTELP---GPDLLITVRKSGVSRTHSLPNDSYMCRHGSTAE 1950
          :||  ||:|||||||||:||| |   |||||:|||||||||||||||||||||||:||||
Db   1898 TAHIGAASGFSLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAE 1957

Qy   1951 GPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPG 2010
          ||||||||||||||||:|||||||||||||||||||||  :|||||:||||||||||||
Db   1958 RSLGHRGWGLPKAQSGSLLSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPG 2017

Qy   2011 RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPPPLARAYSFWGQSSTQAQQHS 2070
          ||||||||||||||||||||||||||||||||:||||| : |||||: ||:|| |||:|
Db   2018 RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLIRSSSFWGGSSIQVQQRS 2077

Qy   2071 RSHSKISKHMTPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPR 2130
          ::||:|||:  |||||| || ||| ||||||||||||||||||||||  ||:|||: ||
Db   2078 GIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPR 2136

Qy   2131 DLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSSQPHLGTDPSNLGGQPLGGPGSR 2190
          |||:||||| ||:|||| |||||||||||||||||||||||:| ||| ||||||||||||
Db   2137 DLKNCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSSQPRLCPSPSSLGGQPLGGPGSR 2196

Qy   2191 PKKKLSPPSITITDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKD 2250
          ||||||||||:| |||||||  | | ||:|||||| ||||||| ::  |  | ||||||||
Db   2197 PKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTRAASPSPKKD 2256

Qy   2251 VLSLSGLSSDPADLDP 2266
          :||||||||||:|:||
Db   2257 TLSLSGLSSDPTDMDP 2272
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                                                     Gaps 6;

Qy     30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISML 89
             || |:||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db     62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121

Qy     90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181

Qy    150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDTLP 209
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRAINRVPSMRILVTLLLDTLP 241

Qy    210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPF 269
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301

Qy    270 ICSQPRENGMRSCRSVPTLRGDGSGGGPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHN 329
          ||||||||||| |||||:|||||:|||||||||||||:|||::|||||||| ::|||||:
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Db  302  ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN  361
Qy  330  PFKGAINFDNLGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLLIVGSFFMINL  389
Db  362  PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLLIVGSFFMINL  421

Qy  390  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR  449
Db  422  CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR  481

Qy  450  RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHIHHHHYHLGN    509
Db  482  RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHYHLGN   541

Qy  510  GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ  569
Db  542  GTLRVPRASPEIQDRDANGSRRIMLPPPSTPTPSGGEPRGAESVHSFYHADCHLEPVRCQ  601

Qy  570  APPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY  629
Db  602  APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF  661

Qy  630  SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD  689
Db  662  SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD  721

Qy  690  SEAVYEFTQDAQHSDLRDPHS-RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG  748
Db  722  SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG   781

Qy  749  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYN  808
Db  782  IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVVGPFGYIKNPTN  841

Qy  809  IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  868
Db  842  IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF  901

Qy  869  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV  928
Db  902  CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV  961

Qy  929  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIIVEGFQAEEISKREDASGQLSCIQLP  988
Db  962  LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIIVEGFQAE------------------ 1003

Qy  989  VDSQGGDANKSESEPDFFSPSLDGGDGDRKKLALVSLGEHPELRKSLLPPLIIHTAATPM 1048
Db 1004  ----GDATKSESEPDFFSPSVDGDGDRKKRLALAVALGEHAELRKSLLPPLIIHTAATPM 1058

Qy 1049  SLPKSTSTGLGEALGPASRRTSSSGAEPGAA-HEMKSPFSARSSPHSPWSAASSWTSRR  1107
Db 1059  SHPKSSSTGVGRALGSGSGRRTSSSGSAEPGAAHHEMKCPFSARSSPHSPWSAASSWTSRR 1118

Qy 1108  SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESGDEEESSEEERASPAGSDHRHRGSLERE 1167
Db 1119  SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESGDEEESSEEDRASPAGSDHRHRGSLERE 1178

Qy 1168  AKSSFDLPDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPLDGDDADDE  1227
Db 1179  AKSSFDLPDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARTLRTDDPQLDGDDNDH  1238

Qy 1228  GNLSKGERVRAWIRARLPACYLRDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIF   1287
Db 1239  GNLSKGERIQAWRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVLVIIF   1298

Qy 1288  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347
Db 1299  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1358

Qy 1348  VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1407
Db 1359  VLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMS 1418


Qy 1408  SLKPIGNIVVICCAFFIFGIIGVQLFKGKFFVCQGEDTRNITNKSDCAEEASYRWVRHKY 1467
Db 1419  SLKPIGNIVVICCAFFIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEEASYRWVRHKY 1478

Qy 1468  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGDQQPIMNHNPWMLLYFISFLLIVAFF  1527
Db 1479  NFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGDQQPIMNHNPWMLLYFISFLLIVAFF  1538

Qy 1528  VLNMFVGVVVENFHKCRQHQEEEARRREKRLRRLEKKR-------KAQCKPYYSDYS   1580
Db 1539  VLNMFVGVVVENFHKCRQHQEEEARRREKRLRRLEKKRRSKEKQMAEAQCKPYYSDYS  1598

Qy 1581  RFRLLVHHLCTSHYLDLFITGVIGLNVTMAMEHYQQPQILDEALKICNYIFTVIFVLES  1640
Db 1599  RFRLLVHHLCTSHYLDLFITGVIGLNVTMAMEHYQQPQILDEALKICNYIFTVIFVFES  1658

Qy 1641  VFKLVAFGPRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIAR  1700
Db 1659  VFKLVAFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRMRVLRIAR  1718

Qy 1701  VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG 1760
Db 1719  VLKLLKMAVGMRALLNTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG 1778

Qy 1761  LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTA 1820
Db 1779  LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTA 1838

Qy 1821  QFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGP 1880
Db 1839  QFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGV 1898

Qy 1881  DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLP 1937
Db 1899  NSTDSPKPGAPHTTAHIGAAGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP  1958

Qy 1938  NDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYIILQLPKDAPHLLQPHSA 1997
Db 1959  NDSYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGA  2018

Qy 1998  PTWGTIPKLPPPGRSPLAQPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPLARAYS   2057
Db 2019  PTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSS  2078

Qy 2058  FWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDL  2117
Db 2079  FWGGSSSTQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDL 2138

Qy 2118  LPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPS  2177
Db 2139  L-PSSQEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPS  2197

Qy 2178  NLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGP 2237
Db 2198  SLGGQPLGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSP 2257

Qy 2238  PDSMAASPSPKKDVLSLSGLSSSDPADLDP 2266
Db 2258  LDSTAASPSPKKDTLSLSGLSSSDPTDMDP 2286
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KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1; MINT31;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; Klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 4; SDC1; SDC4;
KW   chromosome 17.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999; 99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
DR   N-PSDB; AAS01624.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 9; Fig 3B; 125pp; English.
XX
CC   The present sequence representing a novel human T-type calcium channel
CC   CACNA1G maps to chromosome 17. The methylation state of specific regions
CC   within CpG islands associated with the CACNA1G gene correlate with
CC   several cancerous phenotypes involving various tissue and cell types.
CC   Since aberrant methylation of normally unmethylated CpG islands is often
CC   observed in immortalised and transformed cells, CACNA1G is implicated in
CC   cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast
CC   and other cancers. The nucleic acid coding for CACNA1G is useful as a
CC   marker for screening cancer and age related diseases. A diagnostic kit
CC   containing primers (AAS01574-AAS01623) for amplification of a CpG-
CC   containing nucleic acid, where the primer hybridises with a target
CC   polynucleotide sequence (AAS01627-AAS01676), can be used for detecting
CC   aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are
CC   selected from genes encoding CACNA1G, apolipoprotein B (APOB), caudal
CC   type homeobox transcription factor 2 (CDX2), epidermal growth factor
CC   receptor (EGFR), fibrillin-1 (FBN1), G protein-coupled receptor 37
CC   (GPR37), heat shock 70kD protein 6 (HSP70B', HSPA6), RasGAP-related
CC   protein (IQGAP2), klotho (KL), proteinase-activated receptor 2 (PAR2),
CC   paired-like homeodomain transcription factor 2 (PITX2), patched A and B
CC   (PTCHA, PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT 31 sequence
XX
SQ   Sequence 1207 AA;


Query Match           53.1%;   Score 6315.5;   DB 4;   Length 1207;
Best Local Similarity 98.1%;   Pred. No. 0;
Matches 1207;  Conservative  0;   Mismatches  0;   Indels  23;   Gaps  1;

Qy      1 MDEEEDGAGAEESSQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEABGLPYPALAPVV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDEEEDGAGAEESSQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEABGLPYPALAPVV 60

Qy     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Qy    301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy    361 YFVMDAHSFYNFIYPILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YFVMDAHSFYNFIYPILLIIVGSFFMINLCLVVIATQFSETKQRSQLMREQRVRFLSNA 420

Qy    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGGQETQPSS 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGGQETQPSS 480

Qy    481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKYPTVHTSPPPE 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKYPTVHTSPPPE 600

Qy    601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKKLLETQSTGACQSSCKISSPCLKADSG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKKLLETQSTGACQSSCKISSPCLKADSG 660

Qy    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy    721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780

Qy    781 VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMR 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMR 840

Qy    841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDTL 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDTL 900

Qy    901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYLFNLLV 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYLFNLLV 960

Qy    961 AILVEGFQAEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
          |||||                   ------|||||||||||||||||||||||||||||
Db    961 AILVEGFQAE--------------------GDANKSESEPDFFSPSLDGDGDRKKCL 997

Qy   1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057

Qy   1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRRSNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 HEMKSPPSARSSPHSPWSAASSWTSRRSSRRSNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117

Qy   1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1177

Qy   1201 GKSASGRLARALRALRPDDPPLDGDADDEGNL 1230
          |||||||||||||||||||||||||||||||
Db   1178 GKSASGRLARALRALRPDDPPLDGDADDEGNL 1207
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RESULT 15
AAB66476

```
ID   AAB6476 standard; protein; 2359 AA.
XX
AC   AAB6476;
XX
DT   09-APR-2001 (first entry)
XX
DE   Rat alpha-1H calcium channel protein.
XX
KW   Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW   hypotensive; cardiant; nootropic; T-type calcium channel subunit;
KW   cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW   epilepsy; alpha-1H calcium channel.
XX
OS   Rattus sp.
XX
PN   WO200102561-A2.
XX
PD   11-JAN-2001.
XX
PF   04-JUL-2000; 2000WO-CA000794.
XX
PR   02-JUL-1999; 99US-00346794.
XX
PA   (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI   Snutch TP, Baillie DL;
XX
PN   WPI; 2001-123111/13.
DR   N-PSDB; AAF31678.
XX
PT   Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT   cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT   epilepsy.
XX
PS   Disclosure; Page 75-85; 103pp; English.
XX
CC   The present sequence is given in a specification providing sequences and
CC   partial sequences for three types of mammalian (human and rat) T-type
CC   calcium channel subunits. An expression cassette has been generated which
CC   comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC   subunit operably linked to control sequences to effect its expression.
CC   The novel calcium channel nucleic acids and proteins are useful for
CC   treating conditions characterized by undesirable levels of T-type calcium
CC   channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC   hypertension, sleep disorder and epilepsy
XX
SQ   Sequence 2359 AA;

Query Match      52.2%;  Score 6218;  DB 4;  Length 2359;
Best Local Similarity   56.4%;  Pred. No. 0;
Matches 1369;  Conservative 228;  Mismatches 509;  Indels 322;  Gaps 62;


Qy      2  DEEEDGAGAEESGQPRSFMRLNDLS-GAGGRP---GPGS---AEKDPGS---AD---SEA   48
                                   :  | | ||
Db      9  DEVRVPLGASPPA-PAAPVRASPASPGAPGREEQGSGSGGVLAPESPGTECGADLGADEE   67

Qy     49  EGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIA  108
                |||||||| ||| | ||  ||||||| ||||||| :|||||:||||||||||||||| :
Db     68  QPVPYPALAATVFFCLGQTTRPRSWCLRIVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVE  127

Qy    109  CDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYS  168
                :| || ||:|||||||||||||||:||||||:||:|||||||||||||||:|||:|||
Db    128  CRSERCSILEAFDDFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVMAGMMEYS  187

Qy    169  LDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIV  228
             ||  |:| |:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    188  LDGHKVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIV  247

Qy    229  GVQLWAGLLRNRCFLPENFSLPLSVD-LERYYQTENEDESPFICSQPRENGMRSCRSVPT  287
            ||||||||||||||: :  ::| ||  |||||| |  ||:|||| |  :|||: :| | |
Db    248  GVQLWAGLLRNRCFIDSAFVRNNNLITFLRPYYQTEEGEENPFICSSRRDNGMQKCCHIPS  307

Qy    288  --LRGDGGGGPPCGLDYEAY------NSSSNTTCVNWNQYYTNCSAGEHNPFKGAINF  337
              | |       |  :| ||      | :||  || |||| ||||:|| || :|||||
Db    308  RRELR------VQCTLGWEAYGQPQAEDGGAGRNACINWNQYNVCRSGEFNPHNGAINF  361

Qy    338  DNIGYAWTAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQ  397
            |||||||||||||||||||||||| |||||||||||||||||:|||||||||||||||||
Db    362  DNIGYAWTAIFQVITLEGWVDIMYVVMDAHSFYNFIYFILLIIMGSFFMINLCLVVIATQ  421

Qy    398  FSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKLYLVYILRKAARRLAQVSRA  457
            ||||||||.||||.||.|:|||:||||||||||||||||||:|| :||||.|||:|. : |
Db    422  FSETKQRENQLMRRQRARYLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLYAR   481

Qy    458  AGVRVGLLSSP-APLGGQETQPSSCSRSHRR-LSVHHLV-HHHHHHHYHLGNGTLRA     514
              ::    :.. ||:::::|: :: | ||    |||:|| |||||||||: ::| :|
Db    482  WQSRWRKKVDPSSTVHGQ--GPGRPRRAGRRTASVHHLVYHHHHHHYHHFSHGGPRR     539

Qy    515  PRASPEIQDRDANGSRRLM--LPPPSTPALSGAPPGGAGSVHSFYHADCHLEPVRCQAPP  572
            |    |   |. .| ||:   ||.|| |    |.| | :|:|| :|||||.|  : : |.
Db    540  P--SPE----PGAGDNRLVRACAPPSPGPGHGPP-DSESVHSIYHADCHVEGPQBRARV   592

Qy    573  PRSPSEASGRTVGSG---KVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIP----  625
             : .:.||   :.:|   :  |||: .::  | | |.|:::  .||| : :.| :|
Db    593  AHSIATAASLKLASGLGTMNYPTI---LPSGTVNSKG----GTSSRPKGLRGAGAPGAAV  645

Qy    626  ------PGPYSSMHKLLETOSTGACQS------SCKISSPCLKADSGACGPDSCPYC    670
                  | | |  :|:| :|||| || |      || ||||||.:|.|| |.|:|||||
Db    646  HSPLSLSGSPRPYEKIQDVVGEQGLGRASSHLSGLSVPCPLPSP--QAGTLTCELKSCPYC  703

Qy    671  ARA-GAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDP------HS--RRQRSL     716
            | | . .| :| |||| || ||| |:|||| :|.|.|||      ||  ||||: |
Db    704  ASALEDPEFEFSGGSESGDSDAHGVYEFTQDVRHGDCRDPVVQPHEVGTPGHSNERRRTPL  763

Qy    717  GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALE   776
              .|: ||:. |   .:  :.|:||||||| |||||:||||||||:|||||||||||||
Db    764  RKASQPGGIGHIWASFSGKLRRIVDSKYFNRGIMAAILVNTLSMGVEYHEQPEELTNALE  823

Qy    777  ISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTF   836
            |||||||| ||||||||||:  ||:|||:||||||||:||||||||||  . :.|||||
Db    824  ISNIVFTSMFALEMLLKLLLACGPLGYIRNPYNIFDGIVVVISWEIVGVGQADGGQSVLRTF 883

Qy    837  RLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLMLFIFIFSILGMHLFGCKFASRD    896
            ||:|||||||||||| |||||||:|||||||||||||||||||||||||||||||: |
Db    884  RLLRVLKLVRFLPALRRQLVVLMRTMDNVATFCMLMLFIFIFSILGMHLFGCKFSLKTD  943

Qy    897  -GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVL  955
             |||:|||||||||||||||||||||||||||.||||||||||||||||:|||||||||
Db    944  SGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGNYVL  1003

Qy    956  FNLLVAILVEGFQAEEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGD  1015
            |||||||||||||||               |. || .||     .||   :| |  ||
Db   1004  FNLLVAILVEGFQAE-----------GDAATRSDTDEDKTSTQLEGDFD            1040

Qy   1016  RKKCL------ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGLGEALGPAS     1066
                      :  ||.|| | |:||||| ||| |||||| | || |.|.  ||: |
Db   1041  KLRDLRATEMKMYSLAVTPNGHLEGRGSLPPPLITHTAATPMPTPKS-SPNLDVAHALLD  1099

Qy   1067  RRTSSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG  1126
            .|||||| .:| .  |: | |.|| |.| ||. .| | | . ||||||||||||||.  |
Db   1100  SRRSSSGSVDPQLG-DQKSLASLRSSPCTPWGPNSAGSSRRSWNSLGRAPSLKRRSQCG   1158

Qy   1127  ERRSLLSGEGOESODEEESEEERAS----------PAGSDHRHRGSLEREAKSSFDL--  1174
            || ||||||| .| .|| :.:    :          |||  .  |   |    : |
Db   1159  ERESLLSGEGKGSTDDE-AEDSRPSTGTHPGASPGPRATPLRAESLDH--RSTLDLCP   1214

Qy   1175  ----PDTLQVGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPPLLDGDDADDEGNL  1230
                |  . :. ..|.||.|   |||:| .:        |. | | |.. | |  .:
Db   1215  PRPAPPAVQV------HDCNGQMVALPSEFFLRIDSHKEDAAEFDDIED            1258

Qy   1231  SKGERVRAWIRARLPACYLERDSWSAYIPPQSRFRLLCHRIITHKMFDHVVLVIFLNC   1290
            | . : ||:|.| |..| ::|.||||| ||| |:|:  .:|:||||||||||.||||
Db   1259  SCCPRLHKVLEPYAPQWCRSRESWALYLFPPQNRLRVSCQKVIAHKMFDHVVLPIFLNC  1318

Qy   1291  ITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNLD  1350
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Db  1319 ITIALERPDIDPGSTERAFLSVSNYIFTAIFVVEMVKVVALGLLWGEHAYLQSSWNVLD 1378
Qy  1351 GLLVLISVIDILVSMVSDSGTKIIGMRLVLRLLRTLRPLRVISRAQGLKLVVETLMSSLK 1410
Db  1379 GLLVLVSLVDIIVAMASAGGAKIIGVLRVVRLLRTLRPLRVISRAPGLKLVVETLISSLR 1438
Qy  1411 PIGNIVVICCAFFIIFGILGVQLFKGKFYVCQGEDTRNITNKSDCAEASYRWVRHKYNFD 1470
Db  1439 PIGNIVLICCAFFIIFGILGVQLFKGKFYYCEGTDTRNITTKAECHAAHYRWVRRKYNFD 1498
Qy  1471 NLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLN 1530
Db  1499 NLGQALMSLFVLSSKDGWVNIMYDGLDAVGIDQQPVQNHNPWMLLYFISFLLIVSFFVLN 1558
Qy  1531 MFVGVVVENFHKCRQHQEEEARRREEKRLREKKRRKAQCKPYYSDYSRFLLVHHLC 1590
Db  1559 MFVGVVVENFHKCRQHQEAEEARRREEKRLRLERRRRKAQRRPYYADYSHTRRSIHSLC 1618
Qy  1591 TSHYLDLFITGVIGLNVVTMAMEHYQQPQIDEALKICNYIFTVIFVLESVFKLVAFGFR 1650
Db  1619 TSHYLDLFITFIICLNVTMSMHYNQPKSLDEALKYCNYVFTIVFVEAAALKLVAFGFR 1678
Qy  1651 RFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVG 1710
Db  1679 RFFKDRWNQLDLAIVLLSIMGIALEEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATG 1738
Qy  1711 MRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNF 1770
Db  1739 MRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFTNF 1798
Qy  1771 GMAFLTLFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNV 1827
Db  1799 GMAFLTLFRVSTGDNWNGIMKDTLRECTREDKHCLSYLPALSPVYFVTFMLVAQFVLVNV 1858
Qy  1828 VIAVLMKHLEESNKEAKEEABLEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPK 1887
Db  1859 VVAVLMKHLEESNKEAREDAEMDAEIELEM 1888

Qy  1888 PGALHPAAHARSASHFSLEHPTMQPHPT--ELPG----PDLLTVRKSGVSRTHSLPNDS 1940
Db  1889 AQGSTAQPPPTAQESQGTQPDTPNLLVVRKVSVSRMLSLPNDS 1931
Qy  1941 YMCRHGSTAEGPLGHRGWGLP------KAQGSVLSVHSQPADTSYILQLPKDAPHLLQP 1994
Db  1932 YMFRPVAPAAAPHSH----PLQEVEMETYTGPVTSAHSPPLEPRASFQVPSAA------ 1980
Qy  1995 HSAPTWGTIP--KLPPPG--RSPLAQRPLRRQAAIRTDSLD--VQGLGSREDLLAEVSGP 2048
Db  1981 -SSPARVSDPLCALSPRGTPRSLSLSRILCRQEAMHSESLEGKVDDVGG--DSIPDYTEP 2037
Qy  2049 SPPLARAYSFWG--------QSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPP 2098
Db  2038 AENMSTSQASTGAPRSPPCSPRPASVRTRKHTFGQRCISSR--PPT----LGGD 2085
Qy  2099 ETRSSLELDTELSWISGDLLP----PGGQEEPP----------SPRDLKKCYSVEAQSC 2143
Db  2086 EAEAADPADEEVSHITSSAHPWPATEPHSPEASPTASPVKGTMGSGRDPRRFCSVDAQSF 2145
Qy  2144 QRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGQQPLG-----GPGSRPKKKLS 2196
Db  2146 LDKP-GRPDAQRWSSVE---LDNG-ESHLES-----GEVRGRASELEPALGSRRKKKMS 2194
Qy  2197 PPSITIDPP-ESQGPRTPPSP--GICLRRRAPSDSK------------DPLASG 2236
Db  2195 PPCISIEPPTKDEGSSRPPAAEGGNTTLRRRTPSCEAALHRDCPEPTEGPGTGGDPVAKG 2254
Qy  2237 PPDSMAASPSPPKKDVLSLSGLSSDPADL 2264
Db  2255 ERWGQA---SCRAEHLTVPNFAFEPLDM 2279
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Job time : 197.635 secs

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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.3132 Seconds
                                 (without alignments)
                                 3727.727 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5	Sequence 5, Appli
2	6315.5	53.1	1207	3	US-09-398-522-52	Sequence 52, Appl
3	6211	52.2	2353	3	US-08-984-709A-50	Sequence 50, Appl
4	5492.5	46.1	2175	4	US-09-404-650-2	Sequence 2, Appli
5	5492.5	46.1	2175	4	US-09-935-541-2	Sequence 2, Appli
6	5484	46.1	2188	3	US-09-404-650-4	Sequence 4, Appli
7	5484	46.1	2188	4	US-09-935-541-4	Sequence 4, Appli
8	5366	45.1	1835	3	US-09-404-650-5	Sequence 5, Appli
9	5366	45.1	1835	4	US-09-935-541-5	Sequence 5, Appli
10	1750.5	14.7	2343	3	US-09-268-163-4	Sequence 4, Appli
11	1749	14.7	2337	3	US-08-711-118-2	Sequence 2, Appli
12	1749	14.7	2337	3	US-09-452-007-2	Sequence 2, Appli
13	1748.5	14.7	2339	3	US-08-455-543A-47	Sequence 47, Appl
14	1748.5	14.7	2339	2	US-08-223-305C-47	Sequence 47, Appl
15	1746.5	14.7	2339	3	US-09-268-163-6	Sequence 6, Appli
16	1743	14.6	2237	1	US-08-455-543A-48	Sequence 48, Appl
17	1743	14.6	2237	3	US-08-223-305C-48	Sequence 48, Appl
18	1741	14.6	2237	3	US-09-268-163-8	Sequence 8, Appli
19	1722	14.5	2336	3	US-09-268-163-10	Sequence 10, Appli
20	1632.5	13.7	1873	1	US-08-435-675B-4	Sequence 4, Appli
21	1622.5	13.6	1873	3	US-08-336-257A-7	Sequence 7, Appli
22	1619.5	13.6	1984	3	US-08-836-325-10	Sequence 10, Appl
23	1619.5	13.6	1984	4	US-09-457-571-10	Sequence 10, Appl
24	1619.5	13.6	1985	4	US-09-495-714C-6	Sequence 6, Appli
25	1616	13.6	1872	6	5386025-6	Patent No. 5386025
26	1615.5	13.6	1989	3	US-08-836-325-12	Sequence 12, Appl
27	1615.5	13.6	1989	4	US-09-457-571-12	Sequence 12, Appl
28	1607.5	13.5	2516	3	US-08-374-077C-2	Sequence 2, Appli
29	1607.5	13.5	2516	3	US-08-895-590-2	Sequence 2, Appli
30	1607.5	13.5	2516	4	US-09-539-879A-2	Sequence 2, Appli
31	1601	13.4	1977	4	US-09-495-714C-4	Sequence 4, Appli
32	1601	13.4	2509	2	US-08-149-097D-35	Sequence 35, Appl
33	1587	13.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
34	1587	13.3	2016	4	US-09-896-994-2	Sequence 2, Appli
35	1586	13.3	1969	3	US-08-836-325-16	Sequence 16, Appl
36	1586	13.3	1969	4	US-09-457-571-16	Sequence 16, Appl
37	1586	13.3	2016	3	US-09-634-920-4	Sequence 4, Appli
38	1586	13.3	2016	4	US-09-840-125-4	Sequence 4, Appli
39	1583	13.3	1977	4	US-09-976-594-757	Sequence 757, App
40	1583	13.3	1977	4	US-09-919-039-367	Sequence 367, App
41	1573.5	13.2	1912	4	US-09-495-714C-2	Sequence 2, Appli
42	1569.5	13.2	1968	1	US-08-455-543A-45	Sequence 45, Appl
43	1569.5	13.2	1968	2	US-08-223-305C-45	Sequence 45, Appl
44	1560.5	13.1	2161	1	US-08-455-543A-51	Sequence 51, Appl
45	1560.5	13.1	2161	2	US-08-223-305C-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match   99.7%; Score 11862.5; DB 3; Length 2273;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 2260; Conservative 4; Mismatches 4; Indels 2; Gaps 7;

Qy   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TVRVLRFLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy   241 CFLPENFSLPLSVDLERYYQTENEDESPICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CFLPENFSLPLSVDLERYYQTENEDESPICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300

Qy   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

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 361 Qy YFVMDAHSFYNFIYFLLLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 361 Db YFVMDAHSFYNFIYFLLLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

 421 Qy STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 421 Db STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480

 481 Qy SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 481 Db SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

 541 Qy ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 541 Db ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

 601 Qy TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 601 Db TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

 661 Qy ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 661 Db ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

 721 Qy EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 721 Db EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780

 781 Qy VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMR 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 781 Db VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMR 840

 841 Qy VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 841 Db VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900

 901 Qy PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 901 Db PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960

 961 Qy AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 961 Db AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020

1021 Qy ALVSLGEHPELRKSLLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 Db ALVSLGEHPELRKSLLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080

1081 Qy HEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQSQ 1140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 Db HEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQSQ 1140

1141 Qy DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
        | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 Db DQEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200

1201 Qy GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
1201 Db GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP 1260

1261 Qy PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 Db PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320

1321 Qy FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 Db FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380

1381 Qy RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1381 Db RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
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1441 Qy CQGEDTRNITNKSDCAEAASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1441 Db CQGEDTRNITNKSDCAEAASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500

1501 Qy VDQQPIMNHPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1560
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 Db VDQQPIMNHPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL 1560

1561 Qy RRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1613
        ||||||||      :|||||||||||||||||||||||||||||||||||||||||||
1561 Db RRLEKKRRSKEKQMAFAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1620

1614 Qy HYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGIT 1673
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
1621 Db HYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGIP 1680

1674 Qy LEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFM 1733
        ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 Db LEQIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFM 1740

1734 Qy LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 Db LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1800

1794 Qy LRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKERAELEAEL 1853
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 Db LRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKERAELEAEL 1860

1854 Qy ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAAHARSASHFSLEHPTMQPH 1913
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 Db ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAAHARSASHFSLEHPTMQPH 1920

1914 Qy PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1973
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 Db PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1980

1974 Qy QPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQ 2033
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1981 Db QPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQ 2040

2034 Qy GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNW 2093
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2041 Db GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNW 2100

2094 Qy GKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2153
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2101 Db GKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2160

2154 Qy QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP 2213
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2161 Db QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP 2220

2214 Qy PSPGICLRRRAPSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
2221 Db PSPGICLRRRAPSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2273
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RESULT 2
US-09-398-522-52
; Sequence 52, Application US/09398522
; Patent No. 6783933
;
; GENERAL INFORMATION:
;
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1207
; TYPE: PRT

us-09-611-257a-37.rai

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;
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CACNA1G - a gene ecoding a T-type calcium channel
US-09-398-522-52

Query Match             53.1%;  Score 6315.5;  DB 4;  Length 1207;
Best Local Similarity   98.1%;  Pred. No. 0;
Matches 1207;  Conservative    0;  Mismatches    0;  Indels   23;  Gaps    1;

Qy      1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120

Qy    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Qy    301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy    361 YFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480

Qy    481 SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy    601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKISSPCLKADSG 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKISSPCLKADSG 660

Qy    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy    721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780

Qy    781 VFTSLFALEMLKLLVGFPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 VFTSLFALEMLKLLVGFPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR 840

Qy    841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERDGDTL 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERDGDTL 900

Qy    901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
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Qy    961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDRKKCL 1020
            ||||||||||
Db    961 AILVEGFQAE------------------------------GDANKSESEPDFFSPSLDGDRKKCL 997

Qy   1021 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLEALGPASRRTSSSGSAEPGAA 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 ALVSLGEHPELRKSLLPPLIHTAATPMSLPKSTSTGLEALGPASRRTSSSGSAEPGAA 1057

Qy   1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117

Qy   1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1177

Qy   1201 GKSASGRLARALRPDDPPLDGDDADDEGNL 1230
            |||||||||||||||||||||||||||||
Db   1178 GKSASGRLARALRPDDPPLDGDDADDEGNL 1207
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RESULT 3
US-08-984-709A-50
; Sequence 50, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
;   APPLICANT: Williams, Mark E.
;   APPLICANT: Stauderman, Kenneth A.
;   APPLICANT: Harpold, Michael M.
;   TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;   TITLE OF INVENTION: METHODS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Heller Ehrman White & McAuliffe
;     STREET: 4250 Executive Square, Suite 700
;     CITY: La Jolla
;     STATE: California
;     COUNTRY: US
;     ZIP: 92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/984,709A
;     FILING DATE: 02-DEC-1997
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Seidman, Stephanie L.
;     REGISTRATION NUMBER: 33,779
;     REFERENCE/DOCKET NUMBER: 24735-9815  (formerly 6362-9815)
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 450-8400
;     TELEFAX: (619) 587-5360
;   INFORMATION FOR SEQ ID NO: 50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 2353 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: internal
;     ORIGINAL SOURCE:
US-08-984-709A-50

Query Match             52.2%;  Score 6211;  DB 3;  Length 2353;
Best Local Similarity   56.6%;  Pred. No. 0;
Matches 1365;  Conservative  214;  Mismatches  523;  Indels  310;  Gaps   60;

Qy      7 GAGAEESGQP-RSFMRLNDLSGAGGRPGPGSAEKDPGSADSRAEGLPYPALAPVVFFYLS 65
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 27  GASPESPGAPGREAERGSEL-GVSPSESP-AAERGAELGADEEQRVPYPALAATVFFCLG  84       Db
     |||     | |   |  :| :|||       ||||
1053 LKMCSLAVTPNGHLEGRGSLSPPLLMCTAATPMTPKSSPFLDAAPSLPDSRRGSSSSGD  1112

 66  QDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDFIF  125     Qy
     :|||||||||||||||||||||||||   |  |
1076 EPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSRNSIGRAPSLKRRSPSGERRSLLSGE  1135

 85  QTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVECGSERCNILEAFDAFIF  144    Db
     :|||| |||||||||||||| || |||||||||||||||||||  ||
1113 PP--LGDQKPPASLRSSPCAPWGPSGAWSSRRSWSSLGRAPSLKRRGQCGERESLLSGE  1170

126  AFFAVEMVKMVVALGIFGKKCYLGDTWNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVL  185     Qy
     ||||||||||||||||||||||||||||||||||||||||
1136 GQESQDEEESSEEERASPA--GSDHRHRGSLEREAKSSFDLEDTL--- QVPGLH---  1184

145  AFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVVAGMMEYSLDGHNVSLSAIRTVRVL  204   Db
     ||||||| :||| ||||||||||||||||||||| ||||||:|| ::||||||||||||
1171 GKGSTDDE--AEDGRAAPGPRATPLRRAESLDPRLRPAALPPTKCRDRDGQVVALPSDF  1228

186  RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVPFFIFGIVGQIWAGLLRNRCFLPE  245   Qy
     |||||| |||||||| ::| |||||||||||||||||||||||||||| ||||||||||
1185  -RTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRA  1242

205  RPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGQLWAGLLRNRCFLDS  264   Db
     ||||||||||||||| |||||||||||||||||||||||||||| |||||||||||
1229 FLRIDSHREDAAELDDDSEDSCCLRLHKVLEPYKP--- -QWCRS  1268

246  NFSLPLSVD-LERYYQQTENEDESPFICSQPRRENGMRSCRSVP---TLRGDGGGPCGLD  301   Qy
     :| :| |  |||||   |    |       |             :|
1243 RLPACYLERDSWSAYIFPPQSRFLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDP  1302

265  AFVRNNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHIPGRRELR---------  318   Db
     | ||||   ||   :|| : ||||::||  || |  ||:  |||||
1303 HSAERRIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDIL  1362

302  YEAYN------SSSNNTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLE  354   Qy
     ||    :||||||| |||||||||||||||||||||||||||||||
1321 GSTERVFLSVSNYIFTAIFVAEMMVKVVALIGLLSGEHAYLQSSWNLLDGLLVLSLVDIV  1380

319  WEAYTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE  378   Db
     ||:|  |    |     :||||||||:|  || |||||||||||||||||||||||||||
1363 VSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETIMSSLKPIGNIVVICCAF  1422

355  GWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMENLCLVVIATQFSETKQRESQLMREQRV  414   Qy
     ||:|||||||||||||||||| ||| |||||||| |||||||||||||||||||||||||
1381 VAMASAGGAKILGVIRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVVICCAF  1440

379  GWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRA  438   Db
     ||||||||||||||||||||||| |||||| ||||||||||||||||||| |||||
1441 FIIFGILGVQLFKGKFYYCEGPDTRNISTKAQCRAAHYRWVRRKYNFDNLGQALMSLFVL  1500

415  RFLSNASTLIASFSEPGSCYEELLKYLVVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQ  474  Qy
     ||| ||:|||||||||||||||||||| ||||: |    |    | | :: |  |
1483 ASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHK  1542

439  RHLSNDSTLIASFSEPGSCYEELLKYVGHIFRKVKRRSLRLYARWQSRWRKKVDPSAVQCSQ  498  Db
     ||::||||:|||||||||||||:||     ||         |  ||     ||| :||
1501 SSKDGWVNIMYDGLDAVGVDQQPVQNHNPWMLLYISFLLIVSFFVLNMFVGVVVENFHK  1560

475  ETQPSSSCCSRSHRR-LSVHHLV-HHHHHHHHHYHFHGNGTLRAPRASPEIQDRDANGSRRL  532  Qy
     :|           |    :|  |          |           | |       |
1543 CRQHQEEEARRREEKRLRRLEKKRR-----  1596

499  --GPGHRQPRRAGRHTASVHHLVYHHHHHHHHHHHHYHFSHGSPRRPGPEPGACD-----TRLIV  551  Db
      ||   :|      | :|          | |      | |         |       :||
1561 CRQHQFAEEARRREEKRLRRLERRRSTFPSPEAQRRPYAYDYSPTRRSIHSLCTSHYLD  1620

533  MLPPPSTPALSGAPPGGAESVHSFYHADCHLE--PVRCQAPPERSPSEASGR-TVGSGKV  589  Qy
     || |       | |         | |  | |     | |        |   | |||||
1597 LFITGVIGLNVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDR  1656

552  RAGAPPSPSPSPGRGPPDAESVHSIYHADCHIEGPQERARVAHAAATAAASLRLATGLGTM  611  Db
     |||  | | | |  |    |||||::|| | |||  |     |          | | | |
1621 LFITFIICVNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVEAALKLVAFGFRRFFKDR  1680

590  -YPTV--------HTSP------PPETLKEKALVEVAASSGPPTLTSLNIPPGPY  629   Qy
      | |        |  |       | |  |         |  | | |   | | ||
1657 WNQLDIAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLD  1716

612  NYPTILPSGVGSGKGSTSPGPKGKWAGGPPGT------GGHGPLSLNS---PDPY  657  Db
     | |  |   | | || ||||      |          | |||||||    |||
1681 WNQLDAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLD  1740

630  SSMHKLLETQSTGACQS------SCKISSPCLKADSGACGPDSCPYCARA-GAGEVELA  681  Qy
     || |||     |         || |     || | | | | | |     | | | |
1717 TVMQALPQVGNLGLLFMLLFFIFAAILGVELFGDLECDETHPCEGLGRHATFRNFGMAFLT  1776

658  EKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP--PAGTLTCELKSCPYCTRALEDEPEGELS  715  Db
     |   | | |  | | |      |  | |       |   | | | |        | |  |
1741 WNQLDAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLD  1800

682  DREMPDSDSRAVYEFTQDAQHSDLRDP------------HSRRQRSLGPDAEPSSV  725   Qy
     |  |   |  |           |             | | | | | | | |
1777 TVMQALPQVGNLGLLFMLLFFIFYAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLT  1800

716  GSESGSDSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGSPQRRAQQRAAPGEPGWM  775  Db
     | | | | | |      |  |             | |          |    |      |
1801 LFRVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPVYFVTFVLVAQFVLVNVVAVLM  1860

726  LAFWRLICIDTFRKIVDSKYFRGIMIAILVNTLSMGIEYHQPEELTNALEISNIVFTSL  785  Qy
     ||| | | | |   | |||||||| | || | | | | | | | || ||| |||||
1834 KHLEESNKEAKEAEELAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSP------  1890

776  GRLWLWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGVEYHQPEELTNALEISNIVFTSM  835  Db
     | ||  |  | |   | |||||: || | || | | | | | | || || ||| ||| |
1861 KHLEESNKEAREDAELDAEIELEM-------------  1899

786  FALEMLIKLIVVGPFGVIKNPYNIFDGVIVVISVWEIVGQGGGGLSVLRTFRLMRVLKLV  845  Qy
     ||| | || |  || |    | | | | | | ||| | |          |     | |
1891 LHPAAHARSASHFSLEHPTMQPHPTELPG------PDLLTVRKSGVSRTHSLPNDSYMCRHG  1946

836  FALEMLKLLACGPLGLYIRNPYNIFDGIIVVISVWEIVGQADGGGLSVLRTFRLLRVLKLV  895  Db
     |||| | |   || |   | | | | | | | ||| | | |          |     | |
1947 STAEGP------------ PLPQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV  1937

896  RFLPALQRQLVVLMKIMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRK  904  Qy
     |||| |   | ||   |  |   | || || |||| ||| |||  |      | | ||
1938 VPASAPHPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIP----LAVSSPA  1989

905  NFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILV  964  Db
     |||| | ||||||| | ||||| | || |||| | ||| || | || | | | | |
1990 RSGEPLHALSPRGTARSPSLSRLLCRQEAVHTDSLEGK-IDSPRDTLDPAEPGEKTPVRP  2048

956  NFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGNYVLFNLLIAILV  1015  Qy
     |||| | ||||||| | |||| | || |||| | ||| || | || | | | | | |
1998 PTWGTIPKLPPPG--RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLL-AEVSGPSP--P  2051

965  EGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGD------GD  1015  Qy
     |  | | |  | |        |       |          |           |
1990  LARAYSFWG-QSSTQAQCHSRSHSKISKHMTPPAP-CPGPEPNWGKGPPETRSSLELDT  2052

1016 EGFQAE-------- GDANRSDTDEDKTSVHFEEDFHKLRELQTTE  1052  Db
     |  | |       |   |         || ||  |  |  |  |
2052 LARAYSFWG-QSSTQAQCHSRSHSKISKHMTPPAP-CPGPEPNWGKGPPETRSSLELDT  2108

1016 RKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGGSA  1075  Qy
     |  |   |   |  || |    |                                   |
2049 VTQGGSLQSPPRSPRPASVRTKHT-FGQHCVSSRPAAPGGE  2099
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Qy  2109  ELSWISGDLLP------PGGQEEPP---SPRDLKKCYSVSRAQSCQRRPTSWLDERQRRHSI 2159
          ::|:|                 ||:|   :|||||||||||||||:  |:
Db  2100  EVSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGFLDKP-GRADEQWRPSA 2158

Qy  2160  AVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPP-ESQGPRTPPSP-- 2216
          :   :  :     |     :|:  | |||| ||||:||:| :  |||: :|:   ||:
Db  2159  ELGSGEPGEAKAWGPE-----AEP-ALGARRKKKMSPPCISVEPPAEDEGSARPSAAEG 2211

Qy  2217  -GICLRRRAPSSDSK----------DPLASGPPDSMAASPSPKKDVLSLSGLSS 2259
           | |||||:|:       |||||||| |:   |||||| :|:| ||:: :
Db  2212  GSTTLRRRTPSCEATPHRESLEPTEGSGAGGDPAAKGERWGQA---SCRAEHLTVPSFAF 2268

Qy  2260  DPADL-------DP 2266
          :|  |       ||
Db  2269  EPLDLGVPSGDP 2280
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RESULT 4
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R00443B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-2

Query Match   46.1%;   Score 5492.5;   DB 3;   Length 2175;
Best Local Similarity   51.3%;   Pred. No. 0;
Matches 1233;   Conservative 214;   Mismatches 508;   Indels 447;   Gaps 55;

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Qy    31  RPGPGSAEKDPGSADSEAEG---LPYPAIAPVVFFYLSQDSRPRSWCLRTVCNPWFERI 86
          :|||  : ||| ||        | :|:||  |||:||  :|:||||: ||||||||  |
Db    25  QPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIRMVCNPWFECV 84

Qy    87  SMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKC 146
          |||||||||||||| :||:|: || : |:|:|:|||||| |||:||| ||||||||||||
Db    85  SMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKC 144

Qy   147  YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLD 206
          |||||||||||||:|||::||||||||:: ||:||||||||:||||||||||||:|:||
Db   145  YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRIIVNLLLD 204

Qy   207  TLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLFPLSVDLERYYQTENEDE 266
          |||||||||||||||||||||||||||||||||||  |||::  | || | || |:|:|
Db   205  TLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLEENFTIQGDVALPPYYQPEEDDE 264

Qy   267  SPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL----DYEAYNSSSNTT--CVNWNQ 318
            |:||    |:|  ||  :     : ||     |:    | |::  |:    ||||||
Db   265  MPFFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR 321

Qy   319  YYTNCSAGEHNPFKGAINPDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL 378
          || :| :|  || |||||.|||||||::|||||||||||||||||||||||||||||||
Db   322  YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL 381

Qy   379  IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK 438
          |||||||||||||||||||||||||||  :||:||:|:|| : |||:::||| |||:::
Db   382  IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEEIFQ 440

Qy   439  YLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH 498
          |: :||||| :|     ||                ||: : :||||: :
Db   441  YVCHILRKAKR-----RALGLYQALQSRRQALG---------------------- 468
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Qy   499  HHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYH 558
                                              |||:  |:||:         |
Db   469  ------------------------------------PEAPA--PAKPGP---------H 480

Qy   559  ADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPT 618
          |                       :|:      : ::|:       |   |
Db   481  AK---EPRHYQLCPQHSPLDATPHTL---------------------VQPIPATL 511

Qy   619  LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR------ 672
                                            :|:|:  |  ||  |  |: |:
Db   512  -----------------------------ASDPASCPCCQHEDGRRP 529

Qy   673  AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL------ 726
          :| |                           ::||   |:  :: ||  || :
Db   530  SGLGSTD-SGQEGSGSGSAGGE--DEADGDGARSSEDGASSELGKEEEEEQADGAVWL 586

Qy   727  -AFWRLICDTFRKIVDSKYFGRGIMIALLVNTLSMGIEYHEQPEELTNALEISNIVFTS 784
           : |:   | :|| ||||||.||||:|:||||:|||||:|||||||||:||| |:||||
Db   587  CGDVWRETRAKLRGTVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNLEICNVVFTS 646

Qy   785  LFALEMLKLLVVGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKL 844
          :||||::||  .|:| ::|||||||| :||:|:|||||||  ||||||||||:|||||
Db   647  MFALEMIKLAAFGLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVLRTFRLLRVLKL 706

Qy   845  VRFLPALQRQLVVLMKTMDNVATFCMLMLFIFIFSILGMHLFGCKFASERD-GDTLPDR 903
          |||:|||:||||||||||||||||||||||||||||||||:||||||: |: ||:||||
Db   707  VRFMPALRRQLVVLMKTMDNVATFCMLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDR 766

Qy   904  KNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL 963
          ||||||||||||||||||||||||.|||||||||.|||||.||||||||||||||||||||
Db   767  KNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL 826

Qy   964  VEGFQAEISKREDASGQLSCIQLPVDSQGDANKSESEPDEFSPS--------LDGD 1013
          ||||||                          |||:|: |  :           :|
Db   827  VEGFQAE------------------------------GDANRSYSDEDQSSSNIEEFDKLQEGLDSS 863

Qy  1014  GDRKKCLALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRT--- 1069
          ||  | | : : |    |                 |    :   | | | ||
Db   864  GDPKLCPIPMTPNGH----------LDP------SLPLGGHGPGAGAGPAPRLSLQPD 906

Qy  1070  --------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLK 1120
                    ::|:  :    ::| |::|| :::  :|| ::| ||:||||:    |:|:
Db   907  PMLVALGSRKSSVMSLGRMSYDQRSLSSRSSYYGPWGRSAAWASRRSSWN-----SLK 960

Qy  1121  RRSPSGERRSLLSGE-GQESQDEEESSEE-ERASPAGSDH------RHRG 1162
            :|::|  ||| |: | :|::        | :  |                 ||:|
Db   961  HKPPSAEHESLLSAERGGGARVCEVAADEGPRRAAFLHTPHAHHIHHGPHLAHRHRHRR 1020

Qy  1163  SLEREAKSSFDLPDTLQVPGLHRTAGGR--GSASEHQDCNGKSASGRLARALRPDDPPLD 1220
           : : | |  :|:|  :  :|    |:|  |:|:| ||||:  |   :   :|||  |
Db  1021  TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR 1080

Qy  1221  GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDH 1280
          | | ::|     || |||:|||:|  ||:||| ||: | ::: | :||| :|| ||:||
Db  1081  GED-EEEIDYTLCFRVRKMIDVYKPDWCEVREDWSYLFSPENRFRVLCQTIIAHKLFDY 1139

Qy  1281  VVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQA 1340
          |||. ||||||||| |||:|:  |:|||||||||||||:|: ||||:|||:||  |||||
Db  1140  VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQA 1199

Qy  1341  YLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKL 1400
          |||||||||||:||::|:|||:||: :::| |||| |||||||||||||||||||| |||
Db  1200  YLRSSWNVLDGFLVFVSIIDIVVSLASAGAKILGVLRVLRLLRTLRPLRVISRAPGLKL 1259

Qy  1401  VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNIINKSDCAEASY 1460
          ||||:.||||||||||:|||||||||||||||||||||:.| | |||| |:|||| ||:|
Db  1260  VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY 1319

Qy  1461  RWTRHKYNFDNLGQALMSLFVLASKDGWVDIMYGLDAVGVDQQPIMNHNPWMLLYFISF 1520
          ||. |||||||||||||||||||||||||:|||.|||||.|||||::|||||||||||||
Db  1320  RWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISF 1379
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;  PRIOR APPLICATION NUMBER: 09/404,650
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
;
   SEQ ID NO 2
;  LENGTH: 2175
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-935-541-2

Query Match       46.1%;     Score 5492.5;    DB 4;    Length 2175;
Best Local Similarity   51.3%;   Pred. No. 0;
Matches 1233;   Conservative 214;   Mismatches 508;   Indels 447;   Gaps 55;

Qy    31 RPGPGSAEKDPGSADSEAEG---LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFEERI 86
                                :  ::::   :::   ::::|::::|:|||||||||||
Db    25 QPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV 84

Qy    87 SMLVILLNCVTLGMVFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKC 146
            |||||||||||:||||||||||||:  :||||||:|||:|| ::::||||||||||||||
Db    85 SMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKC 144

Qy   147 YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLD 206
            ||||||||||||||:||||||||||:|:|:|||:|:||||||||||:|:|||::|||||
Db   145 YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVNILLD 204

Qy   207 TLPMLGNVLLLCFFVFFIFGIVGVQLMAGLLRNCFLPENFSLPLSVDLERYYQTENEDE 266
            ||||||||||||||||||||||||||||||||||:||||||:::||||||:||::
Db   205 TLPMLGNVLLLCFFVFFIFGIIGVQLMAGLLRNRCFLEENFTIQGDVALPPYYQPEEDDE 264

Qy   267 SPFICSQPRENGMRSCRSVPTLRGDGGGPCGL------DYEAYNSSSNTT--CVNWNQ 318
            :|||:  :::  :|                            ::   : ::::  ::
Db   265 MPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR 321

Qy   319 YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFLL 378
            ||||||:||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   322 YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVDIMYYVMDAHSFYNFIYFILL 381

Qy   379 IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK 438
            ||||||||||||||||||||||||:||:|||:::::|||     :|:|||::|||::::|
Db   382 IIVGSFFMINLCLVVIATQFSETKQRERHRLMLEQRQRYLS--SSTVASYAEPGDCYEEIFQ 440

Qy   439 YLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQEFTQPSSSCSRSHRRLSVHHLVHHH 498
            :: :|::|                 ||:|:  ::
Db   441 YVCHILRKAKR------RALGLVQALQSRRQALG------------------------ 468

Qy   499 HHHHHHYHLGNGTLRAPRASPEIQRDRANGSRRLMLPPSTPALSGAPPGGAESVHSFYH 558
Db   469 ------------------------------PEAPA--PAKPGP------------H 480

Qy   559 ADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPT 618
            :                           :|:||
Db   481 AK---EPRHYQLCPQHSPLDATPHTL-----------VQPIPATL--------------- 511

Qy   619 LTSLNIPPGPYSSMEKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR------ 672
Db   512 ------------------------------ASDPASCPCCQHEDGRRP------------ 529

Qy   673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRQRSLGPDAEPSSVL----- 726
            :                                                :
Db   530 SGLGSTD-SQOEGSGSGSAGGE--DEADGDGARSSEDGASSELGKEEEEEQADGAVWL 586

Qy   727 --AFWRLICDTFRKIVDSKYFGRGLMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 784
              ::|||:||||||||||||||||:|:|:| ||||::||||||||:||||:|:::|||:|
Db   587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPELTNILEICNVVFTS 646

Qy   785 LFALEMLLKLLVYGPFGYIKNPYNIPDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKL 844
            |||||||:||||||||||||||||:||||||||||||||||| ||||||||||:|||||
Db   647 MFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKL 706

Qy   845 VRFLPALQRQLVLVLMKTIMDNVATFCMLLMLFIFSILGMHLFGCKFASERD-GDTLPDR 903
            ||:|||||:||||:||||:|||||||||||||||||||||||||||:|    :||:|||
Db   707 VRFMPALRRQLVVLMKMTDNVATFCMLMLLFIFSILGMHLFGCKFSLRTDTGDTVPDR 766
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Qy  1521 LLIVAFFVLNMFVGVVVENPHKCRQHQEEEARRREEKRLRLEKKKRRKAQCKPYYSDYS 1580
            |||| :||||||||||||||||||||||| |  |::|:::|||||||||||||:|:|:
Db  1380 LLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREKRLRLEKKKRRKAQRLPYYATYC 1439

Qy  1581 RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVLES 1640
            :||||:|||:||||||||||| ||:||||:|| |||||::| ||| |:||| | ||:|
Db  1440 HTRLLIHSMCTSHYLDLFITFICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEA 1499

Qy  1641 VFKLVAFGFRRFPQDRRWNQLDLAIVLLSIMGITLEBIEVNASLPINPTIIRIMRVLRIAR 1700
            ||||||| ||||:|||:|||||||||||:||||||| |::|:::|||||||||||||||||
Db  1500 VLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIRINAALPINPTIIRIMRVLRIAR 1559

Qy  1701 VLKLLKXAVGMRAILLDTVMQALPQVGNLGLLFMLLFPIFAAIGVELFGDLECDETHPCEG 1760
            |||||  :|||| |||||:| |||||||||||||:||||||||||||| :|: |:|||| |
Db  1560 VLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAAIGVELFGKLVCNDENPCEG 1619

Qy  1761 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1817
            | |::|::|  || |||:|||| ||||||||||||:  :|: |: |:   ||:||||||
Db  1620 MSRHATFENFGNAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFV 1679

Qy  1818 LTAQFVLVNVVIAVLMKHLEBSNKEAKEAELBAELELEM-KITLSPQPHSPLGSPFLWPG 1876
            ||||||||||: ||:|||| ||::||||::||::||||| |::|||::|:||:|::|
Db  1680 LTAQFVLINVVAVLMKHLDDSNKEAQEDAEMDABLELEMAHGLGPGPRLPTGSPGA-PG 1738

Qy  1877 VEGPDSPD--------------HPRAHA------------------- 1897
            :  ::|:               |::
Db  1739 -RGPGGAGGGDTEGGLCRRCYSPAQDSLEGELTIIDNLSGSIFHHYSSPPAGCKKCHHDK 1797

Qy  1898 ---------------RSAS------HFSLEHPTMQP----HPTELPGPDLLITVRKSG-- 1929
                           :||:          :::|||      | :||||||| || |:|
Db  1798 QEVQLAETEAFSLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGEC 1857

Qy  1930 ---VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLLPKAQSGSVLSVHSQPADTSYIILQLP 1985
               :||:: ::|  |:::|
Db  1858 FFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPFSPDASSPLLPMP 1913

Qy  1986 LLQPHSAPTWGTIPKLPPPG-----RSPLAQRPLRRQAAIRTDSLDVQG 2034
            |||| :  |:| |:|| | |      :|||:
Db  1914 AEFFHPAVSASQKGPEKGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLD---- 1970

Qy  2035 LGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWG 2094
            :: : ::|: ::|  |: : :
Db  1971 ---------------ASPSSSAGSLQTTLEDSLTLSDSPRRA-------LGPPAPAGPRAGLS 2012

Qy  2095 KGPPETRSSLELDTELSWISGDLLPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQ 2154
            | :    ::::   : :   |
Db  2013 --PAARRRLSL------------RGRGLFSLRGLRA------------------------- 2036

Qy  2155 RRHSIAVSCLDSGSQPHLGTDPSN---LGGQPLGGPGSRPKKKLSPPSIT---IDDPESQ 2208
            : :                                        :
Db  2037 RSHSSGGS-TSPGCTHHDSMDPSDEEGRGGAGGGAGGEHSETLSSLSLITSLFCPPP--- 2092

Qy  2209 GPRTPPSPGICLRRRAPSSDS----KDPLASGGPPDSMAAASPSPKKDVLSLSGLSSDPADL 2264
            |                       |
Db  2093 ---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD------RSKDPPGR 2143

Qy  2265 DP 2266
            :
Db  2144 AP 2145
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RESULT 5
US-09-935-541-2   Sequence 2, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23

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Qy   1898 ------RSAS-----HFSLEHPTMQP------HPTELPGPDLLTVRKSG--  1929
                                                            ::  :::
Db   1798 QEVQLAETEAFSLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDIGEC  1857

Qy   1930 ---VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLP  1985
                                                                    :
Db   1858 FFPLSTAVSPDPENFLCEMEIPFNPV-RSW-LKHDSQAPPSPSFPDASSPLLPMP  1913

Qy   1986 KDAPH------LLQPHSAPTWGTIPKLPPG-----RSPLAQRPLRRQAAIRTDSLDVQG  2034
          ::                                                       :::
Db   1914 AEFFHPAVSASQKGPEKGTGTGTLPKIALQSWASLRSPRVNCTLLRQATGSDTSLD---  1970

Qy   2035 LGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWG  2094
           :                                              ::
Db   1971 --------ASPSSAGSLQTTLEDSLTLSDSPRRA-----LGPPAPAGPPRAGLS  2012

Qy   2095 KGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQ  2154
           :                                                       --HQ  2036
Db   2013 ---PAARRRLSL-----------------------------RGRGLFSLRGLRA

Qy   2155 RRHSIAVSCLDSGSQPHLGTDPSN---LGGQOPLGGPGSRPKKKLSPPSIT---IDPPESQ  2208
           :                              :
Db   2037 RSHSSGGS-TSPGCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSLSLTSLFCPPP--- 2092

Qy   2209 GPRTPPSPGICLRRRAPSDS---KDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADL  2264
           : :                                                --
Db   2093 ---PPPADGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD------RSKDPPGR  2143

Qy   2265 DP  2266
          ::
Db   2144 AP  2145
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RESULT 6
US-09-404-650-4
; Sequence 4, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-4

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Query Match      46.1%;   Score 5484;   DB 3;   Length 2188;
Best Local Similarity   51.1%;   Pred. No. 0;
Matches 1234;   Conservative 212;   Mismatches 509;   Indels 460;   Gaps 56;
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Qy    904 KNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL   963
          ||||||||||||||||||||||||| ||||||||| |:||| |||||||||||||||||
Db    767 KNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL   826

Qy    964 VEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS---------LDGD  1013
          ||||||||                            :    ::
Db    827 VEGFQAE------------------GDANRSYSDEDQSSSNIEBFDKLQEGLDSS   863

Qy   1014 GDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRT----  1069
          || : |  :| ||                    :
Db    864 GDPKLCPIPMTPNGH--------LDP---------SLPLGGHLGPAGAGAPAPRLSLQPD   906

Qy   1070 ------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLK  1120
                 :::  :: :            : :  :         :  ::::    ::: ||
Db    907 PMLVALGSRKSSVMSLGRMSYDQRSLSSRSSYYGPWGRSAAWASRRSSWN------SLK   960

Qy   1121 RRSPSGERRSLLSGE-GQESQDEEESSEE--ERASPAGSDH---------------RHRG  1162
          :   :  : :||::    :                 :              ::::
Db    961 HKPPSAEHESLLSAERGGGARVCEVAADEGPRRAAPLHTPHAHHIHGPHLAHRHRHRR  1020

Qy   1163 SLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRLARALRPDDPLD  1220
          :|       :|       :   :        :   : | ||  : :  :||| ||
Db   1021 TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR  1080

Qy   1221 GDDADDEGNLSKGERVRAWTRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMPDH  1280
          | :  :   |||||| ||  :  : |  ::||||::|:| |:|||:||| | || |:|::
Db   1081 GED-EEBIDYTLCFRVRKMIDVYKPDWCEVREDWSVVLFSPENRFRVLCQTIIAHKLFDY  1139

Qy   1281 VVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQA  1340
          |||  |||||||||:|||:|  : :  ||||:|||||||:|: || :|||:|| :|||||
Db   1140 VVLAFIFLNCITIALERPQIFEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQA  1199

Qy   1341 YLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQCLKL  1400
          |||||||||||:||: |:|||:||: |: | ||||:||||||||||||||||||||  |||
Db   1200 YLRSSWNVLDGFLVFSIIDIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKL  1259

Qy   1401 VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEEASY  1460
          |||||:|||||||||| ||||||||||||||||||||| :| | ||||||:||||: |:|
Db   1260 VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY  1319

Qy   1461 RWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGDVQQPIMNHNPWMLLYFISF  1520
          |||:|||||||||||||||||||||||| |||| |||||||||||: ||||||||||||
Db   1320 RWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVGDVQQPVTNHNPWMLLYFISF  1379

Qy   1521 LLIVAFFVLNMFVGVVVENFHKCRQHOEEEEARRREEKRLRRLEKKKRKAQCKPYYSDYS  1580
          |||:|||||||||||||||||||| ||:|: ||||||||||||||||| |  :|||:||
Db   1380 LLIVSFFVLNMFVGVVVENFHKCRCRQHQEAEARRREEKRLRRLEKKKRRKAQRLPYYATYC  1439

Qy   1581 RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLES  1640
           ||||:| :|||||||:||| :| |||||:|::|||:||: ||| :|||:||||:|||||
Db   1440 HTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNVMFTTVFVLEA  1499

Qy   1641 VFKLVAFGFRRFFQDRWNQLDAIVLLSIMGITLEEIEVNASLPINPTIIRMVLRIAR  1700
          | |||||| |||| |||||||:|||||:|||||||||:||:|||||||||| |||||
Db   1500 VLKLVAFGLRRFFXDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRMRVLRIAR  1559

Qy   1701 VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCBG  1760
          ||||||||:|||||||||:|||||||||||||||||||:|||||||||   |:: ||:|
Db   1560 VLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEG  1619

Qy   1761 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC--DQESTCYNTV--ISPIYFVSFV  1817
            :|||||:|||||||||| ||||||||||||||||||  | ||| |  | :||||||||
Db   1620 MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPIYFVSFV  1679

Qy   1818 LTAQFVLVNVVIAVLMKHLEESNKEAKEAEAELEAEILEM-KTLSPQHSPLGSPFLWPG  1876
          ||||||| |||:||:|||| :||||| : ||  |||:|||    |: :  || || | |
Db   1680 LTAQFVLINVVVAVIMKHLDDSNKEAQDEAEMDAELELEMAHGLGPGPRLPTGSPGA-PG  1738

Qy   1877 VEGPDSPD------------SPKPGAL----------HPAAHA---------  1897
                                :  :                 ::
Db   1739 -RGPGAGGGGDTEGGLCRRCYSPAQDSLEGELTIIDNLSGSIFHHYSSPAGCKKCHHDK  1797

Qy     31 RPGPGSAEKDPGSADSEABG---LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERI   86
          :|||: |  ||:|      :    ||  | | :|| | | ||:  |  : ||||||:  :
Db     25 QPGPRSPPSSPPGLEEPLDGADPHVPHDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV   84

Qy     87 SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKC  146
          ||||||||||||||::|| |::| |||||||||:||||| |||:|||:||||||||||||
Db     85 SMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKC  144

Qy    147 YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLD  206
          |||||||||||||||:|||:||||||||:  :|:|||||||||:|||||||||||| |||
Db    145 YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVNLLLD  204

Qy    207 TLPMLGNVLLCFFVFFIFGIVGVQLMWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE  266
          |||||||||||||||||||||:||||||||||||||| |||::  ||||||||| : :|:
Db    205 TLPMLGNVLLCFFVFFIFGIIGVQLMWAGLLRNRCFLEENFTIQGDVALPPYYQPEEDDE  264
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Qy   267  SPFICSQPRENGMRSCRSVPTLRGDGGGGPCGL------DYEAYNSSSNTT--CVNWNQ  318
              :  |||||:  :  |:       :: |:         | : :|  |:  | |||||
Db   265  MPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR  321

Qy   319  YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL  378
              |||||||||||:||||||||||||||:||||||||||||:|||||:||||||||||||||
Db   322  YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYNFIYFILL  381

Qy   379  IIVGSFFMINLCLVVIATQFSETKQRRSQLMREQRVRFLSNASTLASFSEPGSCYEELLK  438
              ||||||||||||:|||||||||||||||||||||:|||||||||: |::: :  ||||:
Db   382  IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEEIFQ  440

Qy   439  YLVYILRKGAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH  498
              ||:  :  |||:||:      :|| |: :| |  :  | ||| ||:|||||||||||||
Db   441  YVCHILRKAKR------RALGLYQALQSRRQALG                          468

Qy   499  HHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH    558
              |||:
Db   469  ------------------------------------------PEAPA--PAKPGP------H  480

Qy   559  ADCHLEPVRCQAPPRSPSEASGRTVGSGCKVYPTVHTSPPETLKEKALVEVAASSGPPT  618
              |||||
Db   481  AK--EPRHYQLCPQHSPLDATPHTL-------VQPIPATL                      511

Qy   619  LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR------  672
                 ::|||: |     ||:
Db   512  ------------------------ASDPASCPCCQHEDGRRP                    529

Qy   673  AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDARPSSVL------  726
              :|| |:  |      |  |:
Db   530  SGLGSTD-SGQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEEEQADGAVWL   586

Qy   727  -AFWRLICDTFRKIVDSKYFGRGIMIAIIVNTLSMGIEYHEQPELTNALEISNIVFTS    784
              :| |:||||||||||:|||||||:|: |:| |||||||||||||||:||::|| :|||
Db   587  CGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPELTNLEICNVVFTS    646

Qy   785  LFALEMLLKLLLIVYGPFGYIKNPYNIFPDGVIVVISVWEIVQQGGGLSVLRTFRLMRVLKL  844
              :|||||:|||| |: |||||||||||||:|||||||:|||||||||:|||||||||:||
Db   647  MFALEMILKLAAFGLLFDYLRNPYNIFPDSIVVIISIWEIVQQADGGLSVLRTFRLLRVLKL  706

Qy   845  VRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERD-GDTLPDR  903
              ||| ||||||||||||||||:|||||||||||:||||||||||:|||| |  :  ||:
Db   707  VRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFSILGMHIFGCKFSLRTDTGDTVPDR  766

Qy   904  KNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL  963
              |||||||||||||||||||||||||||||||||:||||: ||||||||||||||||||:
Db   767  KNFDSLLWAIVTVFQLLTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL  826

Qy   964  VEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSBSEPDFFSPS-------------LDGD  1013
                |||::       ::  :   :        | | :  :
Db   827  VEGFQAE                                                      863

Qy   1014 GDRKKCLALVSLGEHPELRKSLLPLLIIHTAATPMSLPKSTSTGLGEALGPASRRT----  1069
              ||:| |  :| |:  |  |:: ||
Db   864  GDPKLCPIPMTNGH------------LDP-------SLPLGGHLGPAGAAGPAPRLSLQPD  906

Qy   1070 --------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLK  1120
              ||:
Db   907  PMIVALGSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSAAWASRRSSWN-----SLK  960

Qy   1121 RRSPSGERRSLLSGE-GQESQDEEBSSEE--ERASPAGSDH------------------RHRG  1162
              |:| |:||||||| |
Db   961  HKPPSAEHBSLLSAERGGGARVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHHR  1020

Qy   1163 SLEREAKSSFDLPDTLQVPGLIHRTASGR-GSASEHQDCNGKSASGRLARALRPDDPLD  1220
              |:|  |::
Db   1021 TLSLDNRDSVDLAELVPAVGAHPAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR  1080

Qy   1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDH  1280
              | :
Db   1081 GED-EEEIDYTLCFRVRKMIDVYKPDWCEVREDWSVILFSPENRFRVLCQTIIAHKLFDY  1139

Qy   1281 VVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNVIFTAVFLAEMTVKVVALGWCFGEQA  1340
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Qy   1140 VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQA  1199
              |||  ||||||||| |||:||| |||||||:||:||||:|| ||||||:|||| ||||||
Db   1341 YLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKL  1400

Qy   1200 YLRSSWNVLDGFLVFVSIIDIVVSLASAGGAKIIGVLRVLRLLRTLRPLRVISRAPGLKL  1259
              ||||||||||| ||:||||||:||||:|| |||| |||||||||||||||||||| ||||
Db   1260 VVETLISSLKPIGNIVLICCAFFIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY  1319

Qy   1260 VVETLMSSLKPIGNIVVICCAFFIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASY  1319
              |||| |:||||||||:|||||||||||||||||||||  ::|:|||||:|||| :|:|
Db   1320 RWVEHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVADVDQQPVTNHNPWMLLYFISF  1379

Qy   1320 RWVEHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGDQQPIMNHNPWMLLYFISF  1379
              |||||||||||||||||||||||||||||:|||:|||||:|||||:|||||||||||||
Db   1380 LLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREKRLEKKRRKAQRLPYYATYC  1439

Qy   1380 LLIVAFFVLNMFVGVVVENFHKCRQHQEBEEARRREKRLRLEKKRRRAQCKPYYSDYS  1439
              ||||:||||||||||||||||||||::|||||||||||:|| :|||| ::||| |:|
Db   1440 HTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVVLEA  1499

Qy   1440 RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVFVLES  1499
              | |||:| ||||||||:| |:|| ||||||::|||:||::|||||||||:|||.  ||
Db   1500 VLKLVAFGLRRFFKDRWNQLDLAIVLLSVWGITLEINAALPINPTIIRMRVLRIAR  1559

Qy   1500 VFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEIEVNASLPINPTIIRMRVLRIAR  1559
              |||||||| |||| |||||||||||||||:||||||::| |||||||||||:||||||
Db   1560 VLKLIKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEG  1619

Qy   1560 VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG  1619
              |||| ||| ||||||||::||||||||||||||||||||:||||||| | ::|:  ||||
Db   1620 MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFV  1679

Qy   1620 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV  1679
              : |||| |||||||||| :|||||||||||||||||| :|:||| |: ||| ||||||
Db   1680 LTAQFVLINVVAVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPRLPTGSPGA-PG  1738

Qy   1680 LTAQFVLNVVAVLMKHLEESNKEAKEAEAELAEELELEM--KTLSPQHSPLGSPFLWPG  1738
              |||||||:|||||||||::|||||:|: | |:|||||||   |:     |: | |||| :
Db   1739 -RGPGGAGGGDTEGGLCRRCYSPAQENLWLDSVLLIKDSLEGELTTIIDNLSGSIFHHY  1797

Qy   1739 VEGPD-------------------------------------------SP--------  1760
              ||||                                           |
Db   1797 YLRSSWNVLDGLLVL                                           1817

Qy   1761 -RGPGAGGGGDTEGGLCRRCYSPAQENLWLDSVLLIKDSLEGELTTIIDNLSGSIFHHY  1817
```

Db   1818 LTAQFVLNVVAVLMKHLEESNKEAKEAEAELAEELELEM--KTLSPQHSPLGSPFLWPG 1876

Qy   1858 PPEPMRVGDLGECFFPLSSTAVSPDPENFLCEMBEIPNPV--RSW--LKHDSSQAPPSP 1913

Db   1877 VEGPD--DSPKPGALH---- 1892

Qy   1893 ------HARSAS------------------------------HFSLEHPTMQP----HPTELP 1918

Db   1914 FSPDASSPLLPMPAEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLLRSPRVNCTLLR 1973

Qy   1974 QATGSDTSLD-------------ASPSSSAGSLQTTLEDSLTLSDSPRRA-----------LG 2012

Db   2013 PPAPAPGPPAGLS------------------------------RGRGLFSLRGLRA----- 2047

Qy   2048 SIT--IDPPESQGPRTPSPGICLRRRAPSSDS----KDPLASGCPPDSMAASPSPKKDV 2095

Db   2096 PPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD----- 2148

Qy   2199 HQRSHSSGGS-TSPGCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSL 2251

Db   2252 LSLSGLSSDPADLDP 2266

Db   2149 -----RSKDPPGRAP 2158

RESULT 7
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4

Query Match   46.1%; Score 5484; DB 4; Length 2188;
Best Local Similarity   51.1%; Pred. No. 0;
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

Qy   31 RPGPGSAEKDPGGADSEAEG----LPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERI 86
           :||:||.::||::|||| |||| ::|:|:|||||||: :|::|::|||| ||:::
Db   25 QPGPRSPPSSPPGLEEPLDGADPHVFHPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV 84

Qy   87 SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKC 146
           |||||||||||||||:|| :|:|||.|||||||||||||:||||||:|||||||||||||
Db   85 SMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKC 144

Qy   147 YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLLD 206
           ||||||||||||||:||||||||||||:||||||||||||:|||||||||||:||:|||
Db   145 YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLPLKAINRVPSMRILVNLLLD 204

Qy   207 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE 266
           |||||||||||||||||||||||||||||||||||:|:||||||||:|||||| ||||||
Db   205 TLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGGVALPPYYQPEEDDE 264

Qy   267 SPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL------DYEAYNSSSNTT--CVNWNQ 318
           :|||||| || ::|:.| ||| ||||||| :   :|:|::::: ||||:
Db   265 MPFICSLSGDNGIMGCHEIPLKEQ--GRECCLSKDDVVDFGAGRQDLNASGLCVNWNR 321

Qy   319 YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL 378
           |||:|:|||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db   322 YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYNFIYFILL 381

Qy   379 IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK 438
           |||||||||||||||||||||||||.|:||||||||||:|||:||||||||||||||||:
Db   382 IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS--SSTVASYAEPGDCYEEIFQ 440

Qy   439 YLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGOETQPSSSCSRSHRRLSVHHLVHHH 498
           ||:||| :|: |:   ::||:||:|||::| |:
Db   441 YVCHILRKAKR-------RALGLYGALQSRRQALG--------------------------- 468

Qy   499 HHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRIMLPPPSTPALSGAPPGGAESVHSFYH 558
           ||
Db   469 ------------------------------------PEAPA--PAKPGP--------H 480

Qy   559 ADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPEETLKEKALVEVAASSGPPT 618
           | :|: || : |:
Db   481 AK--EPRHYQLCPQHSPLDATPHTL-----------VQPIPATL------------- 511

Qy   619 LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR---- 672
           :
Db   512 ---------------------------ASDPASCPCCQHEDGRRP 529

```
Db    19 ..........GITEQPGPRSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIKMVCNPW   78
            ||||                                                  :::::: |||||
Qy    83 FERISMLVILLNCVTLGMRFPCEDIACDSQRCRILQAFDDFIPAFFAVEMVKMVALGIF  142
         :||:|||||||||||||:|  ::| ::.    ||  ||||:|:|| |.||.|| ||||||
Db    79 FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKLLQVFDDFIFIFFAMEMVLKMVALGIF  138
Qy   143 GKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSSAVRTVRVLRPLRAINRVPSMRILVT  202
         |||||||||||||||||:|||::||||||||:| | | :|||||||||:||||||||||:
Db   139 GKKCYLGDTWNRLDFFIVMAGMVBYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVN  198
Qy   203 LLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTE  262
         ||||||||||||||||||||||||||:|||||||||||||:|||:| :  ||||  ||
Db   199 LLLDTLPMLGNVLLLCFFVFFIFGIIGVQLIWAGLLRNRCFLEENFTIQGDVALPYYQPE  258
Qy   263 NEDESPFICSQPRENGMRSCRSVPTLRGDGGGPCGL---DYEAYNSSSNNT--CV  314
         :  |.||||| ..|||: .|  :| :: :   .    ||||:|||||||.|  ||
Db   259 EDDEMPFICSLTGDNGIMGCHEIPPLKEQ--GRECCLSKDDVDFGAGRQDLNASGLCV  315
Qy   315 NWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIY  374
         |||:||.||.:|:|||||||||||||||| :|||||:||||||:||||:|||||||:|||
Db   316 NWNRYYNVCRTGNANPHKGAINFDNIGYAGIVIFQVIFQVITLEGWVEIMYYVMDAHSFNFIY  375
Qy   375 FILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYE  434
         |||||||||||||||||||||||||||||:| |::  :|:||::    .:|:: :|:||
Db   376 FILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS--SSTVASYAEPGDCYE  434
Qy   435 ELLKYLVYILRKAAARLAQVSRAAGVRVGLLSSPAPLGGQBTQPSSSCSRSHRRLSVHHL  494
         :||:|| |||:|| |:.:|      ||.||:.:                  ::
Db   435 EIFQVVCHILRKAKRRALGLYQALQNR---------------------------------  461
Qy   495 VHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVH  554
                                                  :::::|:|:|   || |
Db   462 -----------------------------------------RQAMG------PGTPA--PAKPGP--  477
Qy   555 SFYHADCHLEPVRCQAPPPRSPEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASS  614
                                                       ||||
Db   478 ---HAK---EPSHCKLCPRHSPLD---------------------------PTPHTLVQP  504
Qy   615 GPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSAGCGPDSCPYCAR--  672
                                                                  |||||
Db   505 -----------------------------------ISAILASD------PSSCPHCQHEA  523
Qy   673 ----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLA-  727
                                                               ||||  |
Db   524 GRRPSGLGSTD-SGQEGSGSGGSAEEAFANGDG---LQSSEDGVSSDLGKEEBQEDGAAR  578
Qy   728 -FWRLICDTFRKIVDSKYFGRGIMIALLVNTLSMGIEYHQPEELTNALEISNIVFT  783
            ||| |      ||||||||||:||||||||:||||||| |||:|| | ::|:|||
Db   579 LCGDVWRETRKKLRGIVDSKYFNRGIMAILVNTVSMGIEHHQPEELTNILEICNVVFT  638
Qy   784 SLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRIMRVLK  843
          :|||||:|||||.||||| ||| :||||| ||::|||||| |.||||||||:||||||||
Db   639 SMFALEMILKLAAFGLFDYLRNPNIFDSIIVISIWEIVGQADGGLSVLRTFRLLRVLK  698
Qy   844 LVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERD-GDTLPD  902
         ||||:||||||||||||:|||||||||||||||||||||||||||||| :  || |||:|
Db   699 LVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFSLRTDTGDTVPD  758
Qy   903 RKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAI  962
         ||||||||||||:||||||||||||||||||||:||.||||:.||||||||:|:|||||
Db   759 RKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTTPWASLYFVALMTFGNYVLFNLLVAI  818
Qy   963 -----------------------------------------LDG  1012
                                                    :|
Db   819 LVEGFQAE---------------------------------LVEGFQAE  855
Qy  1013 DGDRKKCLALVSLGEHPELRKSLLPPLLIIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071
                                                    |:   .:|||
Db   856 SRDLKLCPIPMTPNGH---------------------------------SLP-------  ...
Qy  1072 SGSSAEPG--..................AAHEMKSPPSARSSPHSPWSAAGSWTSRRSSRNSL 1113
            :|                          |:: :|  |||: :
```

```
Db  1560 ..........VLKLKMATGMRALLDFTVVQALPQVGNIGLLFMLLFFIYAALGVELFGKLVCNDENPCEG  1619
            |||||                                           |||||||  ||
Qy  1761 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV  1817
            :|||:|||||||||||::|||||||||||||||||  :|::||||:   |||||||||
Db  1620 MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFV  1679
Qy  1818 LTAQFVLVNVIAVLMKHLEESNKEAKEAELEAELELEM-KTLSPQPHSPLGSPFLWPG  1876
         |||||||:||::|||||||:.|||||:||| :| :|||| :.:.  ||.|||| ||:|
Db  1680 LTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPGRLPTGSPGA-PG  1738
Qy  1877 VEGPD--------SP--------------------DSPKPGALH--  1892
         :|:||        :|                     |||||:|
Db  1739 -RGPGAGGGGDTEGGLCRRCYSPAQENIWLDSVSLIIKDSLRGELTIIDNLSGSIFHHY  1797
Qy  1893 --PAA-------------HARSAS------HFSLEHPTMQP-----HPTELP  1918
            |:|             ||:||        || |||:| :      ||:||
Db  1798 SSPAGCKKCHHDKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELD  1857
Qy  1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMCRHGSTABGPLGHRGWGLPKAQSGGSVLSVH  1972
         |||:|||:|      |:|::|||  ||: ||:|| :| ||:|||| |:||  |:| |
Db  1858 PPEFMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSP  1913
Qy  1973 SQPADTSYILQLPKDAPH------LLQPHSAPTWGTIPKLPPPG---RSPLAQRPLRR  2021
          :|  :::| :|  :|       |||:|: |||| |:||    :|    |||||||
Db  1914 FSPDASSPLLPMPAEFFHPAVSASQKGPEKGTGTGTLFKIALQGSWASLRSPRVNCTLLR  1973
Qy  2022 QAAIRTDSLDVQGLGSREDLLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMT  2081
         ||| ||||:|:   .|.|||:  | .||                          |:
Db  1974 QATGSDTSLD---------ASPSSSAGSLQTTLEDSLITLSDSPRRA------LG  2012
Qy  2082 PPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQ  2141
         ||||.||| |.| |||  |                 |:| |||::|||||| |:|
Db  2013 PPAPAPGPRAGLS--PAARRRLSL------------RGRGLFSLRGLRA-  2047
Qy  2142 SCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSN--LGGGQPLGGPGSRPKKKLSPP  2198
          |||||  :::    :::.          |: || |   |||:  | .   |:: |||
Db  2048 ----------HQRSHSSGGS-TSPCCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSL  2095
Qy  2199 SIT--IDPPESQGPRTPPSPGICLRRRAPSDSDS----KDPLASGPPDSMAASPSPKKDV  2251
         |::  :| |:.  |.| ||| :|||||||||||     ||| |||||.|:||:||| |
Db  2096 SLTSLFCPPP------PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-  2148
Qy  2252 LSLSGLSSDPADLDP  2266
               :|||  ||
Db  2149 -----RSKDPPGRAP  2158
```

```
  Query Match    45.1%;  Score 5366;  DB 3;  Length 1835;
  Best Local Similarity 56.8%;  Pred. No. 0;
  Matches 1138;  Conservative 183;  Mismatches 346;  Indels 336;  Gaps 38;

Qy    27 GAGGRPGPGSAEKDPGSADSEAEG---LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW   82
```

```
;  CURRENT APPLICATION NUMBER: US/09/935,541
;  CURRENT FILING DATE: 2001-08-23
;  PRIOR APPLICATION NUMBER: 09/404,650
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 5
;    LENGTH: 1835
;    TYPE: PRT
;    ORGANISM: Rattus sp.
;  US-09-935-541-5

Query Match          45.1%;   Score 5366;   DB 4;   Length 1835;
Best Local Similarity  56.8%;   Pred. No. 0;
Matches 1138;   Conservative 183;   Mismatches 346;   Indels 336;   Gaps 38;
```

```
Qy    27  GAGGRPGPGSAEKDPGSADSEAEG----LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW   82
              :  : ||   :|| |||                  |:||:| :|||: || |:| ||||
Db    19  GITEQPGPRSPPPSPPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIKOMVCNPW   78

Qy    83  FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFPDDFIFAFFAVEMVVKMVALGIF  142
              :| :|||:||||||||  | |    ||  | :||:|  | |:||| ||:||||:||||||
Db    79  FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKIIQVFDDFIFIFFAMEMVLKMVALGIF  138

Qy   143  GKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSSAVRTVRLPRLRAINRVPSMRILVT  202
              |||||||||||||||||||| |||| ||||||:| |||:|:|||| |||| |||:||||
Db   139  GKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVN  198

Qy   203  LLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTE  262
              ||||||||||||||||||||||||||||||||||||||||||||                |
Db   199  LLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPPYYQPE  258

Qy   263  NEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL-------DYEAVNSSSNTT--CV  314
              ||:       |::  | :|  |                            : |:| |  |
Db   259  EDDEMPFICSLTGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCV  315

Qy   315  NWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIY  374
              ||| | |||| ||| | |||||||||| | ||||| |||||||||| | |||||||||||
Db   316  NWNRYYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYVVMDAHSFYNFIY  375

Qy   375  FILLIIVGSFFMINLCLVVIATQFSETKQRESOLMREORVRFLSNASTLASFSEPGSCYE  434
              |||||||||||||||||||||||||||||||||||||||:    :: |||| |||| |||
Db   376  FILLIIVGSFFMINLCLVVIATQFSETKQREHRHLMLEQRQRYLS--SSTVASYAEPGDCYE  434

Qy   435  ELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETOPSSSCSRSHRRLSVHHL  494
              |:  |      | |  | |   |    ||
Db   435  EIFQYVVCHILRKAKRRALGLYQALQNR-------------------------------  461

Qy   495  VHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRIMLPPSTPALSGAPPGGAESVH  554
Db   462  --------------------------------RQAMG------PGTPA--PAKPGP---  477

Qy   555  SFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASS  614
Db   478  ---HAK---EPSHCKLCPRHSPLD-----------------PTPHTLVQP---------  504

Qy   615  GPPTTTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-  672
Db   505  ------------------------------------ISAILASD-----FSSCPHCQHEA  523

Qy   673  ---AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLA-  727
Db   524  GRRPSGLGSTD-SGQEGSGSGGSAEAEANGDG----LQSSEDGVSSDLGKEEQEDGAAR  578

Qy   728  ---FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFT  783
Db   579  LCGDVWRETRKKLRGIVDSKYFNRGIMMAILLVNTIVSMGIEHHEQPEELTNILEICNVVFT  638

Qy   784  SLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQOGGGLSVLRTFRLMRVLK  843
Db   639  SMFALEMILKLAAFGLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVLRTFRLLRVLK  698

Qy   844  LVRFLPALQRQLVVLMKTMDNVATFCMLMLFIFIFSIIGMHLFGCKFASERD-GDTLPD  902
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```
Db   893  RLSLQPDPVLVALDSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWN--  950

Qy  1114  GRAPSLKRRSPSGERRSLLSGEGQESQDEE-ESSEEE---RASPAGSDH----------  1158

Db   951  ---SLKHKPPSAEHESLLSGEGGGSCVRACEGAREEAPTRAPLHAPHAHHAHHGPHLA  1006

Qy  1159  ---RHRGSLERFAKSSFDLPDTLQVPGLHRTAS--GRGGASEHQDCNGKSASGRIARAL  1212

Db  1007  HRHRHHRRTLSLDTRDSVDLGELVPVVGAHSRAAWRGACGAPGHEDCNGRMPNIAKDVFT  1066

Qy  1213  RPDDPPLDGDADDEGNLSKGERVRAWTRARLPACYLERDSWSAYIFPPQSRRFLLCHRI  1272

Db  1067  KMDDRRDRGED-EEEIDYTLCFRVRKMIDVYKPDWCEVVREDWSVYLFSPENKFRILCQTI  1125

Qy  1273  ITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL  1332

Db  1126  IAHKLFDYVVLARIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSL  1185

Qy  1333  GWCFGEQAYLRSSWNVLDGLLVLISVDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVI  1392

Db  1186  GLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSVASAGAKILGVLRVLRLLRTLRPLRVI  1245

Qy  1393  SRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILGVQLFKGKFVCQGEDTRNITNK  1452

Db  1246  SRAPGLKLVVETLISSLKPIGNIVLICCAFFIFGILGVQLFKGKFYHCLGVDTRNITNR  1305

Qy  1453  SDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDLDAVGVDQQPIMNDNPW  1512

Db  1306  SDCVAANYRWVRHKYNFDNLGQALMSLFVLASKDGWNIMYNGLDAVADVQQPVTNDNPW  1365

Qy  1513  MLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEBEEEARRREEKRLRRLEKKRRKAQC  1572

Db  1366  MLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREEKRLRRLEKKRRKAQR  1425

Qy  1573  KPYYSDYSRFRFLLVHHLCTSHYLDLFITGVIGLNVTMAMEHYQQPQILDEALKICNYIF  1632

Db  1426  LPYYATYCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMF  1485

Qy  1633  TVIFVLESVFKIVAFGFRRFFQDRWNQLDLAIVLLSSMGITLEEIEVNASLPINPTIIRI  1692

Db  1486  TTVFVLEAVLKLVAFGFKRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRI  1545

Qy  1693  MRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLFFIFAALGVELFGDLEC  1752

Db  1546  MRVLRIARVLKLLKNATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVC  1605

Qy  1753  DETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS  1809

Db  1606  NDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVS  1665

Qy  1810  PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAEAELAELELEM-KTLSPQPHSPL  1868

Db  1666  PLYFVSFVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAE IBLEMAHGLGPCP----  1721

Qy  1869  GSPFLWPGVEGPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTV---  1925

Db  1722  ----------------GPCPG------------------------PCPCPCPCAGPRLPTSSPG  1747

Qy  1926  --RKSGVSRTHSLPNDSYMCRH 1945

Db  1748  APGRGSGGAGAGG-DTESHLCRH 1769
```

RESULT 9
US-09-935-541-5

; Sequence 5, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
;   APPLICANT: Dietrich, Paul S.
;   APPLICANT: McGivern, Joseph G.
;   TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;   TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing

```
Db          |||||  ||||:  | ::     :|||||||:|||||
      1722  ------------------------GPCPG-------------------------PCPCPCPCAGPRLPTSSPG 1747

Qy    1926  ---RKSGVSRTHSLPNDSYMCRH 1945
                 ||:|| ||  :
Db    1748  APGRGSGGAGAGG-DTESHLCRH 1769


RESULT 10
US-09-268-163-4
; Sequence 4, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
;   APPLICANT: Lipscombe, Diane
;   APPLICANT: Schorge, Stephanie
;   TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
;   FILE REFERENCE: B1055/7000
;   CURRENT APPLICATION NUMBER: US/09/268,163B
;   CURRENT FILING DATE: 1999-03-12
;   EARLIER APPLICATION NUMBER: US 60/077,901
;   EARLIER FILING DATE: 1998-03-13
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 2343
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-268-163-4
                                                              Length 2343;

  Query Match            14.7%;  Score 1750.5;  DB 3;  Length 2343;
  Best Local Similarity  24.2%;  Pred. No. 2.4e-133;
  Matches  639;  Conservative 363;  Mismatches 827;  Indels 815;  Gaps  84;
```

```
                                                                              FYLSQDSRP 70
Qy      27  GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVF-------------------------- :: FIFAF 127
                ||||                   :: |           :::
Db      25  GAGGAGGPGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV 84

Qy      71  RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAPDD---FIFAF 127
                |    |   ||:| :: |: |||  :::  |         ::
Db      85  RKYAKRITEWPPFEYMLATTIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFYGI 140

Qy     128  FAVEMVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDLQNVSFSAVRTVR 183
                ::::|  :  :  | |: ||         |: |:::||
Db     141  FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVLTGLATAGTDFDLR----TLRAVR 195

Qy     184  VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFL 243
                | :  |  :  |  :  |::: |   :| ||:|  :|:
Db     196  VLRPLKLVSGIFSLQVVLKSIMKAMVPLLQIGLLLFFAILMPAIIGLEFYMGKFHKACF- 254

Qy     244  PENFSLPLSVDLERYYQTENEDESPPICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYE 303
                ||
Db     255  ----PNSTDAE----------------------------PV--------GDFPCGKEAP 273

Qy     304  AYNSSSNTTCVNMNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363
                |   |   :  |      :::           |      ||:| |::|   || :|
Db     274  ARLCEGDTEC---REYWP---------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNT 323

Qy     364  MD-AHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRES-------QLMREQRVRF 416
                || |  ||||  ::| |||  |||:| :| |                    ::|
Db     324  NDAAGNTWNWLYFIPLIIGSFFMNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE- 382

Qy     417  LSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET 476
                                                                  -EEK 410
Db     383  ------------------------------RELNGYLEWIFKAEEVMLAEEDRNA------ 410

Qy     477  QPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536
                                            :::                  :  :
Db     411  SPLDVLKRAATKKSRNDLIH---------------------------AEEGEDRFAD---- 440

Qy     537  PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTS 596
                                                                    : :
Db     441  ------------------------------------------------------------ 440

Qy     597  PPPEETIKEKALVEVAASSGPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKISSPCLK 656
                                                            ||
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```
Db          |||||  ||||:|:  ||||||  :|:||||::|||:|||||||  ::|||||||||
      699  LVRFMPALRRGQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPD 758

Qy    903  RKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAI 962
                |||||||||||||||||||||||  ::||||||||||| ||||||||||||||||||||
Db    759  RKNFDSLLIWAIVTVFQILTQEDWNVVLYNGMASTTPWASLYPVALMTFGNYLFNLLVAI 818

Qy    963  LVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSEASEPDFFSPS------------LDG 1012
                |||||||||  ::  :|    |:      :|: ::::
Db    819  LVEGFQAE---------------GDANRCSDEDQSSSNLEEFDKLPEGLDN 855

Qy   1013  DGDRKKCLALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071
                :  |: |          :   |:
Db    856  SRDLKLCPIPMTPNGH-------SLP------LGAHLGPAGTMGTAP 892

Qy   1072  SGSAEPG------------------------AAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSL 1113
                                            :::|  ::: :
Db    893  RLSLQPDPVLVALDSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWN-- 950

Qy   1114  GRAPSLKRRSPSGERRSLLSGEGQESQDEE-ESSEEE---RASPAGSDH------------ 1158
                                :::
Db    951  ----SLKHKPPSAEHESLLSGEGGGSCVRACEGAGAREEAPTRTAPLHAPHAHHAHHGPHIA 1006

Qy   1159  -RHRGSLERRAKSSFPLPDTLQVPGLHRTAS--GRGGSASEHQDCNGKSASGRLARAL 1212
                :                        ::|
Db   1007  HRHRHHRRTLSLDTRDSVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPNIAKDVFT 1066

Qy   1213  RPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI 1272
                                    :  |        | :   |::|: |  | || :||||
Db   1067  KMDDRRDRGED-EBEIDYTLCFRVRKMIDVYKPDWCEVREDWSVVLFSPENKFRILCQTI 1125

Qy   1273  ITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVPLAEMTVKVVAL 1332
                | |: |   ||  |||||||| ||      |   |  ::|| |::|: ||  |:| :|
Db   1126  IAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSL 1185

Qy   1333  GWCFPGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVI 1392
                | :  | ||||||||||||| ||||| |:|| |::  |||||||||||||||||||||||
Db   1186  GLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSVASAGGAKILGVLRVLRLLRTLRPLRVI 1245

Qy   1393  SRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK 1452
                |  |||||| ||: |||||||| :|| ||||||||| |||:|||   || | :|| ||||
Db   1246  SRAPGLKLVVETLISSLKPIGNIVIVLCCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR 1305

Qy   1453  SDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPW 1512
                |||  | || |||||||||||||||||:||| ||||| :|  ||:||  |    |  |||:
Db   1306  SDCVAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPW 1365

Qy   1513  MLLYFISFLLIVAFFVLNMFVGVVVENFHKCRCRQHQEEEEARRREEKRLREKKRRKAQC 1572
                |||||||| ||| |||||||||| | ||||||||::|  |||| ||||||||||||||||
Db   1366  MLLYFISFLLIVSFFVLNMFVGVVVENFHKCRCRQHQAEAARRREEKRLRELKKRRKAQR 1425

Qy   1573  KPYYSDYSRFRILVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIF 1632
                |  |:   |       :   ||  :|  :|   :|: || ::|  :::: : |    ||
Db   1426  LPYYATYCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMF 1485

Qy   1633  TVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRI 1692
                |::||: |||||||| |||||||||||||||||| | |||||| :|||||||||||||||
Db   1486  TTVFVLEAVLKLVAFGFLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRI 1545

Qy   1693  MRVLRIARVLKLKLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLEC 1752
                |:|||||||||||||||| |||||||||||||||||||||||||||| |||||||||||||:
Db   1546  MRVLRIARVLKLKLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVC 1605

Qy   1753  DETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS 1809
                :  |: |       : |   |||| |:|::|||||||:|   | |    :  |  :
Db   1606  NDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDRRTCLSSLQFVS 1665

Qy   1810  PIYFVSFVLTAQFVLVNVIAVLMKGHLEESNKEAKEEAEAELLELEM-KTLSPQPHSPL 1868
                |||||||||||||||  || || ||||  | :: |||  ||| |    ::| |:|
Db   1666  PLYFVSFVLTAQFVLINVVVAVLMKGHLDDSNKEAQEDAEMDAEIELEMAHGLGPCP---- 1721

Qy   1869  GSPFLWPGVEGPDSPDSPKPGALHPAAHARKSASHFSLEHPTMQPHPTELPGPDLLTV--- 1925
                ||
Db            ||
```

```
Db   1401  VVYFVVPFPFFVNIFVALIIITF-----QEQGDKVMSE-----CSLEKNERACIDPAISA  1450
                  :|  ||                             :            |  :
Qy    441  ----------------------------------------------------LCAVGSPFAR   450

Qy   1573  KPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKIC  1628
           :|   |  ::                 :         :       :   :|
Db    657  ADSGACGPDSCPYCARAGAGEVELADREMPDSDEAVYEFTQDAQHSDLRDPHSRRQRSL   716

Db   1451  KPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL  1510
                                               :|:
Qy    451  ASLKSGKTESSSYFRR----------------------------KEKMFRF-          473

Qy   1629  NYIFTVIFVLESVFKLVAFGPRRFFQDRWNQLDLAIVLLSIMGITLEI-EVNASLPINP  1687
            |:|  |::|         ::||     ||| :|| ::  |:  ::    : ||
Db    717  GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALE  776

Db   1511  NIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDLVTEIAETN-----NF  1565
                  :|| |        : |:    ::   ||| ||| ||| ::
Qy    474  -FIRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLITTLY                  515

Qy   1688  TIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNIGLLFMLLFFIFAALGVELF  1747
            | :|  ||| |||| |  |||| |||| :||| |||  ||  |||||| :| |
Db    777  ISNIVFTSLFALEMLLKLLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQ-----QGGGLS  831

Db   1566  INLSFLRLFRAARLIKLLRQYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF  1625
             | ||||  ||| :||||| | |:| || || || |:  | |:: :||| |
Qy    516  FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGIS  575

Qy   1748  GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE--STC  1803
            ||    :         :|  :|:| |||| :|| || |:  |:  :|: :  :: :
Db    832  VLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF  891

Db   1626  GNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSLSNQACDEQANATE  1682
            ||:       :  :|      : ||||| :||| ||  :  |  | |:|
Qy    576  VLRALRLLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLIVFALLGMQLFGGQF  635

Qy   1804  YNTVISPIYFVSFVLTAQFVLVNVVIAVLM-----------------KHLEE         1838
            |:::       :| |  |                          | ||
Db    892  ASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIA  946

Db   1683  CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP  1742
            ||      |   ||:     |:||:|||| ||||
Qy    636  NFQDETPT----TNFDTFPAALLTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV  691

Qy   1839  ----------------------------------------------------------   1838
Db    947  LMTFGNYVLFNLLVAILVEGF-QAEEISK----REDASGQ--------LSCIQ         986

Db   1743  AACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISNEDMTVHFTSTLMAL  1802
            :: |        : | : ||                :   :     :::
Qy    692  LTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEAANQKLALQKAKEVAEVSPMSAAN  751

Qy   1839  ----------------------------------------------------------   1838
            :::      |                                :  ||   :
Db    987  LPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGE----------HPELRK   1033

Db   1803  IRTALEIKLAPAGTKQHQCDAELRKEISVVWANI-PQKTLDLLVP-----PHKPDEM   1853
                 |  ||    :      : |    |:|    :    :|:
Qy    752  ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT  811

Qy   1887  KPGALHPA-----------------------AHARSASHFSLEHPTM----QPHTELPGPD  1921
            ||                                :           :|
Db   1034  SLLPPLLIHTAATPMSLP------KSTSTGLGEALGPASR--------RTSSSG-  1073

Db   1854  TVGKVYAALIMIFDFYKQNKTTRDQMQAPGGLSQMGPVSLFHPLKATLEQTQPAVLRGAR  1913
            ||                 |             :          :
Qy    812  HLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHRHRDKDKTPAAGDQDRAEA  871

Qy   1922  LLTVRKSGVSRTHSLPNDSYMCRHGSTABGPLGHRGWGLPKAQSGSVLSVHSQPADTSYI  1981
                  :                      :  |  :         :
Db   1074  ----SAEPGA-------------AHEMKSPPSARS-----------SPH-----------SPWSAASSW  1103

Db   1914  VFLRQKSSTSLSN-------------------GGAIQNQESGIKESV----------SWG  1944
             |                                  :            |
Qy    872  PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGPEGGRRHRRGSPEEAAERE  931

Qy   1982  LQLPKDAPHLLQP----HSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIR----------TDS  2029
            |:                        :                   |
Db   1104  TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEERSSEE--------ERASP-  1153

Db   1945  TQRTQDAPHEARPPLERGHSTEI-------------PVGRSGALAVDVQMQSITRRGPDGEPQPG  1996
             |                                     |     |
Qy    932  PRRHRAHRH--QDPSKECAGAKGERRARHRGGPRAGPREAESGEEPARRHRARHKAQPA  988

Qy   2030  LDVQGLGSREDLLAEVSGP----SPPLARAYSFWGQSSTQAAQQHSRSHSKISKHMTPPAPC  2086
            |                         :|
Db   1154  ----------------AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRG  1191

Db   1997  LESQGRAASMPRLAAETQPVTDASPMKRSI-------STLAQRPRGTHLCST--TPDRPP  2047
                    |             :                 :  |
Qy    989  HEAVEKETTEKEATEKEAEIVEADKEKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL  1048

Qy   2087  PG---------------------PEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSP  2129
                                                   ||
Db   1192  SASEHQDCNGKSASGRLARALRPDDP------------PLDGDADDEGNL-----SKGE  1234

Db   2048  PSQASSHHHHRCHRRDRKQRSLEKGP---SLSADMDGAFSSAVGPGLPPG--EGPTGC  2102
             |                                        :
Qy   1049  QKVEEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTGPLGEATVVPSGNVDLESQAEGK  1108

Qy   2130  RDLKKCYSVEAQSCQRR-PTSWLDEQRRHSIAVSCLDSG-----------SQPHLG  2173
            |                                        :|
Db   1235  R-------VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF  1287

Db   2103  RRERERRQERGRSQERRQPSSSSSEKQRF--YSCDRFGGREPPKPKPSLSSHPTSPTAG  2159
                                              :|
Qy   1109  SMFCLSPINLLRRFCHYIVTMRYFEVVILVVIA                           1161

Qy   2174  TDP---------SNLGGQPL-----------------GGPGSRPKKKLSP-PSITI----DPPESQG  2209
             |                                :|
Db   1288  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN  1347

Db   2160  QEPGPHPQGSGSSVNGSPLLSTSGASTPGRGGRRQLPQTPLTPRPSITYKTANSSFHRA  2219
                 | |          |        :              :
Qy   1162  LSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFFEMVIKMIDLGLLLHPGAYFRDLWN  1220

Qy   2210  PRT--PP-SPG------ICLRRRAPSDSDSKDPLASGPPDSMAASPSPKKDVLSLSGL  2257
             |                        :
Db   1348  VLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLIKLVVETLM  1406

Db   2220  AQTSLPAFSPGRLSRGLSEHNALLQRDPLS-----QPLLAPG                  2258
             |                              :
Qy   1221  ILDFIVVSGALVAFAFSSFVGGSKGDINTIKSLRVLRVLRPLKTIKRLPLKAVFDCVV  1280

Qy   2258  SSDP  2261
            ||
Db   1407  SSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFYCQGE-----DTRN--ITNKSDCAEA  1458

Db   2259  GSDP  2262
            ||
Qy   1281  NSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYLDYEKEEVEA  1340

Qy   1459  SYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYF  1517
            |:                 |     | | | |    |:    :  |
Db   1341  QPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIFY  1400

Qy   1518  ISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREKRLRLEKKRRKA-----SRI  1572
             |                                                  :|
Db        (continued)                                             QC  1572
```

```
APPLICANT:  Sun Chen, Ai Ru
APPLICANT:  Suey, David J.
TITLE OF INVENTION:  NUCLEIC ACID ENCODING HUMAN NEURONAL
TITLE OF INVENTION:  CALCIUM CHANNEL SUBUNITS
NUMBER OF SEQUENCES:  6
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
   STREET:  Two Militia Drive
   CITY:  Lexington
   STATE:  MA
   COUNTRY:  USA
   ZIP:  02173-4799
COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/08/713,118
   FILING DATE:  16-SEP-1996
   CLASSIFICATION:  435
ATTORNEY/AGENT INFORMATION:
   NAME:  Mata, Elizabeth W.
   REGISTRATION NUMBER:  38,236
   REFERENCE/DOCKET NUMBER:  ACC96-01
TELECOMMUNICATION INFORMATION:
   TELEPHONE:  617-861-6240
   TELEFAX:  617-861-9540
INFORMATION FOR SEQ ID NO: 2:
   SEQUENCE CHARACTERISTICS:
   LENGTH:  2337 amino acids
   TYPE:  amino acid
   TOPOLOGY:  linear
   MOLECULE TYPE:  protein
US-08-713-118-2
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Query Match        14.7%;  Score 1749;  DB 3;  Length 2337;
Best Local Similarity   24.3%;  Pred. No. 3.1e-133;
Matches  645;  Conservative 359;  Mismatches 832;  Indels 820;  Gaps 86;

Qy    14  GQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF-----------  61
Db    13  GGPGSGERARG-GGAGGAGGAGGPGPGGLLQPGQGQRVLYKQSIAQRARTMALYNP1PVKQNCFTV  71
Qy    62  ----FYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMRPCEDIACDSQRCRIL  117
Db    72  NRSLFVFSEDNVVRKYAKRITEWPPFEYMILATIIANCIVLAL---EQHLPDGDKTPMS  127
Qy   118  QAFDD---FIFAFFAVEMVVKVVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LD  170
Db   128  ERLDDTEPYFIGIFCFEAGIKIIALGPVFHKGSYLRNGWNVMDFVVVITGILLATAGTDFD  187
Qy   171  LQNVSFSAVRTVRLPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGV  230
Db   188  LR-----TLRAVRVLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAIIMFAIIGL  242
Qy   231  QLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRG  290
Db   243  EFYMGKFHKACF-----PNSTDAE------------------------PV---  263
Qy   291  DGGGGGPCGLDYEAYNSSSNTTCVWNNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQV  350
Db   264  --GDFPGKEAPARLCEGDTEC--REYWP---------GPNFGITNFDNILFAILTVFQC  310
Qy   351  ITLEGWVDIMYFVMD-AHSPYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQRES----  406
Db   311  ITMEGWTDILYNTNDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRR  370
Qy   407  --QIMREQRVRFLSNASTLAASFSEPGSCYEELLKYLVVLRKAARRLAQVSRAAGVRVG  463
Db   371  --RELNGYLEWIFKAEEVMLAEEDRNA----------------------  407
Qy   464  LLSSPAPLGLGQETQPSSSCSRSHRRLSVHHLVHHHHHHYHLGNGTLRAPRASPEIQD  523
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Db   408  ------------------------------------------EEKSPLDVLKRAATKKSRNDLIH-------AEEGED  436
Qy   524  RDANGSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPEASGRT  583
Db   437  RFAD----------------------------------------------------  440
Qy   584  VGSGKVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGA  643
Db   441  -----------------------------------------------------  440
Qy   644  CQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHS  703
Db   441  --LCAVGSPFARASLKSGKTESSSYFRR-------------KEKMRF  473
Qy   704  DLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIE  763
Db   474  FIRRMVKAQSFYWVLCVVALNTLCVAMV  502
Qy   764  YHEQPELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVISWEIV  823
Db   503  HYNQPRRLITTLYFAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVV  562
Qy   824  GQ---QGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLVMKTMDNVATFCMLLMLFIFI  878
Db   563  WAAIKPGSSFGISVLRALRLLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFIVV  622
Qy   879  FSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----  933
Db   623  FALLGMQLFGGQFNFQDETPT----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGG  678
Qy   934  ASTSSWAALYPIALMTFGNYVLFNLLVAILVEGF-QAEEISK---REDASQ-  981
Db   679  VSKGMFSSFYFIVLFLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEAANQKLALQKA  738
Qy   982  --------LSCIQLPVDSQGGDANKSSSEEPDFFSPSLLDGDGDRKKCLALVS-----  1024
Db   739  KEVAEVSPMSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCRALYSEMDPEERLR  798
Qy  1025  ---LGEHPELRKSLLPPLIIHTAATPMSLP---KSTSTGLGEALGPASR-----  1067
Db   799  FATTRHRPDMKTHLDRLVVELGRDGARGPVGGKARPEAAAPEGVDPPRRHRHRDKD  858
Qy  1068  RTSSSG--------------SAEPGA-------------AHEMKSPPSARS-----SPH------  1094
Db   859  KTPAAGDQDRAEAPKAESGEPGAREERPRPHRSHSKEAAGPEARSERGRGPGEGGRRH  918
Qy  1095  SPWSAASSWTSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEE-  1148
Db   919  HRRGSPEEAAERPPRRHAHRH--QDPSKECAGAKGERRARHRGGPRAGPREAESGEEP  975
Qy  1149  ----ERASP------------------AGSDHRHRGSLEREAKSSFDLPDTL  1178
Db   976  ARRHARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTV  1035
Qy  1179  QVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDP---------PLDGDDADD  1226
Db  1036  TVGPMHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPPDNTIVIHIPVMLTGPLGEATVVP  1095
Qy  1227  EGNL-----SKGER------VRAWIRARLPACYLERDSWSAVIFPPQSRFRLLCHRIIT  1274
Db  1096  SGNVDLESQAEGKKEVEADDVMRSGPRPIVPYS------SMFCLSPTNLLRRFCHYIVT  1148
Qy  1275  HKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTKVVALGW  1334
Db  1149  MRYFEVVLVVIALSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDLGL  1207
Qy  1335  CFGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRVIS  1393
Db  1208  LLHPGAYFRDLWNILD----FIVSGALVAFASGSKGKDINTIKSLRVLRVLRPLKTIK  1263
Qy  1394  RAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE------DTR  1447
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RESULT 12

US-09-452-007-2

; Sequence 2, Application US/09452007
; Patent No. 6140485
; GENERAL INFORMATION:
;   APPLICANT: Franco, Rodrigo
;   APPLICANT: Sun Chen, Ai Ru
;   APPLICANT: Suey, David J.
;   TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
;   TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;   STREET: Two Militia Drive
;   CITY: Lexington
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02173-4799
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/452,007
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/713,118
;   FILING DATE: 16-SEP-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mata, Elizabeth W.
;   REGISTRATION NUMBER: 38,236
;   REFERENCE/DOCKET NUMBER: ACC96-01
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-861-6240
;   TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2337 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein

US-09-452-007-2

Query Match   14.7%; Score 1749; DB 3; Length 2337;
Best Local Similarity   24.3%; Pred. No. 3.1e-133;
Matches 645; Conservative 359; Mismatches 832; Indels 820; Gaps 86;

Qy   14 GQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF-----------   61
          |||||| ||||||
Db   13 GGPGSGERARG-GGAGGAGGPGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTV   71

Qy   62 ---FYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIL 117
             : ||:|| | |:|| |:|| |:| | |:| |||||| ||| |:|
Db   72 NRSLFVFSEDNVVRKYAKRITEWPPFEYMILATIIANCIVLAL---EQHLPDGDKTPMS 127

Qy   118 QAFDD---FIFAFFAVEMVVKQMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LD 170
          | || | | || | | | ||| ||| || | ||| | | || ||
Db   128 ERLDDTEPYFIGIFCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVLTGILATAGTDFD 187

Qy   171 LQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGV 230
          || : | | | | | | | || ||| | | || ||| |||| | |
Db   188 LR----TLRAVRVLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGL 242

Qy   231 QLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRG 290
           | | | | | | |: || :
Db   243 EFYMGKFHKACF------PNSTDAE----------------------------------- 263

Qy   291 DGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQV 350
          | ||||| |: ::   :: : : ::
Db   2256 ------SRIGSDP   2256

Qy   1264 RLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCR 1323
          |:|| | | ||: || | | | ||| | ||||| || | :| |
Db   1448 N--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQ 1504

Qy   1324 GQYLDYEKEEVEAQPRQWKKKYDFHYDNVLWALLTLFTVSTGEGWPVLKHSVDATYEEQG 1383
          | |||| | ||||||||| || |:| | |:| :| | | || :: | |:|
Db   1505 PIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKLRRLE 1564

Qy   1384 PSPGYRMELSIFYVYFVVFPFFVNIFVALIIITF------QEQGDKVMSE----CSLE 1433
          | |||| || | |:||||| :
Db   1565 KKRRKA------QCKPY--YSDYSR-FRLLVHHLCTSHYLDLFTTGVIGLNVVTMAMEHY 1615

Qy   1434 KNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVIMMKFY 1493
          | | | |: | | |:| | || |:| :|| ::|: | ||:|| |
Db   1616 QQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDIAIVLLSIMGITLE 1675

Qy   1494 DAPEYELMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDIIVT 1553
          | | | :| : :| | ||| || | |::|| :|| :|:
Db   1676 EIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLL 1735

Qy   1554 EIANNF--IN--LSFLRLFRAARLIKLLRQGYTIRILLLWTFVQSFKALPYVCLLIAML 1607
          | | | | |||||||| |||| | | |||| || || ||| | || |
Db   1736 FFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLR 1795

Qy   1608 FFIYAIIGMQVFGNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSCLS 1664
          || | ||| ||| | | | | | || ||||| ||| | : | |:
Db   1796 D--CDQE--STCVNTVISPIYFVSFVLTAQFVLNVVIAVLM-----------------KHL 1836

Qy   1665 NQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHL 1724
          | |||| |||||| |: :||| |: || | : : | :
Db   1837 EE-- 1838

Qy   1725 DEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISNED 1784
          | | | | |||| | | |:|| || | :
Db   1839 ------------------SNKEAKEAEALEAELELEMKTLSPQPHSPLGSPFLW 1874

Qy   1785 MTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANL-PQKTLDLLVP--- 1840
          : | : | | | : ||||
Db   1875 PGVEGPDSPDSPKPGALHPA-------------------AHARSASHFSLEHPTM----- 1910

Qy   1841 ----PHKPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLFHPLKATL 1895
          |||| | | || |:
Db   1911 -QPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVL 1969

Qy   1896 EQTQPAVLRGARVFLRQKSSTSLSN------------------GGAIQNQESGIKE 1933
          || | | | | |: :| | ||| |:| | |
Db   1970 SVHSQPADTSYILQLPKDAPHLLQP-------HSAPTWGTIPKLPPPGRSPLAQRPLRRQAA 2024

Qy   1934 SV---------SWGTQRTQDAPHEARPLERGHSTEI-------PVGRSGALAVDVQMQSI 1978
          : |
Db   2025 IR------TDSLDVQGLGSREDLLAEVSGP---SPPLARAYSFWGQSSTQAQQHSRSHS 2074

Qy   1979 TRRGPDGEPQPGLESQGRAASMPRLAAETQPVTDASPMKRSI-------STLAQRPRGTHL 2032
          ||
Db   2075 KISKHMTPPAPCPG---------------PEPNWGKGPPETRSSLELDTELSWISGDL 2117

Qy   2033 CST----TDPRPPSQASSHHHHRCHRRRDRKQRSLEKGP---SLSADMDGAPSSAVGPG 2086
          | |
Db   2118 LPPGGQQEEPPSPRDLKKCYSVEAQSCQRR-PTSWLDEQRRHSIAVSCLDSG-------- 2167

Qy   2087 LPPG---EGPTGCRERERRQERSRSQERRQPSSSSSEKQRF---YSCDRFGGGREPPKPKP 2141
          |||
Db   2168 --SQPHLGTDP-------SNIGGQPL-------GGPGSRPKKKLSP-PSITI 2202

Qy   2142 SLSSHPTSPTAGQEPPGPHPQGSGSVNGSPLLSTSGASTPGRGRRQLPQTPLPTPRPSTTY 2201
          | ||||
Db   2203 --DPPESQGPRT--PP-SPG-------ICLRRRAPSSDSKDPLASGPPDSMAASP 2245

Qy   2202 KTANSSPIHFAGAGTSLPAFSPGRLSRGLSEHNALLQRDPLS--QPLAPG------- 2249

Qy   2246 SPKKDVLSLSGLSSDP 2261
          ||||| |:| | |:||
Db   2250 -------SRIGSDP 2256

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Db   264  ---GDFPCGKEAPARLCEGDTEC---REYWP-------GPNFGITNFDNILFAILTVFQC 310
          ::  ||:|| |                  :                 ||| |||:||:||||
Qy   1275 HKMFDHVVIVIFFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTKVVVALGW 1334

Qy   351  ITLEGWVDIMYFVMD-AHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRES-- 406
          || :|||                :|   :| || | :|| ||  ||   || :
Db   1149 MRYFEVVILVVIALSSIALAAEDP-VRTDSPRNNALKYIDYIFTGVFTFEMVIKMIDLGL 1207

Db   311  ITMEGWTDILYNTNDAAGNTWNWLYFIFPILIIIGSFFMNLIVLGVLSGEFAKERERVENRR 370
          ||:|||  ||: |||  || |||||:
Qy   1335 CFGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRVIS 1393

Qy   407  --QLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVG 463
           :  |||:                       |:  :|:   | ||:|
Db   1208 LLHPGAYFRDLWNILD----FIVVSGALVAFAFGSGKGDINTIKSLRVLRVLRPLKTIK 1263

Db   371  AFLKLRRQQQIE---------------RELNGYLEWIFKAEEVMLAEEDRNA----- 407
          |:|||:| :|:                |  || | :| |  ::|  |:||:
Qy   1394 RAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLLGVQLFKGKFFVCQGE------DTR 1447

Qy   464  LLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQD 523
          :| | |     | | ||: :||| |:|| |
Db   1264 RLPFKLAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCR 1323

Db   408  --EBKSPLDVLKRAATKKSRNDLIH- 436
             :|||  ||:|   :| :||:|:
Qy   1324 N--TTNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQ 1448

Qy   524  RDANGSRRRLMLPPSTPALSGAPPGGARSVHSFYHADCHLEPVRCQAPPPRSPSEASGRT 583
          :  |    |: |
Db   1324 GQYLDYEKEEVEAQPRQWWKKYDFHYDNVLWALLLTFVSTGEGWPMVLKHSVDATYEEQG 1383

Db   437  RFAD------------- 440
          :| |
Qy   1505 PIMNFNPWMLLYFISFLLIVAFFVLNMFVGVVVENPHKCRQHQEEEEARRREEKRLRRLE 1564

Qy   584  VGSGKVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGA 643
          :  |                    |
Db   1384 PSPGYRMELSIFYVVYFVVFPFFFNIFVALIIITF-------QEQGDKVMSE----CSLE 1433

Qy   441  ------------- 440
          :    :     :  |
Db   1434 KNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFY 1493

Qy   441  CQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEPTQDAQHS 703
          :  :  |            |:
Db   1434 KNERACIDFAISAKPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFY 1493

Qy   441  --LCAVGSPFARASLKSGKTESSSYFRR--------KERMFRF------- 473
           | | |                      |  |
Db   1616 QQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLLDAIVILLSIMGITLE 1675

Db   704  DLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIE 763
          |:       |                    | ::| :    | ::| |:|||
Qy   1494 DAPYEYELMLKCLNIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDVFIVLGSSITDLIVT 1553

Qy   474  -------------FIRRMVKACQSFYWVVLCVVALNTLCVAMV 502
                      |:  |   :|:||:| ||| ||:|
Db   1676 EIEVNASLPINPTIIRIMRVLRIARVLKLRKMAVGMRALLDTVMQALPQVGNLGLLFMLL 1735

Db   764  YHEQPEELTNALEISNIVFTSLFALEMLLKLLLVYGPFGYIKNPYNIFDGVIVVISVWEIV 823
          :    | ::| :|  :          | |                | |:|  |
Qy   1554 EIANNF--IN--LSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPVCLLIAML 1607

Qy   503  HYNQPRRLTTTLYFAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVV 562
          |    | : | ||  |:   |  ||      |        | |::|   | : ||
Db   1736 FFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRVSTGDNWNGIMKDTLR 1795

Db   824  GQ--------QGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLMLFIFI 878
           |          | |  | | |:  | |::|    |         :  |  | |: |||
Qy   1608 FFIYAIIGMQVFGNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSCLS 1664

Qy   563  WAAIKPGSSFGISVLRALRLLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFIVV 622
          | |:    | |:  | | || |  :||            |: :    |  | ||::| :
Db   1676 D--CDQE--STCYNTVISPIYFVSFVLTAQFVLNVVLAVLM---------KHL 1836

Db   879  FSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM------ 933
          :  :    ||:|   |             :   |::  |    | ||   |:
Qy   1554 EIANNF--IN--LSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPVCLLIAML 1607

Qy   503  HYNQPRRLTTTLYFAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVV 562
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Db   1665 NQACDEQANATECGSDPFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHL 1724

Db   623  ---FALLGMQLFGGQFNFQDETPT-----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGG 678
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Qy   1837 EE--- 1838

Qy   934  ASTSSWAALYFIALMFGNYLFLNLLVAILVEGF-QAEEISK--REDASGQ- 981
          :    ::   |:   || ||: :   |:
Db   1725 DEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMMMPISNED 1784

Db   679  VSKGMFSSFYFIVLTLFGNYTLLNVPLAIAVDNLANAQELTKDEEEMEEAANQKLALQKA 738
          |  :  ||   :   | || |::     |       :|   :::|   :|
Qy   1785 MTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANL-PQKTLDLLVP- 1840

Qy   982  --LSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVS--------- 1024
          :      |                    |
Db   1839 --------------------SNKRAKEEABLEAELELEMKTLSPQHSPLGSPPLW 1874

Db   739  KEVAEVSPMSAANISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLR 798
          :  |   |            ::    ||                   |   ::
Qy   1875 PGVEGPDSPDSPKPGALHPA--------------------AHARSASHFSLEHPTM- 1910

Qy   1025 ----LGEHPELRKSLLPPLLIHTAATPMSLP----KSTSTGLGEALGPASR----- 1067
          ::   ||   | |:
Db   1841 -----PHKPDEMTVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLFHPLKATL 1895

Db   799  FATTRHRRPDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRKD 858
          :
Qy   1911 -QPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVL 1969

Qy   1068 RTSSSG-----SAEPGA-------AHEMKSPPSARS------SPH------ 1094
          :   |       :   |                            :
Db   1896 EQTQPAVLRGARVLRQKSSTSLSN------------------GGAIQNQESGIKE 1933

Db   859  KTPAAGDQDRAEAFPKAESGEPGAR EERRPPHRSHSKEAAGPPEARSERGRGPGPEGGRRH 918
          |
Qy   1970 SVHSQOPADTSYILQQLPKDAPHLLQP---------HSAPTWGTIPKLPPPGRSPLAQRPLRRQAA 2024

Qy   1095 ----SPWSAASSWTSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEE- 1148
                  |             |                    |
Db   1934 SV-----------------SWGTQRTQDAPHEARPPLERGHSTEI----------PVGRSGALAVDVQMQSI 1978

Db   919  HRRGSPEEAAERREPRRHRAHRH--QDPSKECAGAKGERRARHRGGPRAGPREAEASGEEP 975
          :
Qy   2025 IR-----TDSLDVQGLGSREDLLAEVSGP---SPPLARAYSFWGQSSTQAQQHSRSHS 2074

Qy   1149 ----ERASP---------------AGSDHRHRGSLEREAKSSFDLPDTL 1178
          :
Db   1979 TRRGPDGEPQPGLESQGRAASMPRLAAETQPVTDASPMKRSI-------STIAQPRGTHL 2032

Db   976  ARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTV 1035
          :
Qy   2075 KISKHMTPPAPCPG------------------PEPNWGKGPPETRSSLELDTELGWISGDL 2117

Qy   1179 QVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDP-----------PLDGDDADD 1226
          :   :
Db   2033 CST---TPDRPPPSQASSHHHHRCHRRRDRKQRSLEKGP---SLSADMDGAPSSAVGPG 2086

Db   1036 TVGPMHTLPSTCLQKVEEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTGPLGEATVP 1095
          :
Qy   2118 LPPGGQEEPSPRDLKKCYSVEAQSCQRR-PTSWLDEQRHSIAVSCLDDG--------- 2167

Qy   1227 EGNL-----SKGER------VRAWIRARLPACYLERDSWSAYIFPPQSRFLLCHRIIT 1274
          :   :
Db   2087 LPPG-----EGPTGCRRERRERQERSRSQERRQPSSSSSSEKQRF---YSCDRFGGREPPKPKP 2141

Db   1096 SGNVDLESQABGKKEVEADDVMRSGPRPIVPYS--------SMFCLSPTNLLRRFCHYIVT 1148
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Qy  2168  --------SQPHLGTDP--------SNLGGQPL---------GGPGSRPKKKLSP-PSITI  2202
                  :   :|| |        : :|  |         ||  |  : |: ||||
Db  2142  SLSSHPTSPTAGQEPGPHPQQSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITY   2201

Qy  2203  ------DPPESQGPRT--PP-SPG-------ICLRRRAPSSDSKDPLASGPPDSMAASP   2245
                  | :|  || |  || ||         :||  ||  : |: ||
Db  2202  KTANSSPIHFAGAQTSLPAFSPGRLSRGLSEHNAILQRDPLS---QPLAPG---------  2249

Qy  2246  SPKKDVLSLSGLSSDP   2261
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Db  2250  --------SRIGSDP   2256
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RESULT 13
US-08-455-543A-47
; Sequence 47, Application US/08455543A
; Patent No. 5792846
GENERAL INFORMATION:
;   APPLICANT: Harpold, Michael
;   APPLICANT: Ellis, Steven
;   APPLICANT: Williams, Mark
;   APPLICANT: Feldman, Daniel
;   APPLICANT: McCue, Ann
;   APPLICANT: Brenner, Robert
;   TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;   TITLE OF INVENTION: METHODS
;   NUMBER OF SEQUENCES: 57
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Brown, Martin, Haller & McClain
;   STREET: 1660 Union Street
;   CITY: San Diego
;   STATE: California
;   COUNTRY: USA
;   ZIP: 92101-2926
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/455,543A
;   FILING DATE: May 31, 1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/223,305
;   FILING DATE: April 4, 1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/868,354
;   FILING DATE: April 10, 1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/745,206
;   FILING DATE: 15-AUG-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/620,250
;   FILING DATE: 30-NOV-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/482,384
;   FILING DATE: 20-FEB-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/603,751
;   FILING DATE: 04-APR-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US89/01408
;   FILING DATE: 04-APR-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/176,899
;   FILING DATE: 04-APR-1988
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Seidman, Stephanie L.
;   REGISTRATION NUMBER: 33,779
;   REFERENCE/DOCKET NUMBER: 6362-52517
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619)238-0999
;   TELEFAX: (619)238-0062
;
; INFORMATION FOR SEQ ID NO: 47:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2339 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FRAGMENT TYPE: internal
US-08-455-543A-47

Query Match   14.7%; Score 1748.5; DB 1; Length 2339;
Best Local Similarity   24.2%;
Matches 641; Conservative 359; Mismatches 825; Indels 819; Gaps 85;
                                                       Pred. No. 3.4e-133;

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Qy   27  GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF-----------------FYLSQDSRP   70
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Db   25  GAGGAGGPGPGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV   84

Qy   71  RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFDD---FIFAF   127
          | |:| | | |  | |:| | || |: | |  :             |:  |    |:|
Db   85  RKYAKRITEWPPFENMLLATIIANCIVLAL----EQHLPDGDKTPMSERLDDTEPYFIGI   140

Qy  128  FAVEMVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR   183
          | | |:|::|| :|| | ||  : ||:||| |: |: :      |:|   |: |:| |
Db  141  FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR---TLRAVR   195

Qy  184  VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFL   243
          ||||: :   |:  |:::  |   :| ::|||| :| | | |: |  :   |:  :||
Db  196  VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-   254

Qy  244  PENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYE   303
                  :                          | |                 |:
Db  255  ------PNSTDAE----------------------------------PV-------GDFPCGKEAP   273

Qy  304  AYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV   363
             :  :||          :   | : |   |||||:  ||| |:| ::| |: ||:| |
Db  274  ARLCEGDTEC--REYWP--------GPNFGITNFDNILFAILTVFQCITMBGWTDILYNT   323

Qy  364  MD-AHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES-------QLMREQRVRF   416
          :    :  | ||::|:|||||||:|||:| | |  | |           :  : ::|  |:
Db  324  NDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE-   382

Qy  417  LSNASTLASFSRPGSCYEELLKYLYVIYLRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET   476
                                  :|  :|  :| |                            ::|
Db  383  ------------------RELNGYLEWIFKAEEVMLAEEDRNA--------------EEK   410

Qy  477  QPSSSCSRSHRRLSVHHIVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP   536
           |    :     |: | :|                                  |
Db  411  SPLDVLKRAATKKSRNDLIH----------------------------AEEGEDRFAD----   440

Qy  537  PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTS   596
Db  441  ---------------------------------------------------------------   440

Qy  597  PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK   656
Db  441  ---------------------------------------------------------------   440

Qy  657  ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL   716
                     :                  :                        ::
Db  451  ASLKSGKTESSSYFRR-----------------------------KERMFRF--------   473

Qy  717  GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALE   776
                                :  :  :| || |::|| |:||:|| |              |
Db  474  ---------------------FIRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLY   515

Qy  777  ISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQ----QGGGLS   831
           :: :| :|| |::|:||  | || | :  :|  ||:|||  :::|:|       |||:
Db  516  FAEFVLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGIS   575

Qy  832  VLRTPRLMRVLKLVRFLPALQRQLVVLKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF   891
          |||: ||:|::|:::|:  :  :|| |::: : : ::|:|:|:|:|:| |||:||| :|
Db  576  VLRALRLLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFIVFALLGMQLFGGQF   635
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Qy    892 ASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIA  946
Db    636 NFQDETPT----TNFDIFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV  691

Qy    947 LMTFGNYVLFNLLVAILVEGF-QAEEISK-----REDASGQ-----------LSCIQ    986
Db    692 LTLFGNYTLLNVFLAIAVDNLNAQELTKDEEMEEAANQKLALQKAKEVAEVSPMSAAN   751

Qy    987 LPVDSQGGDANKSESEPDFFSFSLDGDGRKKCLALVSLGE---------HPELRK    1033
Db    752 ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT  811

Qy   1034 SLLPPLIIHTAATPMSLP-----KSTSTGLGEALGPASR-------RTSSSG-    1073
Db    812 HLDRPLVVLGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRDKDKTPAAGDQDRAEA  871

Qy   1074 ----SAEPGA-------------AHEMKSPPSARS-------SPH-------SPWSAASSW 1103
Db    872 PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGPEGGRRHHRRGSPEEAAERE  931

Qy   1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEE-----------ERASP- 1153
Db    932 PRRHRAHRH---QDPSKECAGAKGERRARHRGGPRAGPEAEASGEEPARRHRARHKAQPA  988

Qy   1154 -------AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRG 1191
Db    989 HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048

Qy   1192 SASEHQDCNGKSASGRLARALRPDDP---------PLDGDADDEGNL------SKGE 1234
Db   1049 QKVEEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTGPLGEATVVPSGNVDLESQAEGK 1108

Qy   1235 R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKVMFDHVVLVIIF 1287
Db   1109 KEVEADDVMRSGPRPIVPYS----SMFCLSPTNLLRRFCHYIVTMRYFEVVILVVIA 1161

Qy   1288 LNCIITAMERPKIDPHSAERIFLTLSNYITTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347
Db   1162 LSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDLGLLLHPGAYFRDLWN 1220

Qy   1348 VLDGLLVLLISVIDIIVSMV-SDSGTKILGMRLVLRLRLRTLRPLRVISRAQGLKLVVFTLM 1406
Db   1221 ILD----FIVVSGALVAFASFSGSSKGKDINTIKSLRVLRVLRPLKTIKRLPKLKAVFDCVV 1276

Qy   1407 SSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE-----DTRN--IINKSDCAEA 1458
Db   1277 NSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYLDYEKEEVEA 1336

Qy   1459 SYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHPWMLLYF 1517
Db   1337 QPRQWKKYDFHYDNVLWALLLFTVSTGEGWPVLKHSVDATYEEQGPSPGYRMELSIFY 1396

Qy   1518 ISFLLIVAFFVLNMFVGVVENFHKCRQHQEEEEARRREEKRLRLEKKRRKA-----QC 1572
Db   1397 VVVFVVFPFFVNIFVALIIITF-----QEQGDKVMSE-----CSLEKNERACIDFAISA 1446

Qy   1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKIC 1628
Db   1447 KPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL 1506

Qy   1629 NYIFTVIFVLESVFKLVAPGFRRFFQDRKWNQLDIAIVLLSIMGITLEEI-EVNASLPINP 1687
Db   1507 NIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSIITDILVTEIAETN-----NF 1561

Qy   1688 TIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELF 1747
Db   1562 INLSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF 1621

Qy   1748 GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE-STC 1803
Db   1622 GNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678
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Qy   1804 YNTVISPIYFVSFVLTAQFVLNVVIAVLM-----------------------KHLEE----- 1838
Db   1679 CGSDFAYFYFVSPIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1738

Qy   1839 ----------------------------------------------------------- 1838
Db   1739 AACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMP1SNEDMTVHFTSTLMAL 1798

Qy   1839 -----------------------SNKEAKEAELAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSP 1886
Db   1799 IRTALEIKLAPAGTYKQHQCDAELRKEISVVWANL-PQKTLDLLVP----PHKPDEM 1849

Qy   1887 KPGALHPA------------------------AHARSASHFSLEHPTM-----QPHPTELPGPD 1921
Db   1850 TVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLFHPLKATLEQTQPAVLRGAR 1909

Qy   1922 LLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQGSGVLSVHSQPADTSYI 1981
Db   1910 VFLRQKSSTSLSN----------------GGAIONQESGIKESV-----SWG 1940

Qy   1982 LQLPKDAPHLLQP-----HSAPTWGTIPKLPPGRSPLAQPRLRQAAIR-----TDS 2029
Db   1941 TQRTQDAPHEARPPLERGHSTEI-----PVGRSGALAVDVQMQSITRRGPDGEPQPG 1992

Qy   2030 LDVQGLGSREDLLAEVSGP---SPPLARAYSFWGSSTQAQQHSRSHSKISKHMTPPAPC 2086
Db   1993 LESQGRAAASMPRLAAETQPVTDASPMKRSI-----STLAQRPRGTHLCST---TPDRPP 2043

Qy   2087 PG-----------------------PEPNWGKGPPETRSSLELDTELSWISGDLLPGGQEEPSP 2129
Db   2044 PSQASSHHHHRCHRRRDRKQRSLEKGP---SLSADMDGAPSSAVGPGLPPG--EGPTGC 2098

Qy   2130 RDLKKCYSVEAQSCQRR-PTSWLDEQRRHSIAVSCLLDSG-----SQPHLG 2173
Db   2099 RRERERRQERGRSQERRQPSSSSSSEKQRF---YSCDRFGGREPPKPKPSLSSHPTSPTAG 2155

Qy   2174 TDP-----SNLGGQPL-----------------GGPGSRPKKKLSP-PSITI----DPPESQG 2209
Db   2156 QEPGPHPQGSGSVNGSPLLSTSGASTPGRGGRRQLPQTPLTPRPSITYKTANSSPIHFAG 2215

Qy   2210 PRT--PP-SPG-----------ICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL 2257
Db   2216 AQTSLPAFSPGRLSRGLSEHNALLQRDPLS-----QPLAPG-----SRI 2254

Qy   2258 SSDP 2261
Db   2255 GSDP 2258
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/223,305C
  FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/868,354
  FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/745,206
  FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/620,250
  FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/482,384
  FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/603,751
  FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US89/01408
  FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/176,899
  FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
  NAME: Seidman, Stephanie L.
  REGISTRATION NUMBER: 33,779
  REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (619)238-0999
  TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 47:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 2339 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  FRAGMENT TYPE: internal
US-08-223-305C-47
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Query Match        14.7%;  Score 1748.5;  DB 2;  Length 2339;
Best Local Similarity  24.2%;  Pred. No. 3.4e-133;
Matches  641;  Conservative  359;  Mismatches  825;  Indels  819;  Gaps  85;
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Qy    27 GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF--------------------FYILSQDSRP  70
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Db    25 GAGGAGGPGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV  84

Qy    71 RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAF 127
            |:||:||  ||  ||::|::|:  |  |||
Db    85 RKYAKRITEWPPFENMILATIIANCIVLAL----EQHLPDGDKITPMSERLDDTEPYFIGI 140

Qy   128 FAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR 183
            ||::|:||||:|  |:||||||||  ||||||||:||
Db   141 FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR----TLRAVR 195

Qy   184 VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFL 243
            ||:||::|:|:::   |:||  || ||:||:|::|: |||
Db   196 VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFPHKACF 254

Qy   244 PENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYE 303
            ||     ||
Db   255 ---PNSTDAE--------------------PV-----GDFPCGKEAP 273

Qy   304 AYNSSSNNTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363
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Db   274 ARLCEGDTEC--REYWP------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNT 323

Qy   364 MD-AHSFYNFIYFLLIIVGSFFMINLCLVVIATQFSETKQRES------QLMREQRVRF 416
            | |: ||||:   ||||:|||  |  | |||: ::
Db   324 NDAAGNTWNWLYFIPILIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE- 382
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Qy   417 LSNASTLASFSEPGSCYEELLKYLVYILRKAARRILAQVSRAAGVRVGLLSSPAPLGGQET 476
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Db   383 --------------------RELNGYLEWIFKAEEVMLAEEDRNA-----------EEK 410

Qy   477 QPSSSCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536
            ||
Db   411 SPDLVLKRAATKKSRNDLIH---------------------AEEGEDRFAD-- 440

Qy   537 PSTPALSGAPPGGAESVHSPFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTS 596
Db   441 ------------------------------------------------ 440

Qy   597 PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK 656
Db   441 ----------------------------------LCAVGSPFAR 450

Qy   657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL 716
            : :::  :|:
Db   451 ----------ASLKSGKTESSSYFRR---------------KEKMFRF- 473

Qy   717 GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHBQPEELTNALE 776
            |:::::|:|   :  ||| |  |:|::|: ||:|:::|| :||
Db   474 ------------FIRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLY 515

Qy   777 ISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWWEIVGQ-----QGGGLS 831
            ||:||  |:  |  :::|: |  |  || |::  ||:|:|:|: :::
Db   516 FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCPDFGVIVGSVPEVVWAAIKPGSSFGIS 575

Qy   832 VLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF 891
            |||:|||:||  |:||  ||:|::|:||:|
Db   576 VLRALRLLRIFKVTKYWSSLRNLVVSLLNSMKSIISLLFLLFLFIVFALLGMQLFGGQF 635

Qy   892 ASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGM-----ASTSGWAALYFIA 946
            |:|  |   |  |  :| |||:|:|||||||:|||| |:::
Db   636 NFQDETPT----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV 691

Qy   947 LMTFGNVLFNLLVAILVEGF-QAEEISK---REDASGQ-----------------LSCIQ 986
            |:||||| :|| | |  |:  :::| :
Db   692 LTLFGNYTLLNVFLAIAVDNLANAQELTKDEEMEEAANQKLALQKAKEVAEVSPMSAAN 751

Qy   987 LPVDSQGGDANKSESEPDFFPSPLDGDGDRKKCLALVSLGE----------------HPELRK 1033
            | |:::
Db   752 ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT 811

Qy  1034 SLLPPLLIHTAATPMSLP--------KSTSTGLGEALGPASR----------RTSSSG- 1073
            |:::
Db   812 HLDRPLVVELGRDGARGPVGVGKARPEAAAEPGVDPPRRHHRDKDKTPAAGDQDRAEA 871

Qy  1074 ----SAEPGA----------------AHEMKSPPSARS------SPH----------SPWSAASSW 1103
            :|:|
Db   872 PKAESGEPGARERERPRPHRSHSKEAAGPPEARSERGRGPGEGGRRHHRRGSPEEAAERE 931

Qy  1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEE------------ERASP- 1153
            ||:
Db   932 PRRHRAHRH---QDPSKECAGAKGERRARHRGGPRAGPREAESGEPARRHRARHKAQPA 988

Qy  1154 ----------------------------AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRG 1191
Db   989 HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048

Qy  1192 SASEHQDCNGKSASGRLARALRPDDP----------------PLDGDDADDEGNL-----SKGE 1234
Db  1049 QKVEEQPEDADNQRNVTRMGSQPPDPNTVHIPVMLTGPLGEATVVPSGNVDLESQAEGK 1108

Qy  1235 R----VRAWIRARLPACYLERDSWSAVIFPPQSRFLLCHRIITHKMFDHVLVIIF 1287
            :
Db  1109 KEVEADDVMRSGPRPIVPYS------SMFCLSPTNLLRRFCHYIVTMRVFEVVILVVIA 1161

Qy  1288 LNCITIAMERPKIDPHSABRIFLTLSNYIFTAVFLAEMTVKVVAIGWCFGEQAYLRSSWN 1347
            | : :||||| |: :||:|  | :::  :| |: ::
Db  1162 LSSIALAAEDP--VRTDSPRNNALKYLDYIFTGVTTFEMVIKMIDLGLLHPGAYFRDLWN 1220
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Qy   2210 PRT--PP-SPG--------------ICLRRRAPSSDSKDPLASGPPDSMAASPSKKDVLSLSGL 2257
                                      :::   --SRI
Db   2216 AQTSLPAFSPGRLSRGLSEHNALLQRDPLS----QPLAPG------------------------ 2254

Qy   2258 SSDP 2261
Db   2255 GSDP 2258

RESULT 15
US-09-268-163-6
; Sequence 6, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
;   LENGTH: 2339
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-268-163-6

  Query Match   14.7%; Score 1746.5; DB 3; Length 2339;
  Best Local Similarity   24.2%; Pred. No. 5e-133;
  Matches 641; Conservative 359; Mismatches 825; Indels 819; Gaps 85;

Qy   27 GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF------------------FYLSQDSRP 70
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Db   25 GAGGAGGPGPGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV 84

Qy   71 RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFDD----FIFAF 127
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Db   85 RKYAKRITEWPPFEYMILATIIANCIVAL-------EQHLPDGKTPMSRLDDTEPYFIGI 140

Qy 128 FAVEMVVKMVALG--IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR 183
           ||:: |:| :|::| : :| |||:|| ||::|::| |:: |: ::|
Db 141 FCFEAGIKIIALGVFHHKGSYLRNGWNVMDFVVVITGILATAGTDFDLR----TLRAVR 195

Qy 184 VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIGIVGVQLWAGLLRNRCFL 243
           ||||||:| :||:| || :|| |||: ||| | | :||| | | ||| :|
Db 196 VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF 254

Qy 244 PENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGDGGGPPCGLDYE 303
           | -PV-----
Db 255 ------PNSTDAE-------------------------------------GDFPCGKEAP 273

Qy 304 AYNSSSNTTCVRNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363
           || | :: | ::   :: :: | :
Db 274 ARLCEGDTEC---REYWP---------GPNFGITNFDNILFAILIVFQCITMEGWTDILYNT 323

Qy 364 MD-AHSFYNFIYFIPLILIIVGSFEMINLCLVVIATQFSETKQRES----QLMREQRVRF 416
           || |::|| |||: ::||:|| ||| | :::| :| |: :|
Db 324 NDAAGNTWNWLYFIPLIIIGSFEMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE- 382

Qy 417 LSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRGVLLSSPAPLGGQET 476
                                          :: :::   --EEK
Db 383 ---------------------------------RELNGYLEWIFKAEEVMLAEEDRNA-- 410

Qy 477 QPSSSCCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536
                                                             AEEGEDRFAD--
Db 411 SPLDVLKRAATKKSRNDLIH-------------------------------------- 440

Qy 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTS 596
Db 441 --- 440

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Qy   597 PPPETLKEKALVEVAASSGPPTLISLNIPGPYSSMHKLLETQSTGACQSSCKISSPCLK 656
Db   441 ----------------------------------------------LCAVGSPFAR 450

Qy   657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL 716
Db   451 ASLKSGKTESSSYFRR-------------------------KEKMFRF 473

Qy   717 GPDAEPSSVLAFWRLICDTFRKIVDSKYPGRGIMIAILVNTLSMGIEYHEQPEELTNALE 776
Db   474 -----------FIRRMVKAQSFWVVLCVVALNTLCVAMVHYNQPRRLTTTLY 515

Qy   777 ISNIVFTSLFALEMLLKLLVYGPPGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGLS 831
Db   516 FAEFVFLGLFLITEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGIS 575

Qy   832 VLRTFRLRMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF 891
Db   576 VLRALRLLRIFKVTKYWSSLRNLVVSLLNSMKSIISILFLLLFLFIVVFALLGMQLFGGQF 635

Qy   892 ASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGM-----ASTSSWAALYFIA 946
Db   636 NFQDETPT---TNFDTFPAAIITVFQLLTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV 691

Qy   947 LMTFGNYVLFNLLVAILVEGF-QAEEISK-----REDASGQ----------LSCIQ 986
Db   692 LTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEAANQKLALQKAKEVAEVSPMSAAN 751

Qy   987 LPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGE------------HPELRK 1033
Db   752 ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT 811

Qy  1034 SLLPLIIHTAATPMSLP------KSTSTGLGEALGPASR-----------RTSSSG---- 1073
Db   812 HLDRPLVVELGRDGARGPVGGKARPEAEAPEGVDPPRRHHRDKTPAAGDQDRAEA 871

Qy  1074 ----SAEPGA-------AHEMKSPPSARS--------SPH-----------SPWSAASSW 1103
Db   872 PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGEGGRRHHRRGSPEEAAERE 931

Qy  1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEE-------ERASP- 1153
Db   932 PRRHRAHRH---QDPSKECAGAKGERRARHRGPRAGPREAESGEEPARRHRARHKAQPA 988

Qy  1154 --------AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRG 1191
Db   989 HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPRRPHCDLETSGTVTVGPMHTLPSTCL 1048

Qy  1192 SASEHQDCNGKSASGRLARALRPDDP-------------PLDGDDADDEGNL-----SKGE 1234
Db  1049 QKVEEQPEDADNQRNVTRMGSQPPDPNTIVHIPVMLTGPLGEATVVPSGNVDLESQAEGK 1108

Qy  1235 R-------VRAWIRARLPACVLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLIVIF 1287
Db  1109 KEVEADDVMRSGPRPIVPYS------SMFCLSPTNLLRRFCHYIVTMRYFEVVLVVIA 1161

Qy  1288 LNCTTIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVKVALGWCFGEQAYLRSSWN 1347
Db  1162 LSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDLGLLLHPGAYFRDLWN 1220

Qy  1348 VLDGLLVLLSVIDILIVSMV-SDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLM 1406
Db  1221 ILD-----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRVLRPLKTIKRLPKLKAVFDCVV 1276

Qy  1407 SSLKPIGNIVVICCAFFIIFGILGVQLFKGKFVCQGE-----DTRN--ITNKSDCAEA 1458
Db  1277 NSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYLDYEKEEVEA 1336

Qy  1459 SYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYF 1517
Db  1337 QPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIFY 1396


Qy  1518 ISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEKRLRLEKKRRKA----QC 1572
Db  1397 VVYFVVFPFFVNIFVALIIITF------QEQGDKVMSE----CSLEKNERACIDFAISA 1446

Qy  1573 KPY--YSDYSR--FRLLVHHLCTSHYIDLFITGVIGLNVVTMAMEHYQQPQILDEALKIC 1628
Db  1447 KPLTRYMPQNRQSFQYKTWTFVVSPPPEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL 1506

Qy  1629 NYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEI-EVNASLPINP 1687
Db  1507 NIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDILVTEIAETN----NF 1561

Qy  1688 TIIRIMRVLIARVLKLLKMAVGMRALLDTVMQALPQVGNIGLLFMLLFFIFAALGVELF 1747
Db  1562 INLSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF 1621

Qy  1748 GDLECDETHPCEGLGRHATFRNFGMAFLITLLFRVSTGDNWNGIMKDTLRD--CDQE-STC 1803
Db  1622 GNIALDDD--TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678

Qy  1804 YNTVLSPIYFVSFVLTAQFVLVNVVIAVLM-----------------KHLEE------ 1838
Db  1679 CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1738

Qy  1839 ---------- 1838
Db  1739 AACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISNEDMTVHFTSTLMAL 1798

Qy  1839 ------SNKEAKEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSP 1886
Db  1799 IRTALEIKLAPAGTKQHQCDAELRKEISVVWANL-PQKTLDLLVP--PHKPDEM 1849

Qy  1887 KPGALHPA-------------AHARSASHFSLEHPTM---QPHPTELPGPD 1921
Db  1850 TVGKVYAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLFHPKATLEQTQPAVLRGAR 1909

Qy  1922 LLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYI 1981
Db  1910 VFLRQKSSTSLSN----------GGAIQNESGIKESV------SWG 1940

Qy  1982 LQLPKDAPHLLQP---HSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIR-----TDS 2029
Db  1941 TQRTQDAPHEARPPLERGHSTEI----------PVGRSGALAVDVQMQSITRRGPDGEPQPG 1992

Qy  2030 LDVQGLGGSREDLLAEVSGP--SPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPC 2086
Db  1993 LESQGRAAASMPRLAAETQPVTDASPMKRSI------STLAQRPRGTHLCST--TPDRPP 2043

Qy  2087 PG---PEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSP 2129
Db  2044 PSQASSHHHHHCHRRRDRKQRSLEKGP--SLSADMDGAPSSAVGPGLPPG--EGPTGC 2098

Qy  2130 RDLKKCYSVEAQSCQRR-PTSWLDEQRRHSIAVSCLDSG------SQPHLG 2173
Db  2099 RRERERRQRERGRSQERRQPSSSSSSEKQRF--YSCDRFGGREPPKPKPSLSSHPTSPTAG 2155

Qy  2174 TDP-----SNLGGQPL------GGPGPSRPKKKLSP-PSITI----DPPESQG 2209
Db  2156 QEPGPHPQGSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITYKTANSSPIHFAG 2215

Qy  2210 PRT--PP-SPG------ICLRRRAPSDSDSKDPLASGPPDSMAASPSPKKDVLSLSGL 2257
Db  2216 AQTSLPAFSPGRLSRGLSEHNALLQRDPLS-------QPLAPG 2254

Qy  2258 SSDP 2261
Db  2255 GSDP 2258
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Search completed: November 18, 2004, 13:36:33
Job time : 77.3132 secs

GenCore version 5.1.6

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QM protein - protein search, using sw model

Run on:　November 18, 2004, 13:32:41 ; Search time 178.672 Seconds
　　　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　4491.206 Million cell updates/sec

Title:　　　　　　US-09-611-257A-37
Perfect score:　 11904
Sequence:　　　　 1 MDEEDGAGAEESGQPRSFM.........PKKDVLSLGLSSDPADLDP 2266

Scoring table:　 BLOSUM62
　　　　　　　　　 Gapop 10.0 , Gapext 0.5

Searched:　　　　 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters:　　 1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
　　　　　　　　　 Maximum Match 100%
　　　　　　　　　 Listing first 45 summaries

Database :　　　 Published Applications AA:*
　　　　　　　　　 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
　　　　　　　　　 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
　　　　　　　　　 3: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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　　　　　　　　 16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	11815.5	99.3	2377	17	US-10-757-262-16	Sequence 16, Appl
2	11758.5	98.8	2243	16	US-10-408-765A-625	Sequence 625, App
3	11111	93.3	2374	16	US-09-383-894-2	Sequence 2, Appli
4	11111	93.3	2425	10	US-09-383-894-4	Sequence 4, Appli
5	6212	52.2	2353	16	US-10-408-765A-1128	Sequence 1128, Ap
6	5492.5	46.1	2175	9	US-09-935-541-2	Sequence 2, Appli
7	5492.5	46.1	2175	14	US-10-425-800-2	Sequence 2, Appli
8	5484	46.1	2188	9	US-09-935-541-4	Sequence 4, Appli
9	5484	46.1	2188	14	US-10-425-800-4	Sequence 4, Appli
10	5366	45.1	1835	9	US-09-935-541-5	Sequence 5, Appli
11	5366	45.1	1835	14	US-10-425-800-5	Sequence 5, Appli
12	3959.5	33.3	1853	9	US-09-030-482B-19	Sequence 19, Appl
13	3564.5	29.9	1657	14	US-10-369-493-6836	Sequence 6836, Ap

14	1753	14.7	2264	15	US-10-627-370-2	Sequence 2, Appli
15	1750.5	14.7	2343	13	US-10-033-026-4	Sequence 4, Appli
16	1748.5	14.7	2339	15	US-10-375-253-12	Sequence 12, Appl
17	1746.5	14.7	2339	13	US-10-033-026-6	Sequence 6, Appli
18	1746.5	14.7	2339	17	US-10-736-883-32	Sequence 32, Appl
19	1743	14.6	2237	15	US-10-375-253-14	Sequence 14, Appl
20	1741	14.6	2237	13	US-10-033-026-8	Sequence 8, Appli
21	1741	14.6	2237	17	US-10-736-883-34	Sequence 34, Appl
22	1740.5	14.6	2333	17	US-10-736-883-28	Sequence 28, Appl
23	1732.5	14.6	2327	17	US-10-736-883-38	Sequence 38, Appl
24	1729.5	14.5	2331	17	US-10-736-883-44	Sequence 44, Appl
25	1722	14.5	2336	13	US-10-033-026-10	Sequence 10, Appl
26	1722	14.5	2336	17	US-10-736-883-30	Sequence 30, Appl
27	1714	14.4	2288	17	US-10-736-883-40	Sequence 40, Appl
28	1710	14.4	2339	17	US-10-736-883-42	Sequence 42, App
29	1673.5	14.1	1745	15	US-10-627-370-4	Sequence 178, App
30	1667	14.0	2313	16	US-10-322-696-178	Sequence 40, Appl
31	1665	14.0	2270	15	US-10-375-253-40	Sequence 38, Appl
32	1663.5	14.0	2251	15	US-10-375-253-38	Sequence 176, App
33	1659	13.9	2270	16	US-10-322-696-176	Sequence 84, Appl
34	1657.5	13.9	2251	16	US-10-322-696-84	Sequence 22, Appl
35	1632	13.7	1873	13	US-10-029-413A-22	Sequence 1968, Ap
36	1625.5	13.7	1748	16	US-10-408-765A-1968	Sequence 10, Appl
37	1619.5	13.6	1984	10	US-09-457-571-10	Sequence 12, Appl
38	1615.5	13.6	1989	10	US-09-457-571-12	Sequence 2, Appli
39	1602	13.5	2016	16	US-10-632-342-2	Sequence 34, Appl
40	1602	13.5	2510	15	US-10-375-253-34	Sequence 6, Appli
41	1598.5	13.4	2015	16	US-10-632-342-6	Sequence 4, Appli
42	1597.5	13.4	2157	16	US-10-467-491-2	Sequence 4, Appli
43	1596.5	13.4	2151	16	US-10-467-491-4	Sequence 2, Appli
44	1594	13.4	2016	16	US-10-632-342-4	
45	1591	13.4	1854	13	US-10-029-413A-2	

ALIGNMENTS

RESULT 1
US-10-757-262-16
; Sequence 16, Application US/1075762
; Publication No.US20040197825A1
; GENERAL INFORMATION:
;　APPLICANT: Karicheti, Venkateswarlu
;　APPLICANT: Silos-Santiago, Inmaculada
;　APPLICANT: Eliasof, Scott D.
;　TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;　TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
;　TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
;　TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 44373, 51164,
;　TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
;　TITLE OF INVENTION: 18547, 115, 579, 1595, 15625, 760, 18603, 2395, 2554, 8675,
;　TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
;　TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
;　TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
;　TITLE OF INVENTION: 55053
;　FILE REFERENCE: MPI03-007P1RNOMNIM
;　CURRENT APPLICATION NUMBER: US/10/757,262
;　CURRENT FILING DATE: 2004-01-14
;　PRIOR APPLICATION NUMBER: US 60/440,318
;　PRIOR APPLICATION FILING DATE: 2003-01-15
;　PRIOR APPLICATION NUMBER: US 60/444,783
;　PRIOR APPLICATION FILING DATE: 2003-02-04
;　PRIOR APPLICATION NUMBER: US 60/457,901
;　PRIOR APPLICATION FILING DATE: 2003-03-27
;　PRIOR APPLICATION NUMBER: US 60/468,775
;　PRIOR APPLICATION FILING DATE: 2003-05-08
;　PRIOR APPLICATION NUMBER: US 60/471,614
;　PRIOR APPLICATION FILING DATE: 2003-05-19
;　PRIOR APPLICATION NUMBER: US 60/478,742
;　PRIOR APPLICATION FILING DATE: 2003-06-16
;　PRIOR APPLICATION NUMBER: US 60/488,529
;　PRIOR APPLICATION FILING DATE: 2003-07-18
;　PRIOR APPLICATION NUMBER: US 60/491,156

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;   PRIOR FILING DATE: 2003-07-30
;   PRIOR APPLICATION NUMBER: US 60/499,594
;   PRIOR FILING DATE: 2003-09-02
;   PRIOR APPLICATION NUMBER: US 60/506,332
;   PRIOR FILING DATE: 2003-09-26
;   NUMBER OF SEQ ID NOS: 136
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 16
;   LENGTH: 2377
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-757-262-16

Query Match             99.3%;  Score 11815.5;  DB 17;  Length 2377;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 2264;  Conservative 1;  Mismatches 1;  Indels 111;  Gaps 2;
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Qy     1  MDEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEABGLPYPALAPVV    60
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Qy    61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120
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Db   301  DYEAYNSSSNNTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360

Qy   361  YFVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVRFLSNA   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  YFVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVRFLSNA   420

Qy   421  STLASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAAGVRVGLLLSSPAPLGGQETQPSS 480
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Qy   481  SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP    540
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Qy   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
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Qy   601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660
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Qy   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720
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Db   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720

Qy   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780
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Db   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780

Qy   781  VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR  840
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Db   781  VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR  840

Qy   841  VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFFGCKFASERDGDTL 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFFGCKFASERDGDTL 900

Qy   901  PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960

Qy   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020

Qy  1021  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080

Qy  1081  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140

Qy  1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200

Qy  1201  GKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP  1260

Qy  1261  PQSRFRLLCHRIITHKMFDHVVIVIIFLNCTTIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  PQSRFRLLCHRIITHKMFDHVVLVIIFLNCTTIAMERPKIDPHSAERIFLTLSNYIFTAV 1320

Qy  1321  FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMRVL  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMRVL  1380

Qy  1381  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440

Qy  1441  CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500

Qy  1501  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRL 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRL 1560

Qy  1561  RRLEKKR----------------------------KAQCKPYSDYSRFRLLVHHLCTSHYLDLFITGV 1602
          |||||||                            :|||||||||||||||||||||||||
Db  1561  RRLEKKRRRNLMLDDVIASGSASASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGV 1620

Qy  1603  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDL 1662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDL 1680

Qy  1663  AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQAL 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQAL 1740

Qy  1723  PQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST 1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  PQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST 1800

Qy  1783  GDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLESNKE  1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLESNKE  1860

Qy  1843  AKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGPDSPKPGALHPAAHARSASH    1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  AKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGPDSPKPGALHPAAHARSASH    1920

Qy  1903  FSLEHPT---------                                             1909
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Qy   181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240

Qy   241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300

Qy   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360

Qy   361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420

Qy   421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480

Qy   481  SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP   540

Qy   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600

Qy   601  TLKEKAILVEVAASSGPPTLTSLNIPPGYSSMKLLETQSTGACQSSCKISSPCLKADSG  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TLKEKAILVEVAASSGPPTLTSLNIPPGYSSMKLLETQSTGACQSSCKISSPCLKADSG  660

Qy   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720

Qy   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780

Qy   781  VFTSLFALEMLLKLLVVGPFGVIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  VFTSLFALEMLLKLLVVGPFGVIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR  840

Qy   841  VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL  900

Qy   901  PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960

Qy   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGQDANKSESEPDFFSPSLDGDGDRKKCL  1020
          ||||||||||                      |||||||||||||||||||||||||||||
Db   961  AILVEGFQAE------------------------GDANKSESEPDFFSPSLDGDGDRKKCL   997

Qy  1021  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   998  ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA  1057

Qy  1081  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1058  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ  1117

Qy  1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1118  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN  1177

Qy  1201  GKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP   1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1178  GKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP   1237

Qy  1261  PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMER?KIDPHSAERIFLTLSNYIFTAV  1320
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Db  1921  FSLEHPTDRQLFDTISLLIQGSLEWELKLMDELAGPGQPSAFPSASLGGSDPQIPLAE  1980
          |||||||
Qy  1910  ----------------------------MQPHTELPGPDLLTVRKSG            1929

Db  1981  MEALSLTSEIVSEPSCSLALTDDSLPDDMHTLLLSALESNMQPHTELPGPDLLTVRKSG  2040
                                                  ||||||||||||
Qy  1930  VSRTHSLPNDSYMCRHGSTAEGPIGHRGWGLPKAQSGSVLSVHSQPADTSYIIQLPKDAP 1989

Db  2041  VSRTHSLPNDSYMCRHGSTAEGPIGHRGWGLPKAQSGSVLSVHSQPADTSYIIQLPKDAP 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1990  HLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPS  2049

Db  2101  HLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPS  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2050  PPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTE  2109

Db  2161  PPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTE  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2110  LSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQ  2169

Db  2221  LSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQ  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2170  PHLGTDPSNLGGQPLGGPGSRPKKKLSPPSTTIDPPESQGPRTPPSPGICLRRRAPSSDS  2229

Db  2281  PHLGTDPSNLGGQPLGGPGSRPKKKLSPPSTTIDPPESQGPRTPPSPGICLRRRAPSSDS  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2230  KDPLASGPPDSMAASPSPKKDVLSLGSLSSDPADLDP                        2266

Db  2341  KDPLASGPPDSMAASPSPKKDVLSLGSLSSDPADLDP                        2377
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Query Match       98.8%;   Score 11758.5;   DB 16;   Length 2243;
Best Local Similarity  98.9%;   Pred. No. 0;
Matches 2242;   Conservative 0;   Mismatches 0;   Indels 23;   Gaps 1;

Qy    1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAGRGPDGSAEKDPGSADSEAEGLPYPALAPVV  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAGRGPDGSAEKDPGSADSEAEGLPYPALAPVV  60

Qy   61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF  120

Qy  121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
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; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 2374
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-383-894-2

Query Match   93.3%; Score 11111; DB 10; Length 2374;
Best Local Similarity   93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 35; Indels 95; Gaps 24;

Qy   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
          ||||||||||||||||||| ::||||||| ||||::||||||||||||||||||||||||
Db   1 MDEEEDGAGAEESGQPRSFTQLNDLSGAGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120
          |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120

Qy   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
          ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy   181 TVRVLRPLRAINRVPSMRILVTLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TVRVLRPLRAINRVPSMRILVTLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPCGL 300
          |||||||||||||||:|||||||||||||||||||||||||||||||||| :|||||:|
Db   241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPCSL 300

Qy   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
          |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy   361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy   421 STLASFSEPGSCYEELLKYLVILRKAARRLAQVSRAAGVRVCLLSSPAPLGGQETQPSS 480
          |||||||||||||||||||||||||||||||||:||.|||.:||||:..:||:|:||:|
Db   421 STLASFSEPGSCYEELLKYLVILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG 480

Qy   481 SCCRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
          ||:||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db   481 SCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKYPTVHTSPPPE 600
          :.|.:|||:||||||||||||||||||||:|||||.||||||||||||||||||||||||
Db   541 TPSCGPPRGAESVHSFYHADCHLEPVRCCQAPPPRCPSEASGRTVGSGKYPTVHTSPPPE 600

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMEKLLETQSTGACQSSCKISSPCLKADSG 660
          .||:||||||||.:.||||||::|||||:|||:|||||||||||::|||||||||::|||
Db   601 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 660

Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDHS-RRQRSLGPD 719
          ||||||||||||:||||.:.||..:|||||||||||||||||||||||.||||||||||
Db   661 ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPD 720

Qy   720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780

Db   1238 PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1357

Qy   1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   1358 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFPV 1417

Qy   1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1477

Qy   1501 VDQQPIMNENPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEKRL 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1478 VDQQPIMNENPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARRREEKRL 1537

Qy   1561 RRLEKKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYIDLFITGVIGLNVVTMAMEHYQQPQI 1620
          |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db   1538 RRLEKKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQI 1597

Qy   1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 LDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1657

Qy   1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFA 1717

Qy   1741 ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1718 ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1777

Qy   1801 STCNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTL 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778 STCNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEMKTL 1837

Qy   1861 SPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1838 SPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP 1897

Qy   1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGSVLSVHSQPADTSY 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1898 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGSVLSVHSQPADTSY 1957

Qy   1981 ILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1958 ILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED 2017

Qy   2041 LLAEVSGPSPPLARAYSFWGQSTQAQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2018 LLAEVSGPSPPLARAYSFWGQSTQAQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET 2077

Qy   2101 RSSLELDTELSWISGDLLPPGGQOEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2078 RSSLELDTELSWISGDLLPPGGQOEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA 2137

Qy   2161 VSCLDSGSQPHLGTDPDSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRRTPPSPGICL 2220
          |||||||||||||||||:|||||:||||||||||||||||||||||||||||||||||||
Db   2138 VSCLDSGSQPHLGTDPSNLGQOPLGGPGSRPKKKLSPPSITIDPPESQGPRRTPPSPGICL 2197

Qy   2221 RRRAPSSDSKDPLIASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2198 RRRAPSSDSKDPLIASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2243

RESULT 3
US-09-383-894-2
; Sequence 2, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:

```
Db  1861  KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPCVEGVNSPDSKPGAPHTAHIGAA  1920

Qy  1901  SHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG  1957
Db  1921  SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRG  1980

Qy  1958  WGLPKAQSGGVLSVHSQPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQR  2017
Db  1981  WGLPKAQSGGILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR  2040

Qy  2018  PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKIS  2077
Db  2041  PLRRQAAIRTDSLDVQGLGSREDLLSEVSGSPCPLTRSSSFWGGSSIQVQRSGIQSKVS   2100

Qy  2078  KHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGQEEPPSPRDLKKCYS   2137
Db  2101  KHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEFLSPRDLKKCYS  2159

Qy  2138  VEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP  2197
Db  2160  VETQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP  2219

Qy  2198  PSTTIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL  2257
Db  2220  PSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGL  2279

Qy  2258  SSDPADLDP  2266
Db  2280  SSDPTDMDP  2288
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RESULT 4
US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US2003012526 9A1
; GENERAL INFORMATION:
; APPLICANT: Li Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2425
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-4

```
Query Match      93.3%;   Score 11111;  DB 10;  Length 2425;
Best Local Similarity  93.3%;  Pred. No. 0;
Matches 2135;  Conservative  35;  Mismatches  95;  Indels  24;  Gaps  5;

Qy    1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60
Db   52  MDEEEDGAGAEESGQPRSFTQLNDLSGAGRQRGPGSTEKDPGSADSEAEGLPYPALAPVV  111

Qy   61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF  120
Db  112  FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF  171

Qy  121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
Db  172  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  231

Qy  181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFVFFIFGIVGVQLWAGLLRNR   240
Db  232  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFVFFIFGIVGVQLWAGLLRNR   291
```

```
Qy  780  IVFTSLFALEMLKLLVVGPFGYIKNPINIFDGVIVVISVWEIVGQQGGLSVLRTFRLM    839
Db  781  IVFTSLFALEMLKLLLVVGPFGYIKNPINIFDGVIVVISVWEIVGQQGGLSVLRTFRLM   840

Qy  840  RVLKLVRFLPALQRLVVLMKTMDNVATFCMLLMLFIFISILGMHLFGCKFASERDGDT    899
Db  841  RVLKLVRFLPALQRLVVLMKTMDNVATFCMLLMLFIFISILGMHLFGCKFASERDGDT    900

Qy  900  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  959
Db  901  LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL  960

Qy  960  VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGDRKKC   1019
Db  961  VAILVEGFQAEEIGKREDASGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGDRRKR  1020

Qy 1020  LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASGRRTSSSGSAAPGA 1079
Db 1021  LALVALGEHAELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAAEPGA 1080

Qy 1080  A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1138
Db 1081  AHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE  1140

Qy 1139  SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD  1198
Db 1141  SQDEEESSEEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD 1200

Qy 1199  CNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI  1258
Db 1201  CNGKSASGRLARTLRTDPDQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI   1260

Qy 1259  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1318
Db 1261  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1320

Qy 1319  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1378
Db 1321  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1380

Qy 1379  VLRLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILGVQLFKGKF    1438
Db 1381  VLRLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILGVQLFKGKF    1440

Qy 1439  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1498
Db 1441  FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  1500

Qy 1499  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEK   1558
Db 1501  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEAARREEK   1560

Qy 1559  RLRRLEKKR--------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT      1600
Db 1561  RLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1620

Qy 1601  GVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQL  1660
Db 1621  GVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQL  1680

Qy 1661  DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKQMAVGMRALLDTVMQ 1720
Db 1681  DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ  1740

Qy 1721  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1780
Db 1741  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV  1800

Qy 1781  STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  1840
Db 1801  STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN  1860

Qy 1841  KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPCVEGPDSPKPGALHPAAHARSA    1900
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Qy    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
          |||||||||||||||:|||||||||||||||||||||||||||||||||:|||||||
Db    292 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL 351

Qy    301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
          |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352 DYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 411

Qy    361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 471

Qy    421 STLASFSEPGSCYEELLKIVIYLRKAARRLAQVSRAAGVRVGLLSSPAPLGQGETQPSS 480
          |||||||||||||||||||||||||||||||||:||||:|||:||||:||:|||::|:|
Db    472 STLASFSEPGSCYEELLKYIVIYLRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG 531

Qy    481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
          ||:||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db    532 SCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 591

Qy    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKYYPTVHTSPPPE 600
          |:||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    592 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKYYPTVHTSPPPE 651

Qy    601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
          :||:||||||||:||||||||:||||||:||||||||||||||||||||||||:||||||
Db    652 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 711

Qy    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSLGPD 719
          |||||||||||:|||||||||||::||||||||||||||||||||||||||||||||||
Db    712 ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPD 771

Qy    720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAIIVNTLSMGIEYHEQPELTNALEISN 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    772 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAIIVNTLSMGIEYHEQPELTNALEISN 831

Qy    780 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQOGGGLSVLRTFRLM 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    832 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQOGGGLSVLRTFRLM 891

Qy    840 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 899
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    892 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 951

Qy    900 LPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    952 LPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 1011

Qy    960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC 1019
          ||||||||||||:||||||||||||||||:||||||::||||||||||||:|||||||:
Db   1012 VAILVEGFQAEEIGKREDASGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGDRKKR 1071

Qy   1020 LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLEALGPASRRTSSSGSAEPGA 1079
          ||||:|||:|||||||||||||||||||||||||:|||:||||:|:|||||||||||||
Db   1072 LALVALGEHAELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGA 1131

Qy   1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
          | |||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db   1132 AHHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1191

Db   1192 SQDEEESSEERASPAGSDHRHRGSLLEREAKSSFDLP... 1251

Qy   1199 CNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
          ||||||||||||:||:||:|||||:::||||||||||::||:|:|||:  :|||||||||
Db   1252 CNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1311

Qy   1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1312 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1371
```

```
Qy   1319 AVFLAEMTKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLR 1378
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1372 AVFLAEMTKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLR 1431

Qy   1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1432 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1491

Qy   1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1492 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1551

Qy   1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK 1558
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1552 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK 1611

Qy   1559 RLRRLEKKRR------------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT 1600
          |||||||||:                   :|||||||||||||||||||||||||||||
Db   1612 RLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT 1671

Qy   1601 GVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQL 1660
          |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   1672 GVIGLNVVTMAMEHYQQPQIIDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQL 1731

Qy   1661 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKAVGMRALLDTVMQ 1720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1732 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKAVGMRALLDTVMQ 1791

Qy   1721 ALPQVGNLGLLFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1792 ALPQVGNLGLLFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1851

Qy   1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN 1840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1852 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN 1911

Qy   1841 KEAKEEAELBAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSKPGALHPAAHARSA 1900
          |||||||||:||||||||||||||||||||||||||||||:|||:|||||:: : |:|
Db   1912 KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTAHIGAA 1971

Qy   1901 SHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
          |.||||||||.||| :|    |||||||||||||||||||||||||||:||||||.||||
Db   1972 SGFSLEHPTMVPHPEEVVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRG 2031

Qy   1958 WGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQR 2017
          |||||||||:.||||||||||:.||||||||:.||||||.|||:|||||||||||||||
Db   2032 WGLPKAQSGSIISVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR 2091

Qy   2018 PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKIS 2077
          |||||||||||||||||||||||||:||||||.||||||||.|:.|::::||||.:|:|
Db   2092 PLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIOVQQRSGIQSKVS 2151

Qy   2078 KEMTPPAPCPGEPNWGKGPPPETRSSLELDTELSWISGDLLPGGQEPPSPRDLKKCYS 2137
          |:. ||||||.:|.:.|.||||||||||||||||||||||  :||||.||||||||||
Db   2152 KHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLSPRDLKKCYS 2210

Qy   2138 VEAQSCQRRPTSWLDEQRRHSIAVSCLLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP 2197
          ||:||| ||||.||||||||||||||||||||||.|   :|||||||||||||||||||||
Db   2211 VETQSCRRRPGSWLDEQRRHSIAVSCLLDSGSQPRLCFSPSSLGGQPLGGPGSRPKKKLSP 2270

Qy   2198 PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAAGSPPSPKKDVLSLGL 2257
          |||:||||||||.|.|.|||.|||||||:|||||||:...|||||:.||||||||.||||
Db   2271 PSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGL 2330

Qy   2258 SSDPADLDP 2266
          ||||:|.||
Db   2331 SSDPTDMDP 2339
```

GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 3077
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1128

Query Match   52.2%;   Score 6212;   DB 16;   Length 2353;
Best Local Similarity 56.7%;   Pred. No. 0;
Matches 1366; Conservative 214; Mismatches 525; Indels 304; Gaps 61;

```
Qy    7 GAGAEESGQP-RSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLS 65
          ||||| || |  ||  |:||   :||:||: ||:|||::|| :|:||||||| |  ||| |
Db   27 GASPESPGAPGREAAERGSEL-GVSPSESP-AAERGAELGADEEQRVPYPALAAATVFCLG 84

Qy   66 QDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMERPCEDIACDSQRCRILQAFDDFIF 125
          | :||||||| |||||||| :||||| |||||||| |||||:: |:|:| ||:|| |||
Db   85 QTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDEVECGSERCNILEAFDAFIF 144

Qy  126 AFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL 185
          ||||||| :|||||:||:|||||||||||||||| ||| |||||| :||| |||||||
Db  145 AFFAVEMVIRMVALGLFGQKCYLGDTWNRLDFFIVAGMMEYSLDGHNVSLSAIRTVRVL 204

Qy  186 RPLRAINRVPSMRIILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE 245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  205 RPLRAINRVPSMRIILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLDS 264

Qy  246 NFSLPLSVD-LERYYQTENEDESPFICSQPRENGMRSCRSVP---TLRGDGGGGPPCGLD 301
           |:   |  ||||||| :|:|:|||||| ||:||| :||:        :|    |||||
Db  265 AFVRNNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHIPGRRELR------MPCTLG 318

Qy  302 YEAYN------SSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLE 354
           :|| :     :   |||| |||||:|| | :|:| |||||||||||||||||||||||
Db  319 WEAYTQPQAEGVGAARNACINWNQYNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE 378

Qy  355 GWVDIMYFVMDAHSFYNFYFIFLLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRV 414
          |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  379 GWVDIMYYVMDAHSFYNFYFIFLLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRA 438

Qy  415 RFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQ 474
          | ||::||:|||||||||||||||||  | |:| |:  ||: : ||||        :|||
Db  439 RHLSNDSTILASFSEPGSCYEELLKYVGHIPRKVKRRSLRLYARWQSRWRKKVDPSAVQGQ 498

Qy  475 ETQPSSSCCSRSHRR-LSVEHHLV-HHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRL 532
           :  :  | |:: || :|||||| ||||||||||| |   ||: ||::        :|||
Db  499 --GPGHRQRRAGRHTASVHHLVYHHHHHHHHHYHFSHGSPRRGPEPGACD----TRLV 551

Qy  533 MLPPPSTPALSGAPPGGAESVHSFYHADCHLE--PVRCQAPPPRSPSEASGR-TVGSGKV 589
           | || : :||| ||| ||||||:|||||:|   |  :|   |   |  :   | |:|
Db  552 RAGAPPSPPSPGRGPPDAESVHSIYHADCHIEGPQERARVAHAAATAAASLRLATGLGTM 611

Qy  590 -YPTV------HTSP------PPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629
           |||:      ||||                  :|||||| |: ::  | |||
Db  612 NYPTILPSGVGSGKGSTSPGPGKGKWAGGPPGT--------GGHGPLSLNS----PDPY 657

Qy  630 SSMHKLLETQSTGACQS------SCKISSPCLKADSGACGPDSCPYCARA-GAGEVELA 681
          ::   :|:   || |::       |:||||||||:|| ||||||||| |  ||||| |
Db  658 EKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP--PAGTLTCELKSCPYCTRALEDPEGELS 715

Qy  682 DREMPDSDSEAVFETQDAQHSDLRDP-----------HSRRQRSLGPDAEPSSV 725
           | ::|||| || |||||: ||:|||           ||:|| :     | ||
Db  716 GSESGSDSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGSPQRRAQQRAAPGEPGWM 775

Qy  726 LAFWRLICDTFRKIVDSKYFGRGIMIAIIVNTLSMGIEYHEQPELTNALEISNIVFTSL 785
           | | | ||||| |||||||||||| ||||||||||||||||||||||||||||||||:
Db  776 GRLWVTFSGKLRIVDSKYFSRGIMAAILVNTLSMGVEYHEQPELTNALEISNIVFTSM 835

Qy  786 FALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQOGGLSVLRTFRLMRVLKLV 845
          |||||||||| ||| |||:||||||||:|||||||||||: ||||||||||:|||||||
Db  836 FALEMLLKLLACGPLGYIRNPYNIFDGIIVVISWEIVGQADGGLSVLRTFRLLRVLKLV 895

Qy  846 RFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRK 904
          |||||:|||||||:||||||||||  ||||||||||||||||||||::: || ||:|||
Db  896 RFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLFGCKFSLKTDTGDTVPDRK 955

Qy  905 NFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIIV 964
          ||||||||||||||||||||||:|||||||||||||||||||:|||||||||||||||:|
Db  956 NFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAAIYFVALMTFGNYVLFNLLVAILV 1015

Qy  965 EGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFSFSPSLDGD----------GD 1015
          ||||||                ::|::::    ::  ||          :         ||
Db 1016 EGFQAE---------------GDANRSDTDEDKTSVHFEEDFHKLRELQTTB 1052

Qy 1016 RKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSA 1075
           :| | ||: ::| | ||||||:| |||| |:| |||: :    ||| || ||: :||
Db 1053 LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATMPTPKSSPFLDAAPSLPDSRRGSSSSGD 1112

Qy 1076 EPGAAHEMKSPPSARSSPHSPWSAAASWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE 1135
                :  ||||: :|| ||| ::  |:||| ::||||||||||||  | ||::||||
Db 1113 PP--LGDQKPPASLRSSPCAPWGPSGAWSSRRSSWSSLGRAPSLKRRGQCGERESLLSGE 1170

Qy 1136 GQESQDEESSEEERASPA--GSDHRHRGSLEREAKSSFDLPDTL------QVPGLH-- 1184
          |::|:|:  :  || ||:   :: | :      ||: :|  |           | |
Db 1171 GKGSTDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPTKCRDRDGQVVALPSDF 1228

Qy 1185 --RTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRA 1242
            | ::   || :  :   :||: |||||||||| || |:|| |:   :||||  :
Db 1229 FLRIDSHREDAELDDDSBDSCCLRLHKVLEPYKP---------QWCRS 1268

Qy 1243 RLPACYLERDSWSAYIPPPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDP 1302
           | |  |   :|:||: || :||| |  |:||||| ||||| : |||| ||| |||:|||
Db 1269 ------REAWALYLFSPQNRFRVSCQKVITHKMFDHVVLVFIFLNCVTIALERPDIDP 1320

Qy 1303 HSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDIL 1362
           ||||||| :|||||||:|:||| ||||||| | || ||| |:||:|||||||:|::|:
Db 1321 GSTERVFLSVSNYIFTAIFVAEMVKVVALGLLSGHEAYLQSWNLLDGLLVLVSLVDIV 1380

Qy 1363 VSMVDSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAF 1422
          |:| : :  |||| :||||||||||||||||||||:|||||||:|||:|||||||:||||
Db 1381 VAMASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAF 1440

Qy 1423 FIIFGIIGVQLFKGKFFVCQGBDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVL 1482
          |||||::|||||||||:||:| ||||| :|::|  | |||||:||||||||||||||||
Db 1441 FIIFGILGVQLFKGKFYYCEGPDTRNISTKAQCRAAHYRWVRRKYNFDNLGQALMSLFVL 1500

Qy 1483 ASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHK 1542
           |||||:||||||||||||||||: :|||||||||||||||:|| |||||| ||||||||
Db 1501 SSKDGWNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFPFVLNMFGVVVENFHK 1560

Qy 1543 CRQHQEEEEFARRREEKLRLEKKPR-----KAQCKPYYSDYSRFRLLVHHLCTSHYLD 1596
          ||||||  | |||||||:|||::         ||:|||:||| | |  | |||:||||
Db 1561 CRQHQEAEEARRREEKRLRLERRRSTFPSPEAQRRPYYADYSPTRRSIHSLCTSHYLD 1620

Qy 1597 LFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVKIVAFGFRRFFQDR 1656
          ||||  | :|| ||:|||||:||: |||||:|||:||:|  || ||:|||||||||:||
Db 1621 LFITFICVNVIFTMSMEHYNQPKSLDEALKYCNYVFTIVPVFEAALKLIVAFGFRRFFKDR 1680

Qy 1657 WNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLD 1716
          |||||||||||:||||||||||::| ||||||||||||||||||||||||||| |||||
Db 1681 WNQLDLAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLD 1740

Qy 1717 TVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLT 1776
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Db  1741  ||:|||||||    ||||||||  |||||    |:|||| ||||  |||||:|||||||
          TVVQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFSNFGMAFLT  1800
Qy  1777  LFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM   1833
          ||||||||||||||||||:|:    |:         ::|||| |||||||||||:|::|||
Db  1801  LFRVSTGDNWNGIMKDTLRECSREDKHCLSLYLPALSPVYFVTFVLVAQFVLVNVVVAVLM  1860
Qy  1834  KHLEESNKEAKEEABLEARLELEMKTLSPQPHSPLGSPFLWPGVEGPDSP---DSPKPGA   1890
          ||||||||||:|:|:|||:||:|||                 :||   ||||    :::
Db  1861  KHLEESNKEAREDEALDAEIELEM------------------AQGPGSAARRVDADRP--   1899
Qy  1891  LHPAAHARSASHFSLEHPTMQPHPTELPG---PDLLTVRKSGVSRTHSLPNDSYMCRHG   1946
          :                        ::          ||  |::|||||||||| |
Db  1900  ------------------PLPQESFGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV   1937
Qy  1947  STAEGP----------LGHRGWGLPKAQSGSVLGVHSQPADTSYILQLPKDAPHLLQPHSA  1997
          :     ||          |:      ||:||||  |||:  ||| |||     |||||
Db  1938  VPASAPHPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIP------LAVSSPA  1989
Qy  1998  PTWGTIPKLPPPG--RSPLAQPRLRRQAAIRTDSLDVQCLGSREDLL-AEVSGPSP--P   2051
          :||  |  |   |  :|| ::  ||  :||||||| |::  |:::|| || ||||:  |
Db  1990  RSGEPLHAlSPRGTARSPSLSRLLCRQBAVHTDSLEGK-IDSPRDTLDPAEPGEKTPVRP   2048
Qy  2052  LARAYSFWG--QSSTQAQQHSRSHSKISKHMTPPAP-CPGPEPNWGKGPPETRSSLELDT  2108
          :         ||||  || ||   |  | |  ||| |    ||                :
Db  2049  VTQGGSLQSPPRSPRPASVRTRKHT-FGQHCVSRPAAPGGE--------EAEASDPADE   2099
Qy  2109  ELSWISGDLLP------PGGQEEPP---SPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSI  2159
          |:| ::         ||  ||||   ||| ||:||| |:: ::|||:  |  |:: |||
Db  2100  EVSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGFLDKP-GRADEQWRPSA  2158
Qy  2160  AVSCLDSGSGQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPP-ESQGPRTPPSP--  2216
          |:|  |:  |    |   |||| :|||| ||||||:|||| :|: || :||| || ||||
Db  2159  ELGSGEPGEAKAWGPE-----AEP-ALGARRKKKMSPPCISVEPPAEDBGSARPSAAEG   2211
Qy  2217  -GICLRRRAPS--------SDSKDPL--ASGPPDSMA---ASPSPKKDVLSLSGLSSSDPA  2262
          ||| ||||          ||||| |  ||||||||    ||| ||:|| |||| |||||
Db  2212  GSTTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGQASCRAEHLTVPSFAFEPL   2271
Qy  2263  DL-----DP                                                    2266
          ||     ||
Db  2272  DLGVPSGDP                                                    2280
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Qy    87  SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAPDDFIFAFFAVEMVVKMVALGIFGKKC   146
          |||||||||||||| :||:|    |:|| |||| ||||| :||| ||||:||||||||||
Db    85  SMLVILLNCVTLGMYQPCDDMDCLSDRCKILQVPDDFIFIFFAMEMVLKMVALGIFGKKC   144
Qy   147  YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRITVRVLRPLRAINRVPSMRILVTLLLD  206
          ||||||||||||||:||||:|||||||::|:|:||:||||||||:|||||||||||:|||
Db   145  YLGDTWNRLDFFIVMAGMVEYSLDLQNINUSAIRTVRVLRPLKAINRVPSMRILVNLLLD   204
Qy   207  TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE   266
          |||||||||||||||||||||:|||||||||||||||| ||  :|::|  |||| ||:|:
Db   205  TLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPYYQPEEDDE   264
Qy   267  SPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL----------DYEAYNSSSNTT--CVNWNQ   318
          ||||| ||  ||:|| ||:||:  :|||| |||         ||  :::|   |  |||||||
Db   265  MPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVVDFGAGRQDLNASGLCVNWNR   321
Qy   319  YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL   378
          ||  |  ||:||:||||||||||||||  |||||||||| |||:||||||||||||||||
Db   322  YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITILEGWVEIMYYVMDAHSFYNFIYFILL  381
Qy   379  IIVGSFFMINLCLVVIATOFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK   438
          |||||||||||||||||| |||||||| :||  ||  :||  |  ||  ||| |||:  |
Db   382  IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEIFQ   440
Qy   439  YLVYLIRKAARRLAQVSRAAGVRVGLLSSPAPLGGGETQPSSSCSRHRRLSVHHLVHHH   498
          |:: ||||| |         |||  :|||  ||
Db   441  YVCHILRKAKR-------RALGLYQALQSRRQALG                          468
Qy   499  HHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYH  558
          :||                   ||:  |  :
Db   469  ------------------PEAPA--PAKPGP----------H                   480
Qy   559  ADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPT  618
          |:   |   ||                                   ::|      |:
Db   481  AK---EPRHYQLCPQHSPLDATPHTL------------VQPIPATL               511
Qy   619  LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-----   672
          :                                                     |
Db   512  -----------------ASDPASCPCCQHEDGRRP                          529
Qy   673  AGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL-----   726
          :|:|  |                   |  ::           ||| | ||
Db   530  SGLGSTD-SGQDGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEEBEQADGAVWL  586
Qy   727  --AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEELTNALEISNIVFTS   784
            | ||| |   | :|||||||| || |||:|||||||||||||||||||||: ||:||||
Db   587  CGDVWRRTRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS  646
Qy   785  LFALEMLLKLLVVGPFGYIKNPYNIFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLKL   844
          :||||| |:|| | || | ||||||||| || |||||||||::|||||||| ||||||||
Db   647  MFALEMLKLLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFLLRVLKL   706
Qy   845  VRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERD-GDTLPDR  903
          ||| ||| ||||||||||||||||||||||||||||||||||:|||||  |  ||| |||
Db   707  VRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSIIGMHIFGCKFSLRTDGTVPDR   766
Qy   904  KNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVFLNLLVAIL  963
          |||||||||||||||:||||||| :||||||||| ||:|||:||||||||:|||||||||
Db   767  KNFDSLLWAIVTVFQIITQEDWNVVLYNGMASTSPWASLYFVALMTFGNYLFLNLLVAIL  826
Qy   964  VEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS-------------LDGD  1013
          ||||||:          |       |                  |:              :
Db   827  VEGFQAE------------GDANRSYSDEDQSSSNIEEFDKLQEGLDSS---          863
Qy  1014  GDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGTGLGEALGPASRRT----  1069
          || | | :  ||: :                 ||:  |            :|
Db   864  GDPKLCFIPMTPNGH-----LDP-----------SLPLGGHLGPAGAGPAPRLSLQPD   906
Qy  1070  -------SSSGSAEPGAAHEMKSPFSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLIK  1120
                 ||| ||| |     ||  |:|| |:|  ||| :  ||||||| |||:   :||
Db   907  PMLVALGSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSAAWASRRSSWN----SLK   960
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Query Match        46.1%;  Score 5492.5;  DB 9;  Length 2175;
Best Local Similarity  51.3%;  Pred. No. 0;
Matches 1233;  Conservative 214;  Mismatches 508;  Indels 447;  Gaps 55;

Qy    31  RPGPGSAEKDPGSADSRAEG----LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERI   86
          :||| |:|| ||:|  |:||    ||:||| || ||  |:::|:|| |:: ||||||| :|
Db    25  QPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV   84
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Qy   1121  RRSPSGERRSLLSGE-GQESQDEESSEE--ERASPAGSDH----------------RHRG 1162
                ||  |       :: : |  : |  ||  :: :                    |||
Db    961  HKPDSAEHESLLSAERGGGARVCEVAADEGPPRRAPLHTPHAHHIHHGPHLAHRHRHHRR 1020

Qy   1163  SLEREAKSSFDLPDTLQVPGLHRIASGR--GSASEHQDCNGKSASGRLARALRPDDPPLD 1220
                :   :: :: :   |:  |: :      |  ||:  :||  | : : ::: :::::
Db   1021  TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR 1080

Qy   1221  GDDADDEGNLSKGEVRAWIRARLPACYLERDSWSAYIFPPQSRRFLLCHRIITHKMFDH 1280
                :  : :::  | | |  : || |   |: :  | ||  |::   |: || |  | |
Db   1081  GED-EEIDYTLCFRVRKMIDVYKPDWCEVREDWSVYLFSPENRPRVLCQTIIAHKLFDY 1139

Qy   1281  VVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQA 1340
                |||  ||||||| :|  |:   | | : || :||| |  || || ||| ||| |||
Db   1140  VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQA 1199

Qy   1341  YLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKIIGMLRVLRLRTLRPLRVISRAQGLKL 1400
                |||||||||| ||||:|:||:||| |:| | ||| |||||||||||||||| ||| |
Db   1200  YLRSSWNVLDGFLVFVSIIDIVVSLASAGAKIIGVLRVLRLRTLRPLRVISRAPGLKL 1259

Qy   1401  VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASY 1460
                |||| |||||||| |||||||||||||||||| ||||| :   |||| |:||||| |
Db   1260  VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY 1319

Qy   1461  RWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISF 1520
                ||:|||||| :|||||||||||||||||| || |||| || ||||| |||||||||||
Db   1320  RWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVADQQPVTNHNPWMLLYFISF 1379

Qy   1521  LLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKLRRLEKKRKAQCKPYYSDYS 1580
                ||||:|  |||||| ||||| || ||| ||||||| ||||| |||||||:| || |:
Db   1380  LLIVSFFVLNMFVGVVVENFHKCRQHQEAEEARRREEKLRRLEKKRKAQRLPYYATYC 1439

Qy   1581  RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPILDEALKICNYIFTVIFVLES 1640
                 | ||| || ||||| |: || | |||:: ||||:|| :||| | ||||| || ||:|
Db   1440  HTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYQNQPTSLETALKYCNYMFTTVFVLEA 1499

Qy   1641  VFKLVAFGFRRFFQDRMNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIAR 1700
                ||||||||| |||:||||||||||||||| |||| |:|| | :||| | |||||||||||
Db   1500  VFKLVAFGLRRFFKDRMNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIAR 1559

Qy   1701  VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIYAALGVELFGDLECDETHPCEG 1760
                |||||| ||:|||||||||:|||||||||||||||||||||||||||| |||  ||||
Db   1560  VLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEG 1619

Qy   1761  LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYVSFV 1817
                :||||| ||||||||| |:|||||||||||||:|||||  : :: ||    |||| |||
Db   1620  MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYVSFV 1679

Qy   1818  LTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELLEM-KTLSPQHSPLGSPFIWPG 1876
                :||||| || |||| |||: ||:|||| |  | || ||   : |  |  |  ||| |
Db   1680  LTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAEELEMAHGLGPGPRLPTGSPGA-PG 1738

Qy   1877  VEGPDSPD---------SPKPGAL-------------------HPAAHA--------- 1897
                :  |  |         || | |                   || | |
Db   1739  -RGPGGAGGGGDTEGGLCRRCYSPAQDSLEGELTIIDNLSGSIFHHYSSSPAGCKKCHHDK 1797

Qy   1898  ----------RSAS---HFSLEHPTMQP-----HPTELPGPDLLTVRKSG--- 1929
                          :|||   ||| |  ||       ||| ||  |
Db   1798  QEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEMRVGDLGEC 1857

Qy   1930  ---VSRTHSLPN-DSYMCRHGSTABGPLGHRGWGLPKAQGSSVLSVHSQPADTSYIIQLP 1985
                   :| |  | | : | | |  |  | |  | | | :||  |  | |: | :||  ||
Db   1858  FFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSFSPDASSPLLPMP 1913

Qy   1986  KDAPH------LLQPHSAPTWGTIPKLPPPG----RSPLAQRPLRRQAAIRTDSLDVQG 2034
                ||||       ||| ||  | |||||| ||    |||| || ||:||  ||   |
Db   1914  AEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLD--- 1970

Qy   2035  LGSREDLLAEVSGPSPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWG 2094
                              ::::||  :    ||                ||| | | | ||
Db   1971  ----------ASPSSSAGSLQTTLEDSLTLSDSPRRA-------LGPPAPGPGRAGLS 2012

Qy   2095  KGPPETRSSLELDTELSWISGDLLPPGGGQEPPSPRDLKKCYSVRAQSCCRRPFTSWLDEQ 2154
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Qy  1521  LLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRRKAQCKPYYSDYS  1580
          |||| ||||||||||||||||||||||||: |||:||||||||||||||||||| :||
Db  1380  LLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREEKRLRRLEKKRRKAQRLPYYATYC  1439

Qy  1581  RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVFVLES  1640
          : |||:| ::||||||||:|||:||||||||:|||| | |:||||:||||::||.||||
Db  1440  HTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEA  1499

Qy  1641  VFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIAR  1700
          |:|||||| |||| ||||||||||||||::||||||||:||:||||||||||||||||||
Db  1500  VLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIAR  1559

Qy  1701  VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLIFFIFAALGVELFGDLECDETHPCEG  1760
          |||||||| ||||||||| ||||||||||||||:|||| ||||||||| :|| :||PCEG
Db  1560  VLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEG  1619

Qy  1761  LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV  1817
          :.||||| |||||||||| ||||||||||||||||||  ::|:| :: ||||||||||||
Db  1620  MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFV  1679

Qy  1818  LTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEM-KTLSPQHSPLGSPFLWPG   1876
          ||||||| ||| |||||||::|||||:|:|| | ||||||   ||||| |: |||   ||
Db  1680  LTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTGSPGA-PG  1738

Qy  1877  VEGPDSPD------------------SPKPGAL------------------HPAAHA      1897
          ||| :                      ||||
Db  1739  -RGPGGAGGGGDTEGGLCRRCVSPAQDSLEGELTIIDNLSGSIFHHYSSPAGCKKCHHDK  1797

Qy  1898  --------------RSAS-----HFSLEHPTMQP------------HPTELPGDLLTVRKSG-  1929
                        :||:     .:||: |||
Db  1798  QEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELDPPEMRVGDIGEC   1857

Qy  1930  ---VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLP  1985
             :::: |:||  |: :|: ::: :: :|.
Db  1858  FFPLSSTAVSPDDENFLCEMEEIPFNPV--RSW-LKHDSSQAPPSPFSPDASSPLLPMP   1913

Qy  1986  KDAPH------LLQPHSAPTWGTIPKLPPPG--RSPLAQPRLRRQAAIRTDSLDVQG     2034
          :||.|      ||:|: : : : .|:||:       ||::: : :::. |.|||::
Db  1914  AEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLD--   1970

Qy  2035  LGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQHSRSHSKISKHMTPPAPCPGPEPNWG   2094
                                                           ::|||| || |:
Db  1971  -------ASPSSAGSLQTTLEDSLTLSDSPRRA------LGPPAPAPGPRAGLS       2012

Qy  2095  KGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQ  2154
                                                                    :HQ
Db  2013  ------------RGRGLFSLRGLRA--------------------------------HQ  2036

Qy  2155  RRHSIAVSCLDSGSQPHLGTDPSN--LGGQPLGGPGSRPKKKLSPPSIT--IDPPESQ    2208
          | ||:    :|.|:   |||  ::  |||   ||:|| ||| |:|.||:  :|||:
Db  2037  RSHSGGGS-TSPGCTHHDSMDPSDEEGRGGAGGGGAGSEHSETILSSLSLTSLFCPPP--  2092

Qy  2209  GPRTPPSPGICLRRRAPSDS----KDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADL   2264
          ||  |    |  .: ||.|:       |  :|  :  :  :|:|    : ::|: |.|
Db  2093  ---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD------RSKDPPGR  2143

Qy  2265  DP  2266
          .|
Db  2144  AP  2145
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Qy   499  HHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH   558
                                               |||| : |:  : ||||
Db   469  ------------------------------PEAPA--PAKPGP-------------H    480

Qy   559  ADCHLEPVRCQAPPRSPSEASGRTVGGSGKVYPTVHTSPPETLKEKALVEVAASGPPT    618
           |    | | | | :|| .    :         |:  :||    |:|:|  :   ||
Db   481  AK--EPRHYQLCPQHSPLDATPHTL----------------------VQPIATL------ 511

Qy   619  LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----  672
                                                    : ||: |  |  |
Db   512  --------------------------------------ASDPASCPCCQHEDGRRP    529

Qy   673  AGAGEVELADREMPDSDSEAVYFFTQDRAQHSDLRDPHSRRQRSLGPDAEPSSVL----  726
          :|:|:  ::  :: |:|.        :   :     :  .|:| |||||
Db   530  SGLGSTD-SGQEGSGSGSSAGGE-DEADGDGARSSEDGASSELGKEEEBEEQADGAVWL  586

Qy   727  -AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNIVFTS   784
           .   |  : ||:|||||||:||||:|||||| |||||:|||||:||::|||.|::|||
Db   587  CGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS  646

Qy   785  LFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKL  844
          :|||||:| : :.| |.|::|||||||.:|:::|||||||  .|||||||||||:||||
Db   647  MFALEMILLAAFGLFDYLRNPYNIFDSIVIISIWEIVGQADGLSVLRTFRLLRVLKL   706

Qy   845  VRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDR  903
          |||:|||:|||||||||||||||||||||||||||||||||:||||||:|  |||:|||
Db   707  VRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDR  766

Qy   904  KNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL  963
          ||||||||||||||||||||||| |||||||||| ||:||:|||||||||||||||||||
Db   767  KNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL  826

Qy   964  VEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS--------LDGD  1013
          |||||||
Db   827  VEGFQAE-----------------GDANRSYSDEDQSSSNIEEFDKLQBGLDSS      863

Qy  1014  GDRKKCLALVSLGEHPELRKSLLPLLIHTAATPMSLPKSTSTGLGEALGPASRRT----  1069
          ||  .| . ||.:|: |.  ::|:       |   |   : |.|   .|:|
Db   864  GDPKLCPIPMTPNGH------LDP--------SLPLGGHLGPAGAAGPAPRLSLQPD    906

Qy  1070  -------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLK  1120
                 ::|.: ||   .: || ||| ||  |  |::. :| |:.:.| ||  ||||
Db   907  PMLVALGSRKSSVMSLGRMSVDQRSLSSRSSYYGPWGRSAAWASRRSSWN-----SLK  960

Qy  1121  RRSPSGERRSLLSGE-GQESQDEEESEE--ERASPAGSDH----RHRG           1162
          : .||:|| |:|::|    :. | :|   : |  ||.|:|    || .
Db   961  HKPPSAEHESLLSAERGGGARVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRR  1020

Qy  1163  SLEREAKSSFDLLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRLARALRPDDPPLD  1220
          :| . . | ||: .| ::  | ::.| .:  |:|:|: ||||  ::   ||:: ||| 
Db  1021  TLSLDDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR  1080

Qy  1221  GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDH  1280
          |:|  :|  |:||||:| |:|:||||||||||:|| |:||::|||.||| :::|||:||:
Db  1081  GED-EEEIDYTLCFRVRKMIDVYKPDWCEVERDWSVLFSPENRFRVLCQTTIAHKLFDY   1139

Qy  1281  VVIVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQA  1340
          || . ||||||||| ||| |: .: |||||.|||||||:|. ||| ||| ||:  ||.||
Db  1140  VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGSQA  1199

Qy  1341  YLRSSWNVLDGLLVLLISVIDIIVSMVDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKL  1400
          ||||||||||| : : :|:||::||: :.| ||||:|||||||||||||||||||| |||
Db  1200  YLRSSWNVLDGFIVFVSIIDIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKL  1259

Qy  1401  VVETIMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY  1460
          ||||::|||||||||| :|||||||||||||||||||: | ::|||||||:||| |: |
Db  1260  VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFFVCCQGEDTRNITNKSDCAEASY  1319

Qy  1461  RWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISF  1520
          |||:||||||||||||||||||||||||: ||. ||||| ||||| :|||||||||||||
Db  1320  RWVHHKYNFDNLGQALMSLFVLASKDGWNIMNGLDAVAVDQQPVTNHNPWMLLYFISF   1379
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RESULT 8
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23

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Query Match     46.1%;  Score 5484;  DB 9;  Length 2188;
Best Local Similarity 51.1%;  Pred. No. 0;
Matches 1234;  Conservative 212;  Mismatches 509;  Indels 460;  Gaps 56;
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Qy   31  RPGPDGSAEKDPGSADSEAEG----LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERI   86
Db   25  QPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV    84

Qy   87  SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKC  146
Db   85  SMLVILLNCVTLGNYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMWALGIFGKKC  144

Qy  147  YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLD  206
Db  145  YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRIIVNLLLD  204

Qy  207  TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE  266
Db  205  TLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPPYYQPEEDDE  264

Qy  267  SPPICSQPRENGMRSCRSVPTLRGDGDGGGPPCGL------DYEAYNSSSNT--CVNWNQ  318
Db  265  MPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR   321

Qy  319  YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL  378
Db  322  YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYNFIYFILL  381

Qy  379  IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK  438
Db  382  IIVGSFFMINLCLVVIATQFSETKQRERRLMEQRQRYLS-SSTVASYAEPGDCYEEIFQ   440

Qy  439  YLVIYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH  498
Db  441  YVCHILRKAKR-----RALGLYQALQSRRQALG                            468

Qy  499  HHHHHHYHLGNGTLRAPPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYH  558
Db  469  --------------------------PEAPA--PAKPGP--------H             480

Qy  559  ADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPT  618
Db  481  AK---EPRHYQLCPQHSPLDATPHTL---------VQPIPATL                  511

Qy  619  LTSLNIPPGPYSSMHKKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----  672
Db  512  ----------------------------ASDPASCPCCQHEDGRRP              529

Qy  673  AGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL------  726
Db  530  SGLGSTD-SGQEGSGSGGSSAGGE--DEADGDGARSSEDGASSELGKEEEBEQADGAVWL  586

Qy  727  --AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTS  784
Db  587  CGDVWRETRAKLRGIVDSKYFNRGIMAAILVNTVSMGIEHHEQPEELTNILEICNVVFTS  646

Qy  785  LFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQVGGGLSVLRTFRLMRVLKL  844
Db  647  MFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKL  706

Qy  845  VRFLPALQRQLIVLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDR  903
Db  707  VRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDR   766
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Qy  904  KNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL  963
Db  767  KNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL  826

Qy  964  VEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS--------LDGD  1013
Db  827  VEGFQAE-------------------------GDANRSYSDEDQSSSNIEEFDKLQEGLDSS  863

Qy 1014  GDRKKCLALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRT---  1069
Db  864  GDPKLCPIPMTPNGH-------LDP--------SLPLGGHLGPAGAAGPAPRLSLQPD   906

Qy 1070  --------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLK  1120
Db  907  PMLVALGSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSAAWASRRSSWN-------SLK  960

Qy 1121  RRSPSGERRSLLSGE-GQESQDEEESSEE--ERASPAGSDH------------RHRG  1162
Db  961  HKPPSAEHESLLSAERGGGARVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRR  1020

Qy 1163  SLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRLARALRPDDPLD  1220
Db 1021  TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAGHEDCNGRMPSIAKDVFTKMGDRGDR  1080

Qy 1221  GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDH  1280
Db 1081  GED-EEIDYTLCFFVRKMIDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIIAHKLFDY   1139

Qy 1281  VLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQA  1340
Db 1140  VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQA  1199

Qy 1341  YLRSSWNVLDGLLVLISVIDILVSMVSDSGTKIIGMLRVLRLLRTLRPLRVISRAQGLKL  1400
Db 1200  YLRSSWNVLDGFLVFVSIIDIVVSLASAGAKIIGVLRVLRLRTLRPLRVISRAPGLKL   1259

Qy 1401  VVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASY  1460
Db 1260  VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY  1319

Qy 1461  RWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISF  1520
Db 1320  RWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISF  1379

Qy 1521  LLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRRKAQCKPYYSDYS  1580
Db 1380  LLIVSFFVLNMFVGVVVENFHKCRQHQEAEEARRREEKRLRRLEKKRRKAQRLPYYATYC  1439

Qy 1581  RFRLLVHHLCTSHYLDLFITGVIGLNVTMAMEHYQQPOILDEALKICNYIFTVIFVLES  1640
Db 1440  HTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEA  1499

Qy 1641  VFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIAR  1700
Db 1500  VLKIVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIBINAALPINPTIIRIMRVLRIAR  1559

Qy 1701  VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEG  1760
Db 1560  VLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEG  1619

Qy 1761  LGRHATFRNFGMAFLITLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV  1817
Db 1620  MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFV  1679

Qy 1818  LTAQFVLVNVVIAVLMCHLEESNKEAKEEABLEAELELEM-KTLSPQHSPLGSPFLWPG  1876
Db 1680  LTAQFVLINVVVALMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGRLPTGSPGA-PG   1738

Qy 1877  VEGPD------------------SP----------DSPKPGALH--  1892
Db 1739  -RGPGGAGGGDTEGGLCRRCYSPAQENLWLDSVSLLIKDSLEGELTIIDNLSGSIFHHY  1797
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Qy    1893  -PAA-----------------------HARSAS-----HFSLEHPTMQP------HPTELP 1918
Db     205  TLPMLGNVLLLCFFVFFIFGIGVQLWAGLLRNRCFLEENFTIQGDVALPYYQPEEDDE 264

Qy    1798  SSPAGCKKCCHHDKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPPGRKDSKGELD 1857
Db     267  SPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL------------DYEAYNSSSNTT--CVNWNQ 318

Qy    1919  GPDLLTVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLLPKAQSGSVLSVH 1972
Db     265  MFFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR 321

Qy    1858  PPEEMRVGDLGBECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSP 1913
Db     319  YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWIDIMYFVMDAHSFYNFIYFILL 378

Qy    1973  SQPADTSYILQLPKDAPH-----------LLQPHSAPTWGTIPKLPPPG------RSPLAQRPLRR 2021
Db     322  YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFNFIYFILL 381

Qy    1914  FSPDASSPLLPMPARFFHPAVSASQKGPEKGTGTGTLPFKIALQGSWASLRSPRVNCTLLR 1973
Db     379  IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK 438

Qy    2022  QAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWQSSTQAQOHSRSHSKISKHMT 2081
Db     382  IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEBIFQ 440

Qy    1974  QATGSDTSLD----------------ASPSSSAGSLQTTLEDSLITLSDSPRRA------LG 2012
Db     439  YLVIYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVHHLVHHH 498

Qy    2082  PPAPCPGPEPNWGKGPPEETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQ 2141
Db     441  YVCHIRRKAKR-----------RALGLYQALQSRRQALG- 468

Qy    2013  PPAPAPGPRAGLS---PAARRRLSL-------------------RGRGLFSLRGLRA- 2047
Db     499  HHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYH 558

Qy    2142  SCQRRPTSWLDEQRRHSIAVSCLDSGSQOPHLGTDPSN---LGGGQPLGGPGPSGRPKKKLSPP 2198
Db     469  ------------------------PEAPA--PAKPGP----------------------H 480

Qy    2048  ----------HQRSHSSGGS-TSPGCTHHDSMDPSDEEGRGAGGGGAGSEHSETLSSL 2095
Db     559  ADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPETLKEALVEVAASSGPPT 618

Qy    2199  SIT----IDDPESQGRTPPPSPGICLRRRAPSDS----KDPLASGPPDSMAAASPSPKKDV 2251
Db     481  AK--EPRHYQLCPQHSPLDATPHTL------------------------VQPIPATL 511

Qy    2096  SLTSLFCPPP-----------PPFAPGLITPARKFSSTSSLAAPGRPHAAAALAHGLARSPSWAAD- 2148
Db     619  LTSLNIPPGYYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR------ 672

Qy    2252  LSLSGLSSDPADLDP 2266
Db     512  ----------------------------ASDPASCPCCQHEDGRRP 529

Qy    2149  --RSKDPPGRAP 2158
Db     673  AGAGEVELADAREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL-----LDGD 726

Db     530  SGLGSTD-SGQEGSGSGSAGGE--DEADGDGARSSEDGASSELGKEEEEEQADGAVWL 586

Qy     727  --AFWRLICDTFPKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISNIVFTS 784
Db     587  CGDVWRETRAKLRGIVDSKYFNRGIMWAILVNTVSMGIEHHQPEELTNILEICNVVFTS 646

Qy     785  LFALEMLKLLVVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGLSVLRTFRLMRVLKL 844
Db     647  MFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKL 706

Qy     845  VRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDR 903
Db     707  VRFMPALRRQLVLVMKTMDNVATFCMLLMLFIFIFSIIGMHIFGCKFSLRTDTGDTVPDR 766

Qy     904  KNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL 963
Db     767  KNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL 826

Qy     964  VEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS-----------LDGD 1013
Db     827  VEGFQAE------------------------GDANRSYSDEDQSSNIEEFDKLQEGLDSS 863

Qy    1014  GDRKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRT--- 1069
Db     864  GDPKLCPIPMTPNGH----------------------LDP----SLPLGGHLGPAGARGPAPRLSLQPD 906

Qy    1070  --------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLK 1120
Db     907  PMLVALGSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSAAWASRRSSWN---SLK 960

Qy    1121  RRSPSGERRSLLSGE-GQESQDEEESSEE--ERASPAGSDH---------------RHRG 1162
Db     961  HKPPSAEHBSLLSAERGGGARVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRR 1020

Qy    1163  SLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRLARALRPDDPPLD 1220
Db    1021  TLSLDNRDSVDLAEJVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR 1080

Qy    1221  GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFLLCHRIITHKMFDH 1280
Db    1081  GED-EEEIDYTLCFFVRKMIDVYKPDWCEVREDWSVYLFSPENRFRVLCQTIIAHKLFDY 1139
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Qy      31  RPGPGSAEKDPGSADSEAEG---LPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERI 86
Db      25  QPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV 84

Qy      87  SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDPIFAFFAVEMVVKMVALGIFGKKC 146
Db      85  SMLVILLNCVTLGMYQPCDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKC 144

Qy     147  YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLD 206
Db     145  YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSALRTVRVLRPLKAINRVPSMRILVNLLLD 204

Qy     207  TLPMLGNVLLLCFFVFFIFGIGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE 266
Db    1918  ...HPTELP...
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Qy    2252  LSLSGLSSDPADLDP  2266
            |||||   :
Db    2149  ------RSKDPPGRAP  2158
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RESULT 10
US-09-935-541-5
; Sequence 5, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
;   APPLICANT: Dietrich, Paul S.
;   APPLICANT: McGivern, Joseph G.
;   TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;   TITLE OF INVENTION: AND USES
;   FILE REFERENCE: R0043B-REG sequence listing
;   CURRENT APPLICATION NUMBER: US/09/935,541
;   CURRENT FILING DATE: 2001-08-23
;   PRIOR APPLICATION NUMBER: 09/404,650
;   PRIOR FILING DATE: 1999-09-23
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1835
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-935-541-5

Query Match   45.1%; Score 5366; DB 9; Length 1835;
Best Local Similarity   56.8%; Pred. No. 0;
Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;
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Db      27  GAGGRPGPGSAEKDPGSADSEAEG-----LPYALAPVVFFYLSQDSRPRSWCLRTVCNPW   82
            :||||                        :  |:||      ||| ::||  | |:|| |
Qy      19  GITEQPGPGRSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIKMVCNPW   78

Qy      83  FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAPFDFIFAFFAVEMVVKMVALGIF  142
            ||||| ||:|||||||||| ||  |  | :||:: | | ::|||: | |||:||||||||
Db      79  FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIF  138

Qy     143  GKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVT  202
            ||||||||||||||||||| |||||||||||||| |||||||||||||| |||||||:|
Db     139  GKKCYLGDTWNRLDFFIVWAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVN  198

Db     203  LLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTE  262
            ||||||||:||||||||||||||| |||||||||||||||||| ||| ||| :||||||
Qy     199  LLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPYYQPE  258

Db     263  NEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL-----DYEAYNSSSNTT--CV   314
            : || | : ||    |  |  | |  :                :  ::|::|:  |:
Qy     259  EDDEMPFICSLTGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCV  315

Qy     315  NWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIY  374
            ||| ||:||| ||:|||||||||||||| ||||| |||||||| || | |||||||||||
Db     316  NWNRYYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYYVMDAHSFYNFIY  375

Db     375  FILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSBPGSCYE  434
            ||||||| ||||||||||||||||||||||  : |||||| ::  : |: |: | | |||
Qy     376  FILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQYLS-SSTVASYAEPGDCYE  434

Db     435  ELLKYLVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHL  494
            |:|| | |:|: :| | :  |:   | ||
Qy     435  EIFQYVCHILRKAKRALGLYQALQNR-------------------------------  461

Qy     495  VHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVH  554
                                           |||:
Db     462  -----------------------------RQAMG----------PGTPA--PAKPGP-  477

Qy     555  SFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASS  614
             :  | |  :|                            : |||||  |
Db     478  ---HAK--EPSHCKLCPRHSPLD--------------------PTPHTLVQP-------  504

Qy     615  GPPTLTSLNIPPGYPSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR--  672
            | |   :  |                        |::|                 | :
Db     505
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Qy    1281  VVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEQA  1340
            |||  |||||||||| |:|:::  | ::|   ||:|||: |:  |:  |::||||   ||
Db    1140  VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQA  1199

Qy    1341  YLRSSWNVLDGLLVLISVIDILVSMVSDGTKILGMLRVLRLLRTLRPLRVISRAQGLKL  1400
            |||||||||||:||| ||:|:|||| | || |||::|||||||:|||||||||:|| |||
Db    1200  YLRSSWNVLDGFLVFVSIIDIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKL  1259

Qy    1401  VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASY  1460
            |||| ::|||||||||:||||||||||||||||||||||:| | ||||||| |||:|| |
Db    1260  VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANY  1319

Qy    1461  RWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQP1MNHPWMLLYFISF  1520
            ||| ||||||||||||||||||||||||| :||  |||| :||||:|||||||||||||
Db    1320  RWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVDQQPVTNHNPWMLLYFISF  1379

Qy    1521  LLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRKAQCKPYISDYS  1580
            ||||| |||||||||||||||||||| ||  |||||||||||||||||| |||:||:
Db    1380  LLIVSFFVLNMEVGVVVENFHKCRQHQEAEARRREEKRLRLEKKRRKAQRLPYYATYC  1439

Qy    1581  RFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLES  1640
            |||| |||||||||:||||||||| || |:|  | |:||||||||:|||:|||:|:||:
Db    1440  HTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEA  1499

Db    1641  VFKLVAFGFRRFFQDRWNQLDDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIAR  1700
            ||||| | | | |  |||||||:||||| |||||||:||  | ||||||| |||:|||||:
Qy    1500  VLKLVAFGLRRFFKDRKWNQLDDLAIVLLSVMGITLEEINAALPINPTIIRIMRVLRIAR  1559

Db    1701  VLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFPIFAALGVELFGDLECDETHPCEG  1760
            |||||:||| |||||||:||||||||||||||||||||||||||||| ||:|  ||||||
Qy    1560  VLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVCNDENPCEG  1619

Db    1761  LGRHATPRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV  1817
            : | |  |:|||||||| |||:||||||||||||||| |::|:| | |    ||||||||
Qy    1620  MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLYFVSFV  1679

Qy    1680  LTAQFVLNVVLAVLMKGHLEESNKEAKEEAELEAELELEM-KTLSPQPHSPLGSPFLWPG  1738
            ||||||||||||||||| ||: |||| ||| ||| ||||| |||| |   | ||| : |
Db    1818  LTAQFVLINVVVAVLMKCHLDDSNKEAQEDAEMDAELLEMAHGLGPGPRLPTGSPGA-PG  1876

Qy    1739  -RGPGGAGGGGDTEGGLCRRCYSPAQENLWLDSVSLLIIKDSLEGELTIIDNLSGSIFHHY  1797
                                   :  |: ::: |   |:  |::::: |
Db    1877  VEGPD----------------------SP---------DSPKPGALH--            1892

Db    1798  SSPAGCKKCHHDKQEVQLAEFTEAFSLNSDRSSSILLGDDLSLEDPTACPGRKDSKGELD  1857
            : |                   |||| |: || :||
Qy    1893  --PAA-------------------HARSAS-----HFSLEHPTMQP---           1918

Qy    1919  GPDLLIVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVH  1972
            ||| |: | |     ||:   | || |:| :   :|   ::      ::|  |
Db    1858  PPEPMRVGDLGBCFFPLSSTAVSPDPNFLCEMEEIPFNPV--RSW--LKHDSSQAPPSP  1913

Db    1914  FSPDASSPLLPMPABFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLR  1973
                     :    |::|| | |   :   |  |:| |: | | : |:
Qy    1973  SQPADTSYILQLPKDAPH------LLQPHSAPTWGTIPKLPPPG-----RSPLAQRPLRR  2021

Qy    2022  QAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQHSRSHSKISKHMT  2081
             :    ||   :    ||  :|:    : ||:||: : || | | :::| |:    |
Db    1974  QATGSDTSLD-------------ASPSSSAGSLQTTLEDSLTILSDSPRRA------LG  2012

Db    2082  PPAPCPGPEPNWGKGPPETRSSLELDTELSWIISGDLLPPGGQEEPFSPRDLKKCYSVEAQ  2141
            || |   |:    ||   |:|                :: ||||   || || :|:| |
Qy    2013  PPAPADGPRAGLS------PAARRRLSL-----------RGRGLFSLRGLRA-        2047

Qy    2142  SCQRRPTSWLDEQRRHSIAVSCLDSGSGQPHLGTDPSN--LGGQPLGGPGSRPKKKLSPP  2198
            :  ||: | |:|:|          |||   ||  |      |   :|      | | :|
Db    2048  --------HQRSHSSGGS-TSPGCTHHDSMDPSDEEGRGGAGGGGAGSEHSETLSSL  2095

Db    2199  SIT--IDPPESQGPRTPPSPGICLRRRAPSSDS---KDPLASGPPDSMAASPSPKKDV  2251
            :|:   |  :  |   |  : | |: | |:||             |    |    || |
Qy    2096  SLTSLFCPPP------PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-  2148
```

```
Db    505  ----------------------------------------------ISAILASD------PSSCPHCQHEA                523
                                                                          : |||||| |
Qy    673  ----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDFHSRRQRSLGPDAEPSSVLA-                             727
                  : |:|||       : :  :|:|                |:|    |
Db    524  GRRPSGLGSTD-SGQEGSGSGGGSARAEANGDG-----LQSSEDGVSSDLGKEEEQEDGAAR                          578

Qy    728  ----FWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNIVFT                              783
                  : |||||||:||||| :|||||||||||:||||||||||||||||||
Db    579  LCGDVWRETRKKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPELTNILEICNVVFT                              638

Qy    784  SLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISWEIVGQQGGLSVLRTFRLMRVLK                                843
                ||:||||| |:| :||||| :||||:|||:|||||||||:||||:||||||||||
Db    639  SMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLK                             698

Qy    844  LVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPD                             902
                ||| |||||||:||||||||||||||:|||:|||||||||||||:|
Db    699  LVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPD                             758

Qy    903  RKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAI                             962
                |||||||||||||||||||||||||||||||  ::: :|:|||||||||||||||||
Db    759  RKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTTPWASLYFVALMTFGNYVLFNLLVAI                             818

Qy    963  LVEGFQAEEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPS---------------LDG                         1012
                |||||||||
Db    819  LVEGFQAE-------------------------------------------------------                         855

Qy   1013  DGDRKKCCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS                            1071
                                                    |||
Db    856  SRDLKLICPIPMTPNGH-----------LDP-----SLP----LGAHLGPAGTMGTAP                               892

Qy   1072  SGSAEPG------------------------AAHEMKSPPSARSSPHSPWSAAASWTSRRSSRNSL                        1113
                :||                        : :|  | :|  | :|||  | :||||:|
Db    893  RLSLQPDPVLVALDSRKSSVMSLGRMSYDQRSLSSRSSYYGPWGRSGTWASRRSSWN--                              950

Qy   1114  GRAPSLKRRSPSGERRSLLSGEGQESQDEE- ESSEEE---RASPAGSDH---------------                        1158
                                         :|| ||:||
Db    951  ----SLKHKPPSAEHBSLLSGEGGGSCVRACEGARREAPTRTAPLHAPHAHHAHHGPHLA                            1006

Qy   1159  ----RHRGSLEREAKSSFDLPDTLQVPGLHRTAS--GRGSASEHQDCNGKSASGRLARAL                             1212
                      ||  :|              ||||     || |  :|:   :|  |||:
Db   1007  HRHRHRRRTLSLDTRDSVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPNIAKDVFT                             1066

Qy   1213  RPDDPDLGDGDDADDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFPPQSRFRLLCHRI                             1272
                                          |:| |:  |  |||  |||||:||:
Db   1067  KMDDRRDRGED-EEEIDYTLCFRVRKMIDVYKPDWCEVREDWSVVLFSPENKFRILCQTI                             1125

Qy   1273  ITHKMFDHVVLIVIFLNCTIIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL                             1332
                : ||  ||| |||: |||:| |: :|  |    |||: |:|| | |::|||| ||||:|
Db   1126  IAHKLFDYVVLAFIFLNCITIIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSL                            1185

Qy   1333  GWCFGEQAYLRSSWNVLDGLLVLLISVIDIIVSMVSDGTKILGMLRVLRLLRTLRPLRVI                             1392
                  |: ||||||:||||||| |||:|:||||:|:|:|   | |:|||:||||:||||:||
Db   1186  GLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSVASAGGAKILGVLRVLRLLRTLRPLRVI                             1245

Qy   1393  SRAQGLKLVVETLMSSLKPIGNIVVLCCAFFIIFGILGVQLFKGKFFVCCQGEDTRNITNK                            1452
                |: :|||:||::| ||:|||||:| :|||||||| |||||||||| | | : | :||:|:
Db   1246  SRAPGLKLVVETLISSLKPIGNIVLLCCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR                             1305

Qy   1453  SDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPW                             1512
                |||  ||:||:|||||||||||||||||||:|||||:| |:| | | ||:|::||:|||
Db   1306  SDCVAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYDGLDAVDQQPVTNHNPW                               1365

Qy   1513  MLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRKAQC                               1572
                |||||||||||:|||||||||||||||||||||||||||||||||||||:|||||||
Db   1366  MLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRKAQR                               1425

Qy   1573  KPYYSDYSRFLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIF                              1632
                ||  : : :: || |||:|:||:| ||: | :  ||| : |  :  |     ||:|
Db   1426  LPYYAYYCPTRLLIHMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMF                              1485

Qy   1633  TVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIRI                              1692
                |:||||:|| |||| | |:|| ||:||||||:|||:||||||:|| |:|:|||||||||
Db   1486  TTVFVLEAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVSVGTTLEEIEINAALPINPTIRI                             1545

Qy   1693  MRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLEC                             1752
                |||||||||||||| ||||||||||  |||||||||||||||||||| ||||||||| |
Db   1546  MRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVC                             1605

Qy   1753  DETHPCEGLGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS                            1809
                : :|   :||| ||| :||||||||:|| ||||| ||||||||||||  || |  :    |
Db   1606  NDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVS                             1665

Qy   1810  PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELEM-KTLSPQPHSPL                             1868
                |:|:|||:||| |:| ||:|:|||||||:|:|  :|:||| | :|:|:     :| |   |
Db   1666  PLYFVSFVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAEIELEMAHGLGPCP-----                            1721

Qy   1869  GSPFLWPGVEGDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTV---                              1925
                                                            ::|
Db   1722  ------------------------------------------GPCPG----------PCPCPCPCCAGPRLPTSSPG          1747

Qy   1926  ---RKSGVSRTHSLPNDSYMCRH                                                                 1945
                   : |||
Db   1748  APGRGSGGAGAGG-DTESHLCRH                                                                 1769
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RESULT 11
US-10-425-800-5
; Sequence 5, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-425-800-5

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  Query Match             45.1%;  Score 5366;  DB 14;  Length 1835;
  Best Local Similarity   56.8%;  Pred. No. 0;
  Matches 1138;  Conservative 183;  Mismatches 346;  Indels 336;  Gaps 38;

Qy     27  GAGGRPGPGSAEKDPGSADSEAEG---LPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW                              82
                  ||||         :||: |             |   :|| || | |  |  :|||
Db      1  GITEQPGPRSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIKMVCNPW                             78

Qy     83  FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVKMVALGIF                              142
                ||  | : ::||| ||| |: |   ||   ::|||  | |||||||  ||::||||| |
Db     79  FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFFAMEMVLKMVALGIF                               138

Qy    143  GKKCYLGDTWNRLDFFIVIAGMVLEYSLDLQNVSFSAVRTVRVLRPLAINRVPSMRILVT                             202
                ||||||||||||||||||:|||||||||||:|:|||:||||:||||||:|||||||||:
Db    139  GKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSALRTVRVLRPLKAINRVPSMRILVN                             198

Qy    203  LLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTE                              262
                ||||||||||||||||||||||||||:|||||||||||||||||    |  ||: | |
Db    199  LLLDTLPMLGNVLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPPYYQPE                              258

Qy    263  NEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL---------DYEAYNSSSNTT--CV                          314
                :|:| | |  |:| |   | | |   |  |  | |               |: : ||    ||
Db    259  EDDEMPFICSLTGDNGIMGCHEIPPLKEQ----GREECLSKDDVYDFGAGRQDLNASGLCV                            315

Qy    315  NWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIY                             374
                ||| : :||  ||||  |||||||||| |  |  |  |:||| || | :|||||:|||||
Db    316  NWNRYYNVCRTGNANPHKGAINFDNIGYAGIVIFQVIFQVITLEGWVEIMYYVMDAHSFYNFIY                         375

Qy    375  FILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYE                             434
                                                                                                    
Db    486  TTVFVLEAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVSVGTTLEEIEINAALPINPTIRI                            1545
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Db    376 FILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYB 434
Qy    435 ELLKLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHL   494
Db    435 EIFQYVCHILRKAKRRALGLYQALQNR                                  461
Qy    495 VHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVH   554
Db    462 ------------------RQAMG-------PGTPA--PAKPGP------            477
Qy    555 SFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASS 614
Db    478 ---HAK--EPSHCKLCPRHSPLD------------PTPHTLVQP---------------- 504
Qy    615 GPPTLTSLNIPPGPYSSMHKLLETQSTGACQSCKISSPCLKADSGACGPDSCPYCAR--  672
Db    505 ------------ISAILASD-----PSSCPHCQHEA                         523
Qy    673 ----AGAGEVELADREMPDDSDSEAVFEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLA- 727
Db    524 GRRPSGLGSTD-SGQEGSGSGSGSAEARANGDG---IQSSEDGVSSDLGKEBEQEDGAAR 578
Qy    728 --FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFT     783
Db    579 LCGDVWRETRKKLRGIVDSKYFNRGIMAILVNTVSMGIEHEQPEELTNILEICNVVFT   638
Qy    784 SLFALEMLLKLLVYGPPGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLK  843
Db    639 SMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLK 698
Qy    844 LVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMLLFGCKFASERD-GDTLPD 902
Db    699 LVRFMPALRRQJVVLMKTMDNVATFCMLLMLFIFIFSLLGMHIFGCKFSLRTDTGDTVPD 758
Qy    903 RKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYLFNLLVAI  962
Db    759 RKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTTFWASLYFVALMFFGNYVLFNLLVAI 818
Qy    963 LVEGFQAEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS-----------LDG 1012
Db    819 LVEGFQAE-------------------GDANRSCSDEDQSSSNLEEFDKLPEGLDN     855
Qy   1013 DGDRKKCLALVSLGEHPELRKSLLPLLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071
Db    856 SRDLKLCPIPMTPNGH-------SLP------LGAHLGPAGTMGTAP             892
Qy   1072 SGSAEPG----------AAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSL        1113
Db    893 RLSLQPDPVLVALDSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWN--  950
Qy   1114 GRAPSLKRRSPSGERRSLLSGEGQESQDEE-ESSEEE-----RASPAGSDH--------- 1158
Db    951 ---SLKHKPPSAEHESLLSGBGGGGSCVRACEGAREEAPTRTAPLHAPHAHHAHHGPHLA 1006
Qy   1159 ----RHRGSLREEAKSSFDLPDTLQVPGLHRTAS--GRGSASEHQDCNGKSASGRLARAL 1212
Db   1007 HRHRHHRRTLSLDTRDSVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPNIAKDVFT 1066
Qy   1213 RPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI 1272
Db   1067 KMDDRRRDRGED-EEEIDYTLCFRVRKMIDVYKPDWCEVREDWSVYLFSPENKFRILCQTI 1125
Qy   1273 ITHKMFDHVLVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1332
Db   1126 IAHKLFDYVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFIVGEMTLKVVSL     1185
Qy   1333 GWCFGEQAYLRSSWNVLDGLLVLLISVDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVI 1392
Db   1186 GLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSVASAGGAKILGVLRVLRLLRTLRPLRVI 1245
Qy   1393 SRAQGLKLVVETLMSSLKPIGNIVLICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK 1452
Db   1246 SRAPGLKLVVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR 1305
Qy   1453 SDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPW 1512
Db   1306 SDCVAANVRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVADQQPVTNHNPW  1365
Qy   1513 MLLYFISFLLIVAFFVLNMFVGVVENFHKCRQHQEEEARRREKRLRLEKKRRKAQC     1572
Db   1366 MLLYFISFLLIVSFFVLNMFVGVVENFHKCRQHQEAEARRREKRLRLEKKRRKAQR     1425
Qy   1573 KPYYSDYSRFLLVHHLCTSHYLDLFTGVIGLNVVTMAMEHYQQPQLLDEALKICNYIF   1632
Db   1426 LPYYATYCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMF 1485
Qy   1633 TVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRI 1692
Db   1486 TTVFVLRAVLKIVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRI 1545
Qy   1693 MRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLEC 1752
Db   1546 MRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVC 1605
Qy   1753 DETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCNTV--IS  1809
Db   1606 NDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSLQFVS 1665
Qy   1810 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEALELEM-KTLSPQPHSPL  1868
Db   1666 PLYFVSFVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAEIELEMAHGLGPCP---- 1721
Qy   1869 GSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTV--  1925
Db   1722 ------------------------------------------------PCPCPCPCPCAGPRLPTSSPG 1747
Qy   1926 --RKSGVSRTHSLPNDSYMCRH                                       1945
Db   1748 APGRGSGGAGG-DTESHLCRH                                        1769
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RESULT 12
US-09-030-482B-19
; Sequence 19, Application US/09030482B
; Patent No. US20020009772A1
; GENERAL INFORMATION:
; APPLICANT: Snutch, Terry
; APPLICANT: NeuroMed Technologies, Inc.
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS
; FILE REFERENCE: 38109-20007.00
; CURRENT APPLICATION NUMBER: US/09/030,482B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 60/039,204
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1853
; TYPE: PRT
; ORGANISM: Human
US-09-030-482B-19

Query Match   33.3%;   Score 3959.5;   DB 9;   Length 1853;
Best Local Similarity   46.8%;   Pred. No. 2.1e-240;
Matches 908;   Conservative 158;   Mismatches 361;   Indels 515;   Gaps 42;

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Qy    27 GAGGRPG------PGSAEKDPGSADSBAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVC  79
Db    76 GTGMHTGTFQEGAEPGSSQHPEAQATYTAGCTPAPTGDPTCCFVLD----------LVC 124
Qy    80 NPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFAVEMVVKMVAL 139
Db   125 T-WFCCVSMLVILLNCVTLGMYQPCDDMDCLSDRCKIIQVFDDFIFIFFAMEMVLKMVAL 183
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Qy    140  GIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRI  199
           ||||||||||||||||:||::|    ::.|||||:||||||||||||||||||||||
Db    184  GIFGKKCYLGDTWNRLDFFIVMAG------------NINLSAIRTVRVLRPLKAINRVPSMRI  234

Qy    200  LVTLLLDTLPMLGNVLLLCFVFFIFGIVGVQLWAGLLRNCFLPENFSLPLSVDLERYY  259
           ||:||||||||||||||:||:||||||||||||||||||||||:::|
Db    235  LVNLLLDTLPMLGNVLLLCFVFFIFGIIGVQLWAGLLRNCFLEENFTIQGDVALPPYY  294

Qy    260  QTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL------DYEAYNSSSNTT-  312
           : .:                                    ::  :|||
Db    295  QPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASG  351

Qy    313  -CVNMNQYYTNCSAGHENPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN  371
            :                    ||||||||||||||||||||||||:||||||||||||
Db    352  LCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYN  411

Qy    372  FIYFLLLII-----------------  380
           |:|||||||
Db    412  FIYFIILIISELIHLVMPDCSFSTAQSPKCCQGDSLPGVAAESLLLRDSSSSVITDEAAAM  471

Qy    381  ------------VGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLAS  425
                        ||||||||||||||||||:|| :|::.|:.|:||
Db    472  ENLLAGTSKGDESYLLRLAGSQVHSQAQQMLGRGLGPESLETGEEPHSWSPRATRRWDPQ  531

Qy    426  FSEPGSCYEELLKYLVYILRKAARRLLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRS  485
                     .   ::|| :|| :|| ||
Db    532  COPGQPLPLHFMQAQVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVAS  590

Qy    591  YAEPGDCYEEIFQYVCHILRKAKR------RALGLYQALQSRRQALGPEAPAKP----  640
Db    591  RPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFV  1590

Qy    486  HRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGA  545
Db    486  SVIDIVSMVSDSGTKILGMLRVLRLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIV  1416

Qy    641  ------------GPHAKEPRHYPLTVWESILGRQAEECTLRAA----------AHPSSGAS  679
Db    591  SIIDIVVSLASAGGAKIIGVLRVLRLRTLRPLRVISRAPGLKLVVETLISSLKPIGNIV  1650

Qy    546  PPG--GAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKE  604
Db    1417 VICCAFFIIFGLIGVQLFKGKFFVCQQEDTRNITNKSDCAEASYRWRHKYNFDNLGQAL  1476

Qy    680  HPGVSGEEA----------PELC---PQHSPLDATPHTL----------VQPIPATL-  713
Db    1651 LICCAFFIIFGLIGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHHKYNFDNLGQAL  1710

Qy    605  KALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGP  664
Db    1477 MSLFVLASKDGWGVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLIIVAFFVLNMFVGVV  1536

Qy    714  ----------------------------------------------------------ASDP  717
Db    1711 MSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPWMLLYFISFLLIVSFFVLNMFVGVV  1770

Qy    665  DSCPYCAR-------AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGP  718
Db    1537 VENFHKCRQHQEEEARRREEKRLRLEKKRRKAQCKPYYSDYSRFRLLVHHLCTSHYLD  1596

Qy    718  ASCPCCCQHEDGRRPSGLGSTD-SGQEGSGSGSAGGE--DEADGDGARSSEDGASSELGK  774
Db    1771 VENFHKCRQHQEAEEARRREEKRLRLEKKRRKAQRLPYYATYCHTRLLIHSMCTSHYLD  1830

Qy    719  DAEPSSVL-------AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPE-  769
Db    1597 LFITGVIGLNVVTMAMEHYQQP  1618

Qy    775  EEEEEQADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQASA  834
Db    1831 IFITFIICLNVVTMSLEHYNQP  1852

Qy    770  ---------------ELTNALE-------------ISNIV-------  781
           :|.||:               :.|:|
Db    1134 VADEVGDANRSYSDEDQSSSNIEEFDKLQEGLDSSGDPKLCPIMTPNGH---------LDP  1186

Qy    835  AQPGRACGRGQNPDLCMTLKAPCLCHNVPSPGQGVLSHPVTPPHTAPWRMETGKQHGCE  894
Db    1039 LIIHTAATPMSLPKSTSTGLGEALGPA----------------SRRTS  1070

Qy    782  -----FTSLFALEMLLKLLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRT  835
Db    1187 --------SLPLGGHLGPAGAAGPAPRLSLQPDPMLVALGSRKSSVMSLGRMSYDQRS  1236

Qy    895  EGPGQRSSDMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRT  954
Db    1071 ----SSGSAEPGAAHEMKSP------------PSARSSPHSPWSAASSWTSRRSS  1109

Qy    836  FRLLRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASER  895
Db    1237 LVGGLRRATGVQAAFGHLVPQPWVCLWGADPNGNSFQSSRSSYYGPWGRSAAWASRRSS  1296

Qy    955  FRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSLLGMHIFGCKFSLRT  1014
Db    1110 RNSLGRAPSLKRRSPSGERRSLLSGE-GQESQDEEESSEE--ERASPAGSDH----  1158

Qy    896  D-GDTLPDRKNFDSLLWAITVFQIITQEDMNKVLYNGMASTSSWAALYFTALMTFGNYV  954
Db    1297 WN-----------SLKHKPPSAEHESLLSAERGGGARVCEVAADEGPPRAAPLHTPHAHHVHHGP  1350

Qy    1015 DTGDTVPDRKNFDSLLWAITVFQIITQEDMNVVLYNGMASTSPWASLYFVALMTFGNYV  1074
Db    1159 --------RHRGSLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRIA  1209

Qy    955  --------LFNLLVAILVEGFQAE-EISKREDA--------  988
Db    1351 HLAHRHRHRHRTISLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKD  1410

Qy    1075 LFNLLVAILVEGFQAEVTVVLAEEAPPQGLRKTGRGRGLDGGGLQFKLLAGNLS-LKEG  1133
Db    1210 RALRPDDPPLDGDDADD-----------EGNLSKGERVRAWIRARLPACYLERDSWSAYIFP  1260

Qy    989  VDSQGGDANKSESEPDFFSPS-----------LDGDGDRKKCLALVSLGEHPELRKSLLPP  1038
Db    1411 VFTKMGDRGDRGEDEEEIDYVSGGGAGDLTLCFRVRKMIDVVKPDWCEVREDWSVYLFS  1470

Qy    1261 PQSRFR------LLC-------HRIITHKMDHVVLVIIFLNCITIAME  1296
Db    1471 PENRLRDLGWVSLECQGKVGDLVVWVYGQRRQRQTIIAHKLFDYVVLAFIFLNCITIALE  1530

Qy    1297 RPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEQAYLRSSWNVLDGLLVLI  1356
Db    1531 RPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFV  1590
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-6836

Query Match      29.9%;  Score 3564.5;  DB 14;  Length 1657;
Best Local Similarity  42.2%;  Pred. No. 1.5e-215;
Matches  822;  Conservative 231;  Mismatches 430;  Indels 465;  Gaps 50;

Qy    15  QPRSFMRLNDLSGAGGRPG-----------PGSAEKDPG---------------SADSEA   48
Db    56  QSQSTRRHEDVEALGSIEGSKETLQLSEHGRLASSEASPSRWEGRQIEWGNEEQIEEES  115

Qy    49  EGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCED-I  107
Db   116  E-LPYPGFAEPALRCFYQARPPRKWALQMVMSPWFDRITMAVIMINCVTLGMYRPCEDGP  174

Qy   108  ACDSQCRRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEY  167
Db   175  DCDTYRCQILDIIDNCIFVYFAFEMVIKIMALGFYGPAAYMSDTWNRLDFFIVMAGLAEF  234

Qy   168  SLDLQ---NVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMIGNVLLLCFFVFFI  224
Db   235  VLHEYLGGNINLTAIRTVRVLRPLRAVNRIPSMRIIVNLLLDTLPMLGNVLLLCFFVFFI  294

Qy   225  FGIVGVQLWAGLLRNRCF--LPENFS----------LPLSVDLERYYQTENEDESPFICSQPREN  277
Db   295  FGIVGVQLWAGLLRNRRCVINLPKTISENQSALFNNVKLTRFYIPE-DTSLEYICSQPDAN  353

Qy   278  GMRSCRSVPTLRGDGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAG------------  326
Db   354  GLHTCSNLPPYTVD---GVKCNLTLDEYDKVTNDSCINWNIYYNEQVNIYPSLMTIAIS   410

Qy   327  ------EHNPPKGAINPDNICYAWAIAFQVITLEGWVDIMYFVMDAHSFYNFIYFILLII  380
Db   411  CFIKVMQRNPPQGSVSFDNIGFAWVAIFLVISLEGWTDIMYVVQDAHSFWNWIYFVLLIV  470

Qy   381  VGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPG----------S  431
Db   471  IGAFFMINLCLVVIATQFPAETKRRETERMLQERKMLLNRDSISCTGSEIGGASSKEEGDT  530

Qy   432  CYEELLKYLVLYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSV  491
Db   531  VYAAFVRFIGHTFRR-TKRAAKKKYTAYMEE---------------------  560

Qy   492  HHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAE  551
Db   561  ----------RAERKSSERQQR------RKSKLDDMAT--LS----------  584

Qy   552  SVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVA  611
Db   585  ------------------------------RIEEKAEDE-  593

Qy   612  ASSGPPTLTSLNIPPGPYSSMIKLLETQSTGACQSSCKI-SSPCLKADSGACGPDSCPYC  670
Db   594  --EDETTITREN------GDDQIEQNGDGVRIKRVKIEEEPKIKIGN--GNSNGPHY  640

Qy   671  ARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWR  730
Db   641  KHSSSDE--------------ESDEDGEEDQVYDGEEAKKKS-----TPSKL-WW-  675

Qy   731  LICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEM  790
Db   676  -FREKIQKFVICDHFTRGILVAILVNTLSMGVEYHQQPEIITVILEYSNLFFTALFALEM  734

Qy   791  LLKLLVYGPFGYIKNPYNIFDGVIVVLSWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPA  850
Db   735  LLKIIASGLFGYLADGFNLFDGGIVAILSVLELFQEGKGLSVLRTFRILRILKLVRFMPA  794

Qy   851  LQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLRGCKFASERD----GDTLIP-DRKN  905
Db   795  LRYQLVVMLRTMDNVTFFGLLVLFIFSIIGMNLFGCKFCVEEKPLGGLAKKCERKN  854

Qy   906  FDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIIVE  965


Db   855  FDTLLWALITVFQILTQEDWNVLFNGMAQTNPWAALYFVALMTFGNVLFNLLIVAIIVE  914
Qy   966  GFQAEEISKREDASGQLSCIQLPVDSQOGDANKSESEPDFFSPSLDGDGDRKKCLALVSL 1025
Db   915  GFQE---SKEEE---------------------KRQLEEDARKQAVEEEDERKRELELI--  949

Qy  1026  GEHPELRKSLLPLIIHTAATPMSLPKSTGTGLGEALGPASRRTSSSGSAEPGAAHEMKS 1085
Db   950  ----------------IAKTTSPAFNNGVAPA-----ECTCQRPSSPEESPS  980

Qy  1086  PPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLLSGEGQESQ 1140
Db   981  PRLLSANYH----------PSPERKHSANLDAIIDKRLVL-------------- 1010

Qy  1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
Db  1011  --RNSAPFDR-SPV-SEGRDDSRLNRHA--SLVLPVANGVP------YRRQRVH 1052

Qy  1201  GKSASGRLARALRPDDPPLDGDADDEGNLSKGE-RVRAWIRARL-PACYLERDSWSAYI 1258
Db  1053  SWKASQELKQAL---------AEEE--KRNEAKQNTFVRKLLKKTCLHNRTEFSLFL 1098

Qy  1259  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db  1099  MGKNPLRIKCLQTTQKKWFDYTVLFFIGINCITLAMERPSIPPDSFERQFLHISGYIFT 1158

Qy  1319  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1378
Db  1159  VIFTGEMMMK-------------- 1168

Qy  1379  VLRLLRTIRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
Db  1169  ----------VSHRIPTLKPIGNIVLICCTFFIIFGILGVQLFKGMM 1205

Qy  1439  FVCQGEDTRNITNKSDCAEASYR--WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGL 1496
Db  1206  YHCIGPEVGNVTTKADCIE-DYRNKWVNHRYNFDNLGQALMSLFVLSSKDGWVSIMYQGI 1264

Qy  1497  DAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRRE 1556
Db  1265  DAVGVDVQPIENYNEWRMIYFISFLLLVGFFVLNMFVGVVVENFHKCKEALEKEMREKEK 1324

Qy  1557  EKRLRRLEK------------KRRKAQC--- 1590
Db  1325  EKRLKRKLKRQKFEESMAGKRKKNRIVWAGSAIKSIFSVERNYPYYHDYGHTRLFLHGIV 1384

Qy  1591  TSHYLDLFITGVIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVLESVFKLVAFGR 1650
Db  1385  TSKYFDLAIAAVIGINVISMAMEFYMMGLKYVLKALNYFFTAVFTLEAAMKLIALGPK 1444

Qy  1651  RFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVG 1710
Db  1445  RFFIEKWNRLDMFIVILSIAGIIFEEFEA-LELPINPTIIRVMRVLRIARVLKLLKMAKG 1503

Qy  1711  MRAILLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNF 1770
Db  1504  IRSLLDTVGEALPQVGNLGSLFFLLFFIFAALGVELFGKLECSEDHPCDGLGEHAHFKNF 1563

Qy  1771  GMAFLTLFRVSTGDNWNGIMKDTLR-DCD------QESTCYNTVISPIYFVSFVLTAQFVL 1824
Db  1564  GMAFLTLFRIATGDNWNGIMKDALRRDCDCDSSDHCETNCCVDPILAPCFFVIFVLISQFVL 1623

Qy  1825  VNVVIAVLMKHLEESNKEAKEEAELEAE 1852
Db  1624  VNVVAVLMKHLEESN--KRDAEGPAE 1648
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;  APPLICANT: Castle, John C.
;  APPLICANT: Armour, Christopher D.
;  TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B
;  FILE REFERENCE: RS0202Y
;  CURRENT APPLICATION NUMBER: US/10/627,370
;  CURRENT FILING DATE: 2003-07-25
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
   SEQ ID NO 2
;  LENGTH: 2264
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-627-370-2

Query Match         14.7%;  Score 1753;  DB 15;  Length 2264;
Best Local Similarity   24.8%;  Pred. No. 4.6e-101;
Matches   637;  Conservative   358;  Mismatches   830;  Indels   744;  Gaps   85;
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Qy   27 GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF---------------FYLSQDSRP   70
        |||                          :          :         ||:|:
Db   25 GAGGAGGPGPGPGGLQPFGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV   84

Qy   71 RSWCLRTVCNPWFERISMLVILLNCVTLGMWFRPCEDIACDSQRCRILQAFDD---FIFAF  127
        | :  :  ||||:  ::|||| ||:|||||   :| :     :      :         ||||
Db   85 RKYAKRITEWPPFEYMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI  140

Qy  128 FAVEMVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR  183
        | ||  |:|||| |: ||  :|: |||||||||| | |::     |||||:|:|||||
Db  141 FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR-----TLRAVR  195

Qy  184 VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFL  243
        |||||: |:  |:  : ||:  :  : |||:|||| | :|||| :||:: || | : ||
Db  196 VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-  254

Qy  244 PENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYE  303
        | |                                            ::
Db  255 -----PNSTDAE------------------------------PV-------GDFPCCKEAP  273

Qy  304 AYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV  363
        | |::  ||     :| ||  :|::| |: :|||||||| ||:|:||||:|||||||||||
Db  274 ARLCBGDTEC---REYWP--------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNT  323

Qy  364 MD-AHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES--------QLMREQRVRF  416
        :  |:|| ||: | |||||||||||||:|||: : || :|:       ||:||:|
Db  324 NDAAGNTWNWLYFIFLIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE-  382

Qy  417 LSNASTLASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET  476
        |   |    :                  |: ||  |
Db  383 --------RELNGYLEWIFKAEEVMLAEEDRNA---------------EEK  410

Qy  477 QPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP  536
        ||   ||| |: : ::|| :: : :                          |:
Db  411 SPLDVLKRAATKKKSRNDLIH--------------------AEEGBDRFAD--------  440

Qy  537 PSTPALSGAPPGGABSVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTS  596
Db  441 -------------------------------------------------------  440

Qy  597 PPPETLKEKALVEVAASSGPPTLITSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK  656
                                                          ||
Db  441 ------------------------------------------------LCAVGSPFAR  450

Qy  657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL  716
                                                         : :
Db  451 ASLKSGKTSSSSYFRR---------------------------KEKMFRF--------  473

Qy  717 GPDAEPSSVLAFWRLICDITFRKIVDSKYPFGRGIMIAILVNTLSMGIEYHEQPEELTNALE  776
                 : : ::    :::   ::  :   |:|:::  :|||:| ||::           ||
Db  474 -----FIRRMVKAQSFTWVLCVVALNTLCVAMVHYNQPRRLTTTLY  515

Qy  777 ISNIVFTSLFALEMLLKILVYGPFGYIKNPYNIFDCGVIVVISWEIVG-----QGGGLS  831
        |:|:||  ||:||| |:| | | |  :   ::|| ||||| :|  |||      |||||
Db  516 FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSSVFEVWAAIKPGSSFGIS  575

Qy  832 VLRTFRIMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLMLFIFIFSILGMHLFGCKF  891
        ||| :|::|||||||||||| |:|||||:|:|:::|:||||||||:|:||||||||| |
Db  576 VLRALRLLRIFKVTKWSSLRRNLVVSLLNSMKSIISLLFLLFIVVFALLGMQLFGGQF  635

Qy  892 ASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM--------ASTSSWAALYFIA  946
        :                 ||  ::  |||||||||:||| :|        | |: | | |::|
Db  636 NFQDETPT----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV  691

Qy  947 LMTFGNYVLFNLLVAILVEGF-QABEISK---REDASGQ-----------LSCIQ  986
        |  |||| : ||:|  |:     ||::      ::                ::::
Db  692 LTLFGNYTLLNVFLAIAVDNLANAQELTKDEBEMEEAANQKLALQKAKEVAVSPMSAAN  751

Qy  987 LPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGE----------HPELRK 1033
        :    :                              |||||          |::|:
Db  752 ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT  811

Qy 1034 SLLPPLIIHTAATPMSLP---------------KSTSTGLGEALGPASR---------RTSSSG----- 1073
        ||:                             |:|:|||::||:|:|:          |::::|
Db  812 HLDRPLVVELGRDGARGPVGKARPEAAEAPEGVDPPRRHHRHRDKDKTPAAGDQDRAEA  871

Qy 1074 ---SAEPGA---------------AHEMKSPPSARS---------SPH---------SPWSAASSW 1103
           :||                                         |           |:|:| |
Db  872 PKAESGEPGARRERRPRPHRSHSKEAAGPPEARSERGRGPGPEGGRRHRRGSPEEAAERE  931

Qy 1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQSSQDEESSEE---------ERASP- 1153
        :    :   :  |    :||:    |||: |:|:::|:|:|:               |||:
Db  932 PRRHRAHRH--QDPSKECAGAKGERRARHRGPRAGPREABSGEEPARRHRARHKAQPA  988

Qy 1154 ---------------------------AGSDHRHRGSLEREAKSSFPLDPTLQVPGLHRTASGRG 1191
                                   |||:|:|::|  :|: :|:| || :   | :: |  |
Db  989 HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048

Qy 1192 SASEHQDCNGKSASGRLARALRPDDP----------PLDGDDADDEGNL--------SKGE 1234
        ::|::|:                   |          || || || ||:        |:||
Db 1049 QKVEEQPEDADNQRNVTRMGSQPPPDPNTIVHIPVMLTGPLGEATVVPSGNVDLESQAEGK 1108

Qy 1235 R--------VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMPDHVVLVIIF 1287
        |        ||  :|:|  |  : | :|:|  ::  ::  | || : |:|:: :: |:::|
Db 1109 KEVEADDVMRSGPRPIVPYS--------SMFCLSPTNLLRRFCHYIVTMRYFEVILVVIA 1161

Qy 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347
        | ::|:|| ::   |  :  ||::|||||||:||: || |:|:|:||| ||:|||||:||
Db 1162 LSSIALAAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDLGLLLHPGAYFRDLWN 1220

Qy 1348 VLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETIM 1406
        :|      :|::|:: :    |   ||:|:|||||||||:|:|::|  |::|:|  : |:
Db 1221 ILLD----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRVLRPLKTIKRLPKLKAVFDCVV 1276

Qy 1407 SSLKPIGNIVVICCAFFIIFGLGVQLFKGKFPVVCQGE------DTRN--ITNKSDCAEA 1458
        ::||:|::::::  ||:::|| |:|||||||| :| :|        |:   | | :|  |
Db 1277 NSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYLLDYEKEEVEA 1336

Qy 1459 SYR--WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDLDAVGVDQQPIMNHNPWMLLYF 1517
         :|   :::|:: ||:  ||: :|:|: ||||:::::    |  ::|| : |  |:||::|
Db 1337 QPRQWKKYDFHYDNVLWALLLTFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIFY 1396

Qy 1518 ISFLLIVAFFVLNMFVGVVVENFHKCRQHQBEEEARRREEKRLRRLEKKRRKA------QC 1572
        : :::|| || ||:|  | ::||::                   |  :: ::
Db 1397 VVYFVVFPFFFVNIFVALIIITF---------QBGGDKVMSE----CSLEKNERACIDFAISA 1446

Qy 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVTMAMEHYQQPLIDEALKIC 1628
        ||   :    ::  ||:: :  : |: :  :: :: ::|:::|:|  ::|: :|:|:|
Db 1447 KPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVLMMKFVDAPYEYELMLKCL 1506

Qy 1629 NYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSMGITLEEI-EVNASLPINP 1687
        | |||:||::| |:|::||| || | | |||: || |:|||||| ::   : |:   ||
Db 1507 NIVFTSMFSMECVLKIIAFGVLNYFRDAWNVPDFVTVLGSITDILVTEIAETN-----NF 1561

Qy 1688 TIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFIFAALGVELF 1747
        |:||::|||| ||||||||: |||||| :   |::   ::   | ::::::||::|::|
Db 1562 INLSFLRLFRAARLIKLLRQYTIRILLWTFVQSFKALPYVCLLIAMLFFYAIIGMQVF 1621
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Qy    1748  GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE--STC  1803
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Db    1622  GNIALDDD--TSINRHNNFRTFLQAIMLLFRSATGEAWHEIMLSCLSNQACDEQANATE  1678

Qy    1804  YNTVISPIYFVSFVLTAQFV-----------LVNVVIAVLMKHLE-----ESNK       1841
                 :::  ||  |: ||||::||            | ||:|||:|:|:     ||||
Db    1679  CGSDFAYFYFVSFIFLCSFLRLVRMMPISNEDMTVHFTSTMALIRTALEIKLAPAGTK  1738

Qy    1842  EAKEEAELEAELELEMKTLSDQPHSPLGSPFLWPGVEGPDSPKPGALHPA---------  1894
                 ||::| ||||:::  ::   |   ::::   ||::| |||:| ||||:||
Db    1739  QHQCDAELRKELSVVWANL-PQKTLDLLVP--------PHKPDEMTVGKVYAALMIFDFY  1789

Qy    1895  ----AHARSASHFSLEHPTM---QPHPTELPGPDLLTVRKSGVSRTHSL           1936
                  ||||:|   :    |:  :||     :| |||:::|:|| : |:::|
Db    1790  KQNKTTRDQMQQAPGGLSQMGFPVSLFHPLKATLEQTQPAVLRGARVFLRQKSSTSLLSN--  1847

Qy    1937  PNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGSVLSVHSQPADTSYILQLPKDAPHLLQP--  1994
                 :   ::      |  ||||:|        || ||: |: :::|:|::: |:|: |:||||
Db    1848  ----------GGAIQNQESGIKESV-----------SWGTQRTQDAPHEARPPL       1880

Qy    1995  --HSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIR------TDSLDVQGLGSREDLLAE    2044
                  || | |    |      ||  ||  :: |:|         :| ::|   |:|::||
Db    1881  ERGHSTEI------------PVGRSGALAVDVQMQSITRRGPDGEPQPGLESQGRAASMPRLAA  1932

Qy    2045  VSGP---SPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPG---------    2088
                 |:||    |  ||:: |  ::||: :   ::|   |:|::
Db    1933  ETQPVTDASPMKRSI-----STLAQRPRGTHLCST---TEDRPPPSQASSHHHHHRCHR  1983

Qy    2089  ----PEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQ  2144
                  |  | ||:   :||     |  ||:|    |:|| |:|::    ||:  |:
Db    1984  RRDRKQRSLEKGP--SLSADMDGAPSSAVGPGLPPG--EGPTGCRRERERRQERGRSQE  2038

Qy    2145  RR-PTSWLDEQRRHSIAVSCLDSG-----------SQPHLGTDP--------SNLGG    2181
                 ||   :||::| |:: |    ||             ::|::: |         :|:||
Db    2039  RRQPSSSSSSEKQRF--YSCDRFGGREPPKPKPSLSSHPTSPTAGQEPGPHPQGSGSVNG  2095

Qy    2182  QPL------------------GGPGSRPKKKLSP-PSITI-----DPPESQGPRT--PP-SPG---  2217
                 ||:                  ||| |  :|  | |:   |      : :| ||
Db    2096  SPLLSTSGASTPGRGGRRQLPQTPLTPRPSIITYKTANSSPIHFAGAQTSLPAFSPGRLSR  2155

Qy    2218  ------ICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDP  2261
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Db    2156  GLSEHNALLQRDPLS---QPLAPG-----------------SRIGSDP  2183
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RESULT 15
US-10-033-026-4

; Sequence 4, Application US/10033026
; Publication No. US2002014730909A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-13
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
US-10-033-026-4

; SEQ ID NO 4
; LENGTH: 2343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-026-4

Query Match   14.7%; Score 1750.5; DB 13; Length 2343;
Best Local Similarity 24.2%; Pred. No. 6.9e-101;
Matches 639; Conservative 363; Mismatches 827; Indels 815; Gaps 84;

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Qy       1                                                         |||| |||

Db      71  RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD--FIFAF  127
                 :  |||  | |||    ||:  : :||  :||                      :: ||
Qy      25  GAGGAGPGPGGLQPGQPRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVVSEDNVV  84

Db      85  RKYAKRITEWPPFEYMILATIIANCIVLAL----EQHLPDGDKTPMSERLDDTEPYFIGI  140
                 :    :||:     |:|:::|| | |:: ||
Qy      71  RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD--FIFAF  127

Db     128  FAVEMVKMVALG-IFGKKCYLGDTWNRLDFFTVIAGMLEYS--LDLQNVSFSAVRTVR  183
                 |  |  |::|| :|||    |    |  || |:||::|||:   |     :|| ||
Qy      85  RKYAKRITEWPPFEYMILATIIANCIVLAL----EQHLPDGDKTPMSERLDDTEPYFIGI  140

Db     141  FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR---TLRAVR  195
                 |  | ||| :|| | |||||||  || |||| ::||::| |||| ||:   |||| |
Qy     128  FAVEMVKMVALG-IFGKKCYLGDTWNRLDFFTVIAGMLEYS--LDLQNVSFSAVRTVR  183

Db     196  VLRPLKLIVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-  254
                 ||||  ::||:|||::|:||:   ||||||  |    ::|||| ::|:||||| ||: |
Qy     184  VLRPLRAINRVPSMRILVTLLDDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFL  243

Db     255  ------PNSTDAE-------------------------------PV--------GDFPCGKEAP  273
                 |     :::| |                                 |         ||| |:||
Qy     244  PENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGLDYE  303

Db     274  ARLCEGDTEC--REYWP-------GPNFGITNDNILFAILTVFQCITMEGWTDILYNT  323
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Qy     304  AYNSSSNTTCVWNQYYTNCSAGEHNPFKGAINFDNIGYAWAIAFQVITLEGWVDIMYFV  363

Db     324  NDAAGNTWNWLYFIPLIIIGSFFMLNLVGLVLSGEFAKEREVENRRAFLKLRQQQIE-  382
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Qy     364  MD-AHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRES------QLMREQRVRF  416

Db     383  ------RBLNGYLEWIFKAEEVMLAEEDRNA                         -EBK  410
                                                                           |||
Qy     417  LSNASTLASFSEPGSCYEBLLKYLVIYIIRKAAARLAQVSRAAGVRVGLLSSPAPLGGQET  476

Db     411  SPLDVLKRAATKKSRNDLIH----------------------------------AEEGEDRFAD  440
                                                                           :||| |||
Qy     477  QPSSSCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP  536

Db     441  ----------------------------------------------------KEKMRFP  473
                                                                      :|:|||
Qy     537  PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVPTVHTS  596

Db     451  ASLKSGKTESSSSYFRR------------------------------  473
                 :|
Qy     441                                                      -PP-SPG---  440

Db     474  ----------------------------FIRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLY  515
                 |||:|::|::::::||:|:||
Qy     597  PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYYSSMHKLLETQSTGACQSSCKISSPCLK  656

Db     516  FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGIS  575
                 :| |:|:| :|::|| ::|
Qy     657  ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRSL  716

Db     717  GPDAEPSSVLAFWRLICDTFRKIVDSKYPGRGIMIAILVNTLSMGIEYHEQPEELTNALE  776
                 ||   ::    :||: ||||::|||   |||:::|:::|| ||||||: :| ||::|::|
Qy     717  GPDAEPSSVLAFWRLICDTFRKIVDSKYPGRGIMIAILVNTLSMGIEYHEQPEELTNALE  776

Db     777  ISNIVFTSLFALEMLLKLLVYGPPGYIKNPYNIFDGVIVISVWEIVGQ---QGGGLS  831
                 |||:|||| :||:| | |:|||||||||||||||||||||:|||||||    ||| ||
Qy     777  ISNIVFTSLFALEMLLKLLVYGPPGYIKNPYNIFDGVIVISVWEIVGQ---QGGGLS  831

Db     832  VLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFSILGMLFGCKF  891
                 |||:|||||||||||||||||||||||||||||||:|||||||||||||||||||||
Qy     832  VLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFSILGMLFGCKF  891

Db     892  ASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM--------ASTSSWAALYFIA  946
                 |||||||||||||||:|||:|||||||||||||||||||||||       ||||||||||||
Qy     892  ASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM--------ASTSSWAALYFIA  946

Db     947  LMTFGNYVLFNLLVAILVEGF-QAEEISK---REDASGQ----------LSCIQ  986
                 |||||||||| :|:|||| |: |::||:|    :|:|:           ||| |
Qy     947  LTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEAANQKLALQKAKEVAEVSPMSAAN  751

Db     987  LPVDSQGGDANKSESEPDFFSPSLLDGDGDRKKCLALVSLGE----------HPELRK  1033
                  :|:     :|:  :   |::  :| ::::::  |:|:::          |||||
Qy     752  ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT  811

Db    1034  SLLPPLIHTAATPMSLP----------------KSTSTGLGEALGPASR--------RTSSSG-  1073
                 ::||   |::|| :||                 ::|:|| ||  |||              :::
Qy      27  GAGGRPGGSGAEKDPGSADSEAEGLPYPALAPVF-----------------FYLSQDSRP  70
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Qy  1922  LLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYI  1981
          :  ||| :       :
Db  1914  VFLRQKSSTSLSN---------------------------GGAIQNESGIKESV------SWG  1944

Qy  1982  LQLPKDAPHLLQP-------HSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIR-----TDS  2029
          :||||| ||            :  ||
Db  1945  TQRTQDAPHEARPPLERGHSTEI-------PVGRSGALAVDVQMQSITRRGPDGEPQPG  1996

Qy  2030  LDVQGLGSREDLLAEVSGP---SPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPC  2086
          |: ||              :||        :|||
Db  1997  LESQGRAASMPRLAAETQPVTDASPMKRSI---------STLAQRPRGTHLCST---TPDRPP  2047

Qy  2087  PG---------------------PEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSP  2129
          :                     :
Db  2048  PSQASSHHHHRCHRRRDRKQRSLEKGP---SLSADMDGAPSSAVGPGLPPG--EGPTGC  2102

Qy  2130  RDLKKCYSVEAQSCQRR-PTSWLDEQRHSIAVSCLDSG-----------------SQPHLG  2173
          |  :|  |                :|: |  :
Db  2103  RRERERRQERGRSQERRQPSSSSSEKQRF---YSCDRFGGREPPKPKPSLSSHPTSPTAG  2159

Qy  2174  TDP-------SNLGGQPL--------------------GGPGSRPKKKLSP-PSITI---DPPESQG  2209
          :|          :|:         :|:  |: ||
Db  2160  QEPGPHPQGSGSGVNGSPLLSTSGASTPGRGGRRQLPQTPLTPRPSITYKTANSSPIHFAG  2219

Qy  2210  PRT--PP-SPG-----------ICLRRRAPSSDSKDPLASGPPPDSMAASPSPKKDVLSLSGL-SRI  2257
          :|: |  ||            |||
Db  2220  AQTSLPAFSPGRLSRGLSEHNALLQRDPLS--QPLAPG----------------------SRI  2258

Qy  2258  SSDP  2261
          ||||
Db  2259  GSDP  2262


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Job time   : 210.672 secs
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Db   812  HLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHRHRDKDKTPAAGDQDRAEA  871

Qy  1074  ----SAEPGA-----------AHEMKSPPSARS-------SPH------------SPWSAASSW  1103
          :                  ||||                       ||||
Db   872  PKAESGEPGARRERPRPHRSHSKEAAGPPEARSERGRGPGEPGGRRHHRRGSPEEAAERE  931

Qy  1104  TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEE--------ERASP-  1153
          |: | :         ||||||                          :
Db   932  PRRHRARRH--QDPSKECAGAKGERRARHRGGPRAGPREAESGEEPARRHRARHHKAQPA  988

Qy  1154  ------------------AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRG  1191
                            |:  ||
Db   989  HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL  1048

Qy  1192  SASEHQDCNGKSASGRLARALRPDDP-----------PLDGDDADDEGNL-----SKGE  1234
          ||                                         :|:
Db  1049  QKVEEQPEDADNQRNVTRMGSQPPDNTIVHIPVMLTGPLGEATVVPSGNVDLESQAEGK  1108

Qy  1235  R-------VRAWIRARLPACYLERDSWKSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF  1287
          :|          :  |: ||  : |::|  :|  ||: :|:|
Db  1109  KEVEADDVMRSGPRPIVPYS-------SMFCLSPTNLLRRFCHYIVTMRYFEVVLLVVIA  1161

Qy  1288  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN  1347
          | :   | |: |     :| ::| |::|||  |  : |:|:|  |      ||
Db  1162  LSSIALAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDLGLLLHPGAYFRDLWN  1220

Qy  1348  VLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLM  1406
          :||::|| :|: :   :      |  || |: ||||||| | ||  |: ||| :||
Db  1221  ILDFIVVSGALVAFAFSSFVGGSKGKDINTIKSLRVLRVLRPLKFTIKRLPLKIKAVFDCVV  1280

Qy  1407  SSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE--------DTRN--ITNKSDCAEA  1458
          :|||  ||:||:  |:||:|  :  ||||||||:|  :        |:||
Db  1281  NSLKNVLNILIVYMLFMFIAVIAVQLFKGKFFYCTDESKELERDCRGQYLDYEKEEVEA  1340

Qy  1459  SYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYF  1517
          :|    :| ||:||:  |  :|  ::||||  :|:      :  |:  |::  ||::::|
Db  1341  QPRQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIFY  1400

Qy  1518  ISFLLVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRRKA-----QC  1572
          :  ::|  |:::|||  :|:||           :|::          |:|      ||
Db  1401  VVYFVVFPFFFVNIFVALIIITF-----QEQGDKVMSE----CSLEKNERACIDFAISA  1450

Qy  1573  KPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDERALKIC  1628
          ||     :|       :  |::   | ::  |: ::|| |:|   |   |  |: | |
Db  1451  KPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL  1510

Qy  1629  NYIFTVIFVLESVFKLVAFGFRRRFQDRWNQLDLAIVLLSIMGITLEEI-EVNASLPINP  1687
          | :||:  ::  |:|::|||  :  :|:|| ||  |||::  ||:|  |    ||
Db  1511  NIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDILVTEIAETN-----NF  1565

Qy  1688  TIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELF  1747
          :|  ::|:|| |:|:|||::    ||:  ||:|:   |  ||||:|:||::|| :|| |:|
Db  1566  INLSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF  1625

Qy  1748  GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE--STC  1803
          |::  ||  ||      | ||:| ||:|||||::||: | :||  ::      |::
Db  1626  GNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE  1682

Qy  1804  YNTVISPIYFVSFVLTAQFVLVNVIAVLM------------KHLEE-----------  1838
          :: : | :||||: : | |::|:::|:|:
Db  1683  CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP  1742

Qy  1839  -------------------------------------------  1838

Db  1743  AACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNMPISNEDMTVHFTSTIMAL  1802

Qy  1839  ------------SNKEAKERAELEAELELEMKTLSPQHSPLGSPFLWPGVEGPDSPDSP  1886
                      :     : :  |::    :|:|||  |
Db  1803  IRTALEIKLAPAGTKQHQCDABLRKEISVVWANL-PQKTLDLLVP------PHKPDEM  1853

Qy  1887  KPGALHPA----------------------------AHARSASHFSLEHPTM---QPHPTELPGPD  1921
          :|                                  |::|| |: |:| |
Db  1854  TVGKVYAALMIFDFYKQNKTRDQMQQAPGGLSQMGPVSLFHPLKATLEQTQPAVLRGAR  1913
```

OM protein - protein search, using sw model

```
             GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:     November 18, 2004, 13:14:21 ; Search time 50.2671 Seconds
                                (without alignments)
                          4337.375 Million cell updates/sec

Title:      US-09-611-257A-37
Perfect score:  11904
Sequence:   1 MDEEEDGAGAEESGQPRSFM.........PKKDVLSLSGLSSDPADLDP 2266

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:   283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :      PIR_79:*
            1:  _pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description		
1	10945	91.9	2254	2	T09053	low voltage-activa		
2	3564.5	29.9	1657	2	T15838	hypothetical prote		
3	1746.5	14.7	2339	2	A42566	omega-conotoxin-se		
4	1741	14.6	2237	2	T45115	N-type calcium cha		
5	1711	14.4	2336	2	A45386	omega-conotoxin-se		
6	1706	14.3	2288	2	S41080	calcium channel al		
7	1697	14.3	2259	2	S29236	calcium channel pr		
8	1689	14.2	1810	2	T30193	probable voltage-g		
9	1681	14.1	2178	2	S29237	calcium channel pr		
10	1681	14.1	2272	2	C54772	voltage-dependent		
11	1665	14.0	2270	2	A54972	voltage-dependent		
12	1664.5	14.0	1891	2	T43262	calcium channel al		
13	1663.5	14.0	2251	2	B54972	voltage-dependent		
14	1656	13.9	2223	2	A47447	calcium channel pr		
15	1651.5	13.9	2222	2	A37490	voltage-dependent		
16	1633	13.7	1911	2	T43048	calcium channel al		
17	1632	13.7	1873	2	A30063	dihydropyridine re		
18	1626	13.7	1993	2	T30902	sodium channel SCA		
19	1625.5	13.7	1852	2	A37860	calcium channel pr		
20	1612	13.5	2143	2	JH0427	voltage-dependent		
21	1602.5	13.5	2139	2	A44467	voltage-dependent		
22	1597.5	13.4	1559	2	T30535	calcium channel al		
23	1596.5	13.4	2166	2	S11339	calcium channel pr		
24	1591	13.4	2019	2	A33996	sodium channel pro		
25	1590	13.4	1783	2	T37258	probable voltage-d		
26	1586	13.3	2016	2	A38195	sodium channel pro		
27	1583.5	13.3	1873	2	A55645	calcium channel, v		
28	1583	13.3	1977	2	S54771	sodium channel alp		
29	1581.5	13.3	2171	2	S05054	calcium channel al		
30	1578	13.3	1917	2	C88728	protein C48A7.1 [i		
31	1573.5	13.2	1983	2	A60054	sodium channel pro		
32	1572.5	13.2	2212	2	A41098	calcium channel pr		
33	1568.5	13.2	1687	2	S41742	calcium channel al		
34	1566.5	13.2	2203	2	T42742	voltage-dependent		
35	1565.5	13.1	1951	2	S00320	sodium channel pro		
36	1564.5	13.1	2181	2	A38198	calcium channel al		
37	1561	13.1	2326	2	B47447	calcium channel pr		
38	1560.5	13.1	1610	2	A46227	voltage-dependent		
39	1557.5	13.1	2161	2	JH0564	calcium channel al		
40	1555	13.1	2220	2	A45290	calcium channel pr		
41	1554	13.1	2262	2	T30890	calcium channel al		
42	1553.5	13.1	2005	2	A46269	sodium channel alp		
43	1550	13.0	1957	2	S68453	sodium channel pro		
44	1549.5	13.0	2009	2	A25019	sodium channel pro		
45	1549	13.0	1646	2	JH0422	voltage-dependent		

ALIGNMENTS

```
RESULT 1
T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09053
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox
Nature 391, 896, 1998
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium
A;Reference number: ZI6538; MUID:98154730; PMID:9495342
A;Accession: T09053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2254 <PER>
A;Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Map position: 17
A;Note: CACNA1G
C;Superfamily: calcium channel; voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel; voltage-gated ion channel

Query Match             91.9%;  Score 10945;  DB 2;  Length 2254;
Best Local Similarity   92.5%;  Pred. No. 0;
Matches 2107;  Conservative 34;  Mismatches 101;  Indels 36;  Gaps 6;

Qy      1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDEEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy     61 FFYLSQDSRPRSWCLRTVCNPWFERISMEIVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 FFYLSQDSRPRSWCLRTVCNPWFERVSMIVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
          |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db    241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL 300

Qy    301 DYEAYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DYETYNSSSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy    361 YFVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFESTKQRESQLMREQRVRFLSNA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   361 YFVMDAHSFYNFIYFILLIIVGSFEMINLCLVVIATQFSETKQRESQLMREQVRFLSNA  420
Qy   421 STLASFSEFGSCYEELLKLYLVYILRKAAARLAQVSRAAGVRGLLSSPAPLGGQETQPSS  480
         ||||||||||||||||||||||||||||||||||| ||| ||| || ||| :  | || |
Db   421 STLASFSEFGSCYEELLKLYLVYILRKAAARLAQVSRAIGVRAGLLSSPVARSGQEPQPSG  480

Qy   481 SCGRSHRRLSVHHLVHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP  540
         || ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   481 SCTRSHRRLSVHHLVHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP  540

Qy   541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
         : ||  | ||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   541 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPE  600

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660
         :||:||||||| |:||||||||| |||||||||||||||||||||| |||||||| ||||
Db   601 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG  660

Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSLGPD  719
         |||||||||||:||||| | ||  :||||||||||||||||||||||||| || |||||
Db   661 ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPD  720

Qy   720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN  779
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN  780

Qy   780 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLM  839
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLM  840

Qy   840 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT  899
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT  900

Qy   900 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGWASTSSWAALYFIALMTFGNVLFNLL  959
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGWASTSSWAALYFIALMTFGNVLFNLL  960

Qy   960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC 1019
         |||||||||||                      ||:||||||||||||||||||||||||
Db   961 VAILVEGFQAE----------------------GDATKSESEPDFFSPSVDGDGDRKKR  997

Qy  1020 LALVSLGEHPELRKSLLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGAEPGA 1079
         ||||:||||:|||||||| |||||||||| ||:|:||:||||| ||||||||| :||||
Db   998 LALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGA 1057

Qy  1080 A-HEMKSPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
         | |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1058 AHHEMKCPPSARSSPHSPWSAAASWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1117

Qy  1139 SQDEEESSEERARSPAGSDHRHRGSLEREFAKSSFDLPDTLQVPGLHRTASGRGASEHQD 1198
         |||||||||||| ||||||||||||||||| |||||||||||||||||||||||:||||
Db  1118 SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSASEHQD 1177

Qy  1199 CNGKSASGRLARALRPDDPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
         ||||||||||||:||:|||||||::|||||||||||:|:|:|||||| | |||||||||
Db  1178 CNGKSASGRLARTLRTDDPLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1237

Qy  1259 FPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1238 FPPQSRFRLLCHRIITHKMFDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297

Qy  1319 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVDSGTKILGMLR 1378
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1298 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVDSGTKILGMLR 1357

Qy  1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1358 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417

Qy  1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1418 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1477
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Qy  1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEEARRREEK 1558
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1478 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEEARRREEK 1537

Qy  1559 RLRRLEKKR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1611
         ||||||||       |:|||||||||||||||||||||||||||||||||||||||||
Db  1538 RLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1597

Qy  1612 MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG 1671
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1598 MEHYQQPQILDEALKICNYIFTVIFVFPESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG 1657

Qy  1672 ITLBEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLL 1731
         ||||||||| |||||||||||||||||||||||||||||||| :||||||||||||||||
Db  1658 ITLBEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLL 1717

Qy  1732 FMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1718 FMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1777

Qy  1792 DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLESNKEAKEEABLEA 1851
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1778 DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLESNKEAKEEABLEA 1837

Qy  1852 ELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALIPAAHARSASHFSLEHPTMQ 1911
         |||||||||||||||||||||||||| :| : ||||| || ||:| |:| |||||||:||
Db  1838 ELELEMKTLSPQPHSPLGSPFLWPGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV 1897

Qy  1912 PHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSV 1968
         |||  ||   ||||||||||||||||||||||||||:||||| |||||||||||||||||
Db  1898 PHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI 1957

Qy  1969 LSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTD 2028
         ||||||||||| ||||||| ||||||| ||||||||||||||||||||||||||||||||
Db  1958 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD 2017

Qy  2029 SLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQHSRSHSKISKHMTPPAPCPG 2088
         |||||||||||||:||||||| ||:|:  |||:||:| |:||||: || | ||:|||||
Db  2018 SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQRGIQSVKSKHIRLPAPCPG 2077

Qy  2089 PEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPT 2148
         ||| | | ||||||||||||||||||||| |   |||| |||||||||||:|||:||| 
Db  2078 LEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLFPRDLKKCYSVETQSCRRRPG 2136

Qy  2149 SWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQ 2208
         :||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Db  2137 FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPPESQ 2196

Qy  2209 GPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASSPSPKKDVLSLSGLSSDPADLDP 2266
         | | | ||| |||||||:||||||| ||| ||:|||||| |||:||||||||||| :|||
Db  2197 GSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASSPKKDTLSLSGLSSDPTDMDP 2254
```

```
Query Match       29.9%;  Score 3564.5;  DB 2;  Length 1657;
Best Local Similarity   42.2%;  Pred. No. 6.5e-210;
Matches  822;  Conservative  231;  Mismatches  430;  Indels  465;  Gaps   50;

Qy    15 QPRSFMRLNDLSGAGGRPG---------------PGSAEKDPG-------------SADSEA 48
         |:||:|||                        :||::|
Db    56 QSQSTRRHEDVEALGSIEGSKETLQLSEHGRLASSEASPSRWEGRQIEWGNEEQIEEES 115

Qy    49 EGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCED-I 107
         |:|||   ||:||||:||:  |  : |: || ||:|:|:||:| ||:|||:|:|::|
Db   116 E-LPYPGFAEPALRCFYQARPPRKWALQMVMSPWFDRITMAVIMINCVTLGMYRPCEDGP 174

Qy   108 ACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEY 167
         | || | ||:  || :|| |::|::||:: |  :| || |:|||:|||||:|:|||:|:
Db   175 DCDTYRCQILDIIDNCIFVYFAFEMVIKIMALGFYGPAAYMSDTWNRLDFFIVMAGIAEF 234

Qy   168 SLDLQ---NVSFSAVRTVRVLRPLRAINRVPSMRIILVTLLLDTLPMLGNVLLLCFFVFFI 224
         |||:|   |  : |:|||:||||||:||||:|||:||:|:|||||||||||||||||||:|
Db   235 VLHEYLGGNINLTAIRTVRVLRPLRAVNRIPSMRIILVNLLLDTLPMLGNVLLLCFFVFFI 294

Qy   225 FGIVGVQLWAGLLRNRCF--LPENFS------LPLSVDLERYYQTENEDESPFICSQPREN 277
         ||||||||||||||||      :||         |:|: :  ::: ||| |: |||:||:|
Db   295 FGIVGVQLWAGLLRNRCVINLPKTISENQSALFNNVKLTRFYIPE-DTSLEYICSQPDAN 353

Qy   278 GMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAG------------ 326
         |:  | |||       | |        :: | | | |:|:
Db   354 GLHTCSNLPPYTVD----GVKCNLTLDEYDKVTNDSCINWNIYYNECQVNIYPSLMTIAIS 410

Qy   327 ------EHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLII 380
              ||:|||| |::||||||||::|||:|||||||||||||||| ||||||||||||
Db   411 CFIKVMQRNFPQGSVSFDNIGFAWVAIFLVISLEGWTDIMYVVQDAHSFWNWIYFVLLIV 470

Qy   381 VGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPG---------S 431
         ||:|||||||:|||||||:|| :: ||| | | |:|:| :    :||
Db   471 IGAFFMINLCLVVIATQFAETKRRETERMLQERKMLLNRDSISCTGSEIGASSKEEGDT 530

Qy   432 CYEELLKYLVVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRHRRLSV 491
         ::::|| |:|
Db   531 VYAAVRFIGHTFRR-TKRAAKKKYTAYMEE------------------------------- 560

Qy   492 HHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAE 551
         |:
Db   561 ---------------RAERKSSERQQR-----RKSKLLDDMAT--LS------------- 584

Qy   552 SVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVA 611
                                                    :|||
Db   585 ---------------------------------------------RIEEKAEDE-- 593

Qy   612 ASSGPPTLTTSLNIPPGPYSSMHKLLETQSTGACQSSCKI-SSPCLKADSGACGPDSCPYC 670
                                                      :|
Db   594 --EDETTITREN------------GDDQIEQNGDGVRIKRVKIEEEPKIKIGN--GNSNGPHY 640

Qy   671 ARAGAGEVELADREMPDSDSEAVEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWR 730
                                          : :  || :: ::||| ::  :|
Db   641 KHSSSDE------------------ESDEDGEEDQVYDGEEAKKKS-----TPSKL-WW- 675

Qy   731 LICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEM 790
         |:| |||:|||:| || | : |||||||||:::::|| ||:||:||||:|::|:|:|||
Db   676 -FREKIQKFVICDHFTRGILVAILVNTLSMGVEYHQQPBILTVILEYSNLFFTALFALEM 734

Qy   791 LLKLLVYGPFGYIKNPYNIIPDGVIVVISVWEIVQGQQGGGLSVLRTFRLMRVLKLVRFLPA 850
         ||||| | ||||:||| | ||| |:::|::|| | |:| |:|:|||||||:||||||| :|
Db   735 LLKIIASGLFGYLADGFNLFDGGIVALSVLELFQEGKGGLSVLRTFRLLRILKLVRFMPA 794

Qy   851 LQRQLVVLMKTMDNVATFCMLLMFLFIFSILGMHLFGCKFASERD---GDTLP--DRKN 905
         | ||||:|||:|||| ||  |:||:||||||||||||||   |:: ||:|   |:||
Db   795 LRYQLVVMLRTMDNVTVFFGLLVLFIFIFSILGMNLFGCKFCVEEKFLGGLAKKCERKN 854

Qy   906 FDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVE 965
         || ||| |:|||||||||||:: | ::|| : :||| |:|||||||||||||:||||||:
Db   855 FDTLLWALITVFQIITQEDWNMVLFNGMAQTNPWAALYFVALMTFGNYVLFNLLVAILVE 914
```

```
Qy   966 GFQAEEISKREDASGQLSCIQLPVDSQGQDANKSESEPDFFSPSLDGDGDRKKCLALVSL 1025
         ||||       :::||||                        ::|:  |
Db   915 GFQB--------SKEEE------------------------------KRQLEEDARKQAVEEEDERKRELELI- 949

Qy  1026 GEHPELRKSLLPPLLIHTAATPMSLPKSTGLGEALGPASRRTSSSGAEPGAAHEMKS 1085
                                                :||::||:||
Db   950 --------------IAKTTSPAFNGVAPA--------------ECTCQRPSSPEESFS 980

Qy  1086 PPSARSSPHSPWSAAASSWTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLLSGEGQESQ 1140
                                                         :|:
Db   981 --------------------PSPERKHSANLDAIIDKRLVL---------------- 1010

Qy  1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
                            :||:|                    ::|:|
Db  1011 --RNSAPFDR-SPV-SEGRDDSRLNRHA--SLVLPVANGVP----------YRRQRVH 1052

Qy  1201 GKSASGRLARALRPDDPPLDGDADDEGNLSKGE-RVRAWIRARL-PACYLERDSWSAYI 1258
                                   :|::|
Db  1053 SWKASQELKQAL----------AEEE---KRNEAKQNTFVRKLLKKTCLHNRTEFSLFL 1098

Qy  1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
         ||  |||| :|   |  ||  :|| |:|:|||||||||||:  : |::|||:|:||:||:
Db  1099 MGPKNPLRIKCLQTTQKKWFDYTVLFFIGINCITLAMERPSIPPDSFERQFLHISGYIFT 1158

Qy  1319 AVPFLAEMTVKVKVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLR 1378
         :|  |  ||:|
Db  1159 --VIFTGEMMMK------------------------------------------------- 1168

Qy  1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKF 1438
         |||| |||:||||||| ||||||:|||:|||||||:| | :||| |||||||||||:
Db  1169 -----VSHRIPTLKPIGNIVLICCTFFIIFGILGVQLFKGMM 1205

Qy  1439 FVCQGEDTRNITNKSDCAEASYR--WTRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGL 1496
         : || || ||:|  || |:  :|    |  :||||||:|||:|||:| ||||||:|  |:
Db  1206 YHCIGPEVGNVTTKADCIE-DYRNKWVNHRYNFDNLGQALMSLFVLSSKDGWVSIMYGI 1264

Qy  1497 DAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRRE 1556
         |||||||||||:||||:|||||||:|||||||||||||||||||||||:|::::::|:|
Db  1265 DAVGVDVQPIENYNEWRMIYFISFLLLVGFFVLNMFVGVVVENFHKCKEALEKEMREKEK 1324

Qy  1557 EKRLRRLEK--------KRRKAQC---------------------KPYYSDYSRFRLLVHHLC 1590
         ||:|:|:|:        ||:|:                       ||::| ||:||:|:||
Db  1325 EKRLKRKLRQKFEESMAGKRKKNRIVWAGSAIKSIFSVERNYPYYHDYGHTRLFLHGIV 1384

Qy  1591 TSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFR 1650
         ||:|| || :|:|:|||:|:|:| |||||  :||: |||| |||:||:|:|| ::|
Db  1385 TSKYFDLAIAAVIGINVISMAMEFYMMPMGLKYVLKALNYFFTAVFTLEAAMKLIALGFK 1444

Qy  1651 RFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIARVLKLLKMAVG 1710
         ||||:|:||::|:|::|:| :|||:||||||||||||||||:||||||||||||||:||
Db  1445 RFFIEKNRLDMFIVLSIAGI-IFEFEA--LPINPTIIRVMRVLRIARVLRLLKLLKMAKG 1503

Qy  1711 MRALLDTVMQALPQVGNLGLJFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNF 1770
         : :||||||:|||||||||| ||||||||||||:|||:   :::|| | :: |: |||
Db  1504 IRSLLLDTVGEALPQVGNLGSLFFLLFFIFAALGVELFGKLECSEDHPCDGLGEHAHFKNF 1563

Qy  1771 GMAFLTLFRVSTGDNWNGIMKDTLR-DCD---------QESTCYNTVISPIYFVSFVLTAQFVL 1824
         ||||||||:|||||||||||||::| |||                :||||| :||:|::|||
Db  1564 GMAFLTLFRIATGDNWNGIMKDALRDDCDSSDHCETNCCVDPILAPCFFVFLISQFVL 1623

Qy  1825 VNVVIAVLMKHLEESNKEAKEAEELEAE 1852
         ||||:||||||||||||
Db  1624 VNVVAVLMKHLEESN---KRDAEGPAE 1648
```

```
RESULT 3
A42566
omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively splice
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: A42566
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McCu
Science 257, 389-395, 1992
```

```
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-typ
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: A42566
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2339 <WIL>
A;Experimental source: IMR32, hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:109168)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match            14.7%;  Score 1746.5;  DB 2;  Length 2339;
Best Local Similarity  24.2%;  Pred. No. 2.2e-98;
Matches 641;  Conservative 361;  Mismatches 823;  Indels 819;  Gaps 86;
```

```
Qy    27  GAGGRPGPGSAEKDPGGADSEAEGLPYPALAPVVF------------FYLSQDSRP    70
              :  :::   :: ::    ::    ::   :        ||:||:::
Db    25  GAGGAGGPGPGGLQPGGQRVLYKQSIAQRARTMALYNFIPVKQNCFTVNRSLFVFSEDNVV   84

Qy    71  RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAF   127
              ||:   : ::|| ::::| |:|||:|:|  | : :      :|| ::    |::|:
Db    85  RKYAKRITEWPPFEYMILATIIANCIVLAL---EQHLPDGDKIPMSERLLDDTBPYFIGI   140

Qy   128  FAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR   183
           | ||  : :||| :|  | ||  :|| :|||:|:| |:|      |:|  ||| |:|
Db   141  FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR------TLRAVR   195

Qy   184  VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQMAGLLRNRCFL   243
          ||||::   ::|::: ::  ::  : |:: :||| | |:|:| |:|:|: | |  :: ||
Db   196  VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-   254

Qy   244  PENFSLPLSVDLLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPCGLDYE   303
                                  |:               |:       ||: ::|
Db   255  ------------PNSTDAE---------------PV----GDFPCQKEAP             273

Qy   304  AYNSSSNNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWTDILYNT   363
            :  :   ||      :    | ::    || :|||||:  |:|: |::|:|||||||||
Db   274  ARLCEGDTEC---REYWP--------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNT   323

Qy   364  MD-AHSFYNFIYFLILIIVGSFFMINLCLVVIATQFSETKQRES-------QLMREQRVRF   416
              |    :   : ||||:||||||:|| |||:   |::   :|          : :: :
Db   324  NDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRQQQIE-   382

Qy   417  LSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET   476
                                    :  : |      |  |  : : |      :::| |
Db   383  ---------------REINGYLEWIFKAEEVMLAEEDRNA                        410

Qy   477  QPSSSCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP   536
                 : ::   : |: ::: :          : |: :    |: | |  :::
Db   411  SPLDVLKRAATKKSRNDLIH----------------AEEGDRDFAD----------      440

Qy   537  PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTS   596
                                                                 | ||| |:
Db   441  ----------------------------------------------------LCAVGSPFAR   450

Qy   597  PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMKLLETQSTGACQSSCKISSPCLK   656
                                                      :       |    ::  :
Db   657  ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL   716

Qy   657  ASLKSGKTESSSYFRR------------------------KEKMFRF                473
                                                       : ::|:
Db   717  GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALE   776

Qy   474  ----FIRRMVKAQSFTWVLCVVALNTLCVAMVHYNQPRRLTTTLY                  515
              |:||      :|| |:| | :|:| |: :|:|
Db   777  ISNIVFTSLFALEMLLKLLLVGPFGYIKNPYNIFDGVIVVISWEIVG--QQGG-GLS     831

Qy   516  FAEFVFGLLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVVWAAIKPGGSFGIS   575
          ::  |  :: : ::|| |    |:|:    :  :|:| :|: | |::| ||  ||| ||
Db   832  VLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF   891

Qy   832  VLRALRLLRIFKVTKYWSSLRNLVVSSLLNSMKSIISLLFLLFIVVFALLGMQLFGGQF   891
          |||:::  |:||:||:       :| ||||:|| | ||::|| |:|:|| |||| || |
Db   576  VLRLRRFLRVFKFTKYWSSLRNLVVSSLLNSMKSIISLLFLLFIVVFALLGMQLFGGQF   635
```

```
Qy   892  ASERDGDTLPDRKNFDSLLWAIVVFQLLTQEDWNKVLYNGM----ASTSSWAALYFIA    946
            :  | :|     ||| | | |||:|:|| |:|||| :|          ||| ||||:
Db   636  NFQDETPT----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV   691

Qy   947  LMTFGNYVLFNLLVAILVEGF-QAEEISK---REDASGQ-                        986
          | ||||| | |:: || :     :|::     ||
Db   692  LTLFGNYTLLNVFLAIAVDNLANAQELTKDEEMEEAANQKLALQKAKEVAEVSPMSAAN   751

Qy   987  LPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGE------------HPELRK   1033
           : :  |  :||: :| |:||   |||| ||:         |            ||::|
Db   752  ISIAARQQNSAKARSVWEQRASQLRIQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT   811

Qy  1034  SLLPLIIHTAATPMSLP----KSTSTGLGEALGPASR----RTSSSG-              1073
           :| |:: :  :::| |     |:| || : ::   ::      ::::
Db   812  HLDRPLVVELGRDGARGPVVGKARPEAAEAPEGVDPPRRHRHRDKDKTPAAGDQDRAEA   871

Qy  1074  ----SAEPGA---------------AHEMKSPPSARS-------SPH-              1103
              ||  |                 : : ::   |:         ||
Db   872  PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGPEGGRRHRRGSPEEAAERE   931

Qy  1104  TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQSQDEEESSEE------ERASP-     1153
              :::: :| |:     :| : :|  || :   | :::|||::|      ||:|
Db   932  PRRHRAHRH---QDPSKECAGAGKGRRARHRGGPRAGPREAESGEEPARRHRARHAQPA   988

Qy  1154  ------AGSDHRHRGSLEREAKSSPDLPDTLQVPGLHRTASGRG                 1191
                :: : :|  | :| : :| |  :  | ::
Db   989  HEAVEKETTEKEATEKEAEIVEADKKKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL  1048

Qy  1192  SASEHQDCNGKSASGRLARALRPDDP----------PLDGDADDEGNL---SKGER-     1235
           ||  |      |: :|| ||| |:|           || ||| :| :     ||||
Db  1049  QKVEEQEPEDADNQRNVTRMGSQPPDNTIVHIPVMLTGPLGEATVVPSGNVDLESQAEQK  1108

Qy  1236  --------VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMEPDHVLVLIIF  1287
                    :    |     ||         |:  |:| :  || : ||  | |||:::
Db  1109  ------SMFCLSPTNLLRRFCHYIVTMRYFEVVIIVVIA                        1161

Qy  1288  LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN  1347
           :  :|| | :: |  : :| ||| ||||||:||: || |:|: |   | || |: ||
Db  1162  LSSIAIAAEDP-VRTDSPRNNALKYLDYIFTGVFTFEMVIKMIDLGLLLHPGAYFRDLWN  1220

Qy  1348  VLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLM  1406
           ::   :|:|: ||:     |: |  | | :||||:||| |:|| :: | :|| |:  :|
Db  1221  ILD---FIVVSGALVAFAFSGSSKGKDINTKSLRVLRVLRPLKTIKRLPKLKAVFDCVV   1276

Qy  1407  SSLKPIGNIVICCAFFIIFGILGVQLFKGKFFVCQGE--------DTRN--TTNKSDCAEA  1458
           |||  :  ::  ||| |:| |: |:|||||||:| |:        ||    :| : : ||
Db  1277  NSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGGYLDYEKEVEA   1336

Qy  1459  SYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYF  1517
              | :: |:: || |::| :||: :: ||| ::  ::        : | | | ||:||:
Db  1337  QPRQWKKYDFHYDNVLWALLILFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIFY  1396

Qy  1518  ISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLREKKRRKA---QC     1572
          :|::::| ||:|:|||  :| || ||  :           :  |:: :            ||
Db  1397  VVYFVVFPFFFVNIFVALIIITF-----QEQGDKVMSE----CSLEKNERACIDFAISA  1446

Qy  1573  KPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKIC  1628
          ||    : : |  |  |: |: || : : || ::|:|:||:: |   :  ::::: |:|
Db  1447  KPLTRYMPQNRQSFQYKTWTFVVSPPFEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL  1506

Qy  1629  NYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEI-EVNASLPINP  1687
          | :||:::: : |:|::|||: ::|:|:|| :||: ||  :  |:| :     ||:
Db  1507  NIVFTSMFSMECVLKIIAFGVLNYFRDAWNVFDFVTVLGSITDILVTEIAETN----NF   1561

Qy  1688  TIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELF  1747
          : ||::|: |:||  |||:: :| ||: | | |:|  :|:| : ::: ||:: |: ||::|
Db  1562  INLSFLRLFRAARLIKLLRQGYTIRIILWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF  1621

Qy  1748  GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE-STC  1803
          |:  :|:   : ::  |  :: |  |::|:||:|||: |: || |: |      |::  :
Db  1622  GNIALDDD---TSINRHNFRTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE  1678
```

```
Qy   1804  YNTVISPIYFVSFVLTAQFVLVNVVIAVLM-----------------KHLEE----------  1838
                :  ||||:  |||||: :||: :|:|
Db   1679  CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSIIGPHHLDEFIRVWAEYDP  1738

Qy   1839  ------------------------------------------------------------  1838

Db   1839  ------------------------------------------------------------  1838
```

```
Matches  629;   Conservative  361;   Mismatches  836;   Indels  780;   Gaps  80;
```

```
Qy    27  GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF-----------------FYLSQDSRP   70
           ||||:|||: ||:    :    :|:||:    ||:
Db    25  GAGGAGGPGPGGLQPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV   84

Qy    71  RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDD---FIFAF  127
           |:|:|      ::||||:|||:   :||  :|||||::|:::  :|  |||    |||||
Db    85  RKYAKRITEWPPFEYMILATIIANCIVLAL----EQHLPDGDKTPMSERLDDTEPYFIGI  140

Qy   128  FAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR  183
           |||:||| ||||  |   :||:|  ||::    |:    |:    ||:   ::|   |||
Db   141  FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR-----TLRAVR  195

Qy   184  VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGVVGVQLWAGLLRNRCFL  243
           |||||||| |  |::|:   :|:|:|||     ||||||:|||:| ||:| |||:|||||
Db   196  VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF-  254

Qy   244  PENFSLPLSVDLERYYQTNEDESPFICSQPRENGMRSCRSVPFLRGDGGGPCGLDYE    303
                                            :|||:|||||  |:|:    ||: :
Db   255  ------PNSTDAE-----------------------------PV----GDFPCGKEAP    273

Qy   304  AYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV  363
             |    :  |:|  :  :||  ::|        |:|||:|  ||||:|:||| |||:|:
Db   274  ARLCEGDTEC---REYWP------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNT   323

Qy   364  MD-AHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES-----QLMREQRVRF  416
           |:    || ||| :|::|||:| :|||:  |||:|||||        :     |::|:
Db   324  NDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE-  382

Qy   417  LSNASTLASFSEPGSCYEELLKYLVYIIRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET  476
                                 |:|| ||: | |           :|      |||:
Db   383  ------------------------RELNGYLEWIFKAEEVMLAEEDRNA------EEK   410

Qy   477  QPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP   536
              :| |: :|::|                            :| :|
Db   411  SPLDVLKRAATKKSRNDLIH-------------------------AEEGEDRFAD----  440

Qy   537  PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTS  596
            |
Db   537  ------------------------------------------------------------  440

Qy   597  PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK  656

Db   441  ------------------------------------------------------------  441

Qy   657  ADSGACGPDSCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL  716
                                                           :|    :|
Db   451  ------------------------------------------ASLKSGKTESSSSYFRR  473

Qy   717  GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALILVNTLSMGIEYHEQPELTNALE  776
            :      :||| :|  |   |||||:||||||:|| :|:|||||||:::     |  ::
Db   474  ------------------------FIRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPRRLTTTLY  515

Qy   777  ISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISWEIVGQ-----QGGGLS  831
             :  |||::|:|  :   :||:|  ||:|| | :|||  |:  :|| ||    :
Db   516  FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSVFEVVWAAIKPGSSFGIS  575

Qy   832  VLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF  891
           ||| ||:||| :::|:| :   |  |:||:|||::  |:|  || |:|| |:|:|:||
Db   576  VLRALRLLRIFKVTKWSSLRNLVVSLLNSMKSIISLLFLLFLFIVFALLGMQLFGGQF   635

Qy   892  ASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----ASTSSWAALYFIA  946
                                :|:| :|:|||::|      :     :::   || |:
Db   636  NFQDETPT----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV  691

Qy   947  LMTFGNYVLFNLLVAILVEGF-QAEEISK----REDASGQ-------LSCIQ  986
            | |||||:|::| ||::     ||:|:      ||||:        |:|| |
Db   692  LTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEAANQKLALQKAKEVASPMSAAN  751

Qy   987  LPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGE-----HPELRK  1033
            :     |::  ::      : :     : |: :  ::|     :  :|:|:
Db   752  ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPDMKT  811
```

```
RESULT 4
T45115
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45115
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McCue, A.F.
Science 257, 389-395, 1992
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: T45115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2237 <WIL>
A;Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g179797
A;Experimental source: cell line IMR32; neuroblastoma
C;Genetics:
A;Note: CCHL1A2
C;Function:
A;Description: calcium influx
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match     14.6%;   Score 1741;   DB 2;   Length 2237;
Best Local Similarity   24.1%;   Pred. No. 4.6e-98;
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Qy 1034 SLLPLIIHTAATPMSLP-------KSTSTGLGEALGPASR------------RTSSSG-------- 1073
Db  812 HLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHRHRDKDTPAAGDQDRAEA 871

Qy 1074 ---SAEPGA-----------AHEMKSPPSARS----SPH------SPWSAASSW 1103
Db  872 PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGPEGGRRHRRGSPEEAAERE 931

Qy 1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGEGSQDEEESSEE--------ERASP- 1153
Db  932 PRRHRAHRH--QDFSKECAGAKGERRARHRGGPRAGPREEAESGEEPARRHRARHKAQPA 988

Qy 1154 ------------AGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRG 1191
Db  989 HEAVEKETTEKEATEKEAEIVEADKEKEELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048

Qy 1192 SASEHQDCNGKSASGRLARALRPDDP-------------SKGE 1234
Db 1049 QKVEEQPEDADNQRNVTRMGSQPPDPNTIVHIPVMLTGPLGEATVVPSGNVDLRSQAEGK 1108

Qy 1235 R--------VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIF 1287
Db 1109 KEVEADDVMRSGPRPIVPYS---SMFCLSPTNLLRRFPCHYIVTMRYFEVVLILVVIA 1161

Qy 1288 LNCTTIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347
Db 1162 LSSIALAAEDP-VRTDSPRRNALKYLDYIFTGVFTFEMVIKMIDLGLLLHPGAYFRDLWN 1220

Qy 1348 VLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTLRPLRVISRAQCLKLVVETLM 1406
Db 1221 ILD-----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRVLRPLKTIKRLPKLKAVFDCVV 1276

Qy 1407 SSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCCGE------DTRN--ITNKSDCAEA 1458
Db 1277 NSLKNVINILIVYMLFMFIAVIAVQLFKGKFFYCCTDESKELERDCRGQYILDYEKEEVEA 1336

Qy 1459 SYR--WVRHKINFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYF 1517
Db 1337 QPRQWKKYDFHYDNVLWALLLFLFTVSTGEGWPELMLKHSVDATYEEQGPSGYRMELSIFY 1396

Qy 1518 ISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRRLEKKRKA-----QC 1572
Db 1397 VVYFVVFPFFFVNIFVALIIITF------QEQGDKVMSE----CSLEKNERACIDFAISA 1446

Qy 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKIC 1628
Db 1447 KPLTRYMPQNRQSFQYKTWTFVVSPPEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL 1506

Qy 1629 NYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEI-EVNASLPINP 1687
Db 1507 NIVFTMSFMSMECVLKIIAFGVLNYFRDAWNVFDFVVLGSITDILVTEIAETN-----NF 1561

Qy 1688 TTIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELF 1747
Db 1562 INLSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF 1621

Qy 1748 GDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE-STC 1803
Db 1622 GNIALDDD---TSINRHNNFRTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678

Qy 1804 YNTVISPIYFVSFVLTAQFVLVNVVIAVLM----KHLEE 1838
Db 1679 CGSDFAYFYFVSFIFLCSFLMNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1738

Qy 1839 ------------------- 1838
Db 1739 AACGRISYNDMFEMLKIMSPPLGLGKKCPARVAYKRLVRMNMPISNEDMTVHFTSTLMAL 1798

Qy 1839 ------------------- 1886
Db 1799 IRTALEIKLAPAGTKHQCDAELRKEISVVWANL-PQKTLDLLVP-----PHKPDEM 1849
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Qy 1887 KPGALHPA-----------------------AHARSASHFSLEHPTM 1921
Db 1850 TVGKVYVAALMIFDFYKQNKTTRDQMQQAPGGLSQMGPVSLFHPLKATLEQTQPAVLRGAR 1909

Qy 1922 LLTVRKSGVRTHSLPENDSYMCRHGSTAEGPLGHRGWGLPKAQSGGVLSVHSQPADTSYI 1981
Db 1910 VFLRQKSTSLSN---------------------GGAIQNOESGIKESV-----SWG 1940

Qy 1982 LQLPKDAPHLLQP-------HSAPTWGTIPKLPPGRSPLAQRPLRRQAAIR-------TDS 2029
Db 1941 TQRTQDAPHRARPPLERGHSTEI-------PVGRRSGALAVDVQMQSITRRGPDGEPQPG 1992

Qy 2030 LDVQGLGSREDLLAEVSGP---SPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTTPPAPC 2086
Db 1993 LESQGRAASMPRLAAETQPVTDASPMKRSI-------STLAQRPRGTHLCST--TPDRPP 2043

Qy 2087 PG------------------PEPNWGKGPPETRSSLEIDTELSWISGDLLPPGGQEEPSP 2129
Db 2044 PSQASSHHHHRCHRRRDRKQRSLEKGP----SLSADMDGAFSSAVGPGLPPG--EGPTGC 2098

Qy 2130 RDLKKCYSVEAQSCQRR-PTSWLDEQRRHSIAVSCLDSGS------QPHLGTDPSN-LG 2180
Db 2099 RRERERRQERGRSQERRQPSSSSSEKQRF--YSCDRFGGREPPKPKPSLSSHPTSPTAG 2155

Qy 2181 GQPLGGPGSRPKKKLSPPSITIDPPESQGPRTPPSP------------------GIC 2219
Db 2156 QEP--GPHPQAGSAVGFPNTT--PCCRETPSASPWPLALEALALTLTWGSVWTVRPLSTPC 2211

Qy 2220 LRRRAPSDSKDPLASGPPDSMAASP 2245
Db 2212 LRTRSLSRRLWPPTRAAPPGLPTCPP 2237
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RESULT 5
A45386
omega-conotoxin-sensitive calcium channel alpha-1 subunit rbB-I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45386
R;Dubel, S.J.; Starr, T.V.; Hell, J.; Ahlijanian, M.K.; Enyeart, J.J.; Catterall, W.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5058-5062, 1992
A;Title: Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensitive calc
A;Reference number: A45386; MUID:92279265; PMID:1317580
A;Accession: A45386
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2336 <DUB>
A;Cross-references: UNIPROT:O89089
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:104355)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   14.4%;   Score 1711;   DB 2;   Length 2336;
Best Local Similarity 24.0%;   Pred. No. 3.3e-96;
Matches 644;   Conservative 365;   Mismatches 810;   Indels 860;   Gaps 93;

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Qy  27 GAGGRPGGSAEKDPGSADSEAEGLPYPALAPVVF------------FYLSQDSRP 70
Db  25 GAGGAGGPGQGGLPPGGQRVLYKQSIAQARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV 84

Qy  71 RSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFFD---FIFAF 127
Db  85 RKYAKRITEWPPFEYMILATIIANCIVLAL-----EQHLPDGDKTPMSERLDDTEPYFIGI 140

Qy 128 FAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS--LDLQNVSFSAVRTVR 183
Db 141 FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTEILATAGTDFDLR----TLRAVR 195

Qy 184 VLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIGIVGVQLWAGLLRNRCFL 243
Db 196 VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYMGKFHKACF 254

Qy 244 PENFSLPLSVDLERYYQTENEDRSPFICSQPRENGMRSCRSVPTLRGDGGGPCGLDYE 303
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Db   255  ||||  |                                                   |||  :
          -----PNSTDAE------                    PV------GDFPCGKEAP   273
Qy   304  AYNSSSNTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVTTLEGWVDIMYFV   363
Db   274  ARLCDSDTEC--REYWP------GPNFGITNFDNIFAIITVFQCITMEGWTDILYNT     323

Qy   364  MD-AHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES----QLMREQRVRF    416
Db   324  NDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLNVRRQQQIE-  382

Qy   417  LSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET  476
Db   383  RELNGYLEWIFKAEEVMLAEEDKNA------EEK                            410

Qy   477  QP-SSSCSRHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRIMLP     535
Db   411  SPLDAVLKRAATKKSRNDLIH------AEEGEDR                            438

Qy   536  PPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHT  595
Db   439  ------                                                        438

Qy   596  SPPPEETLKEKALVEVAAASGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCL 655
Db   439  ------FVDLCAAGSPFARASL------KSGKTESS                          462

Qy   656  KADSGACGPDSCPYCARAGAGEVELADREMFDSDSEAVYEFTQDAQHSDLRDPHSRRQRS  715
Db   463  ------SYFRR------KBKMFRF                                      474

Qy   716  LGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL  775
Db   475  ------LIRRMVKAQSFWVVLCVVALNTLCVAMVHYNQPQRLTTAL                515

Qy   776  EISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQ----QGGGL    830
Db   516  YFAAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIVGSIFEVVWAAIKPGTSFGI 575

Qy   831  SVLRTRLRMRVLKLVFLPALQRQLVVLMKTMDNVATFCMLLMLFIFISLIGMHLFGCK    890
Db   576  SVLRALRLRIFKVTKYWNSLRNLVVSLLNSMKSIISLLFLLFFIFIVVFALLGMQLFGGQ  635

Qy   891  FASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM------ASTSSWAALYFI 945
Db   636  FNFQDETPT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFI   691

Qy   946  ALMTFGNYLVLFNLLVAILVEGF-QAEEISK------REDASGQ------LSCI        985
Db   692  VLTLFGNYTLLNVFLAIAVDNLANAQELTKDEEEMEEAANQKLALQKAKEVAEVSPMSAA  751

Qy   986  QLPVDSQGGDANKSESEPDFFSPSLLDGDGDRKKCLALVSLGE------HPELR       1032
Db   752  NISTAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRYASTRHVRPDMK  811

Qy  1033  KSLLPPLIIH------TAATP------                                  1047
Db   812  THMDRPLVVEPGRDGLRGPAGNKSKPEGTEATEGADPPRRHRHRDRDKTSASTPAGGEQ   871

Qy  1048  --MSLPKSTSTGLGEALGPASRRTSSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTS 1105
Db   872  DRTDCPKAESTETGAREERARPRRSHSKEA-PGADTQVRCERSRRHHRRGSPEATEREP   930

Qy  1106  RR------SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESEEERASPAG      1155
Db   931  RRHRAHRHAQDSSKEGKEGTAPVL---VPKGERRARHRGPRTGPRETENSEEPTR       982

Qy  1156  SDHRHRGSLEREAKSSFDLLPDTLQVPGLH------RTASGRGSASEHQ----DCNGKSA 1204
Db   983  --RHR------AKHKVPPTLEPPEREVAEKESNVVEGDKETRNHQKEPRCDLEAIAV    1031

Qy  1205  SGRLARALRP------DDPPLDGDADDEGNLSK------GER                   1235
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Db  1032  TGVGSLHMLPSTCLQKVDEQP--EDADNQRNVTRMGSQPSDPSTTVHVPVTLTGPPGEA  1088
Qy  1236  ------VRAWIRARLPACYLERDSWSAYI-FPPQSRFRLL                     1268
Db  1089  TVVPSANTDLEGQAEGKKEAEAADDVLRRGRPIVP------YSSMFGCLSPTNLLRRF   1140

Qy  1269  CHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVK 1328
Db  1141  CHYIVTMRYFEMVILVVIALSSIALAAEDP-VRTDSFRNNALKYMDYIFTGVFTFEMVIK 1199

Qy  1329  VVALGWCFGEQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLR 1387
Db  1200  MIDLGLLLHPGAYFRDLWNILDFIVVSGALVAFAFSSFMGGSKGKDINTIKSLRVLRVLR 1259

Qy  1388  PLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFYCVCQGE--- 1444
Db  1260  PLKTIKRLPKLKAVFDCVVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGKFFYCTDESKE 1319

Qy  1445  --DTRN--ITNKSDCAEASYR-WVRHKYHYFDNLGQAIMSLFVLASKGDWVDIMYDGLDA 1498
Db  1320  LERDCRGQYLDYEKEEVEAQPRQWKKYDFHYDNVLWALLLTLFTVSTGEGWPMVLKHSVDA 1379

Qy  1499  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEK  1558
Db  1380  TYEEQGPSPGFRMELSIFYVVVIFVVFPFFVNIFVALLIITF------QEQGDKVMSE-   1431

Qy  1559  RLRRLEKKRRKA------QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVT 1609
Db  1432  --CSLEKNERACIDFAISAKPLTRYMPQNKQSFQYKTWTFVVSPPFEVFIMAMIALNTVV  1489

Qy  1610  MAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVARFGFRRFFQDRWNQLDIAIVLLSI 1669
Db  1490  LMMKFYDAPYEYELMLKCLNIVFTSMFSLECILKIIAFGVLNYFRDAWNVFDVTVLGSI   1549

Qy  1670  MGITLBEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLG  1729
Db  1550  TDILVTEIANNF---IN---LSFLRLFRAARLIKLCRQGYTIRILLWTFVQSFKALPYVC  1603

Qy  1730  LLFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGI   1789
Db  1604  LLIAMLFFIYALIGMQVFGNIALDDG--TSINRHNNFRTFLQALMLLFRSATGEAWHEI   1660

Qy  1790  MKDTL--RDCD--QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLM------        1833
Db  1661  MLSCLGNRACDPHANASEC-GSDFAYFYFVSPIFLCSFLMLNLFVAVIMDNFEYLTRDSS  1719

Qy  1834  ----KHLEE------                                              1838
Db  1720  ILGPHHLDEFIRVWAEYDPAACGRISYNDMEFMLKHMSPPLGLGKKCPARVAYKRLVRMN  1779

Qy  1839  ---SNKE------AKEEAELEAELEMKTL--SPQPHSPL                      1868
Db  1780  MPISNEDMTVHFTSTLMALIRTALEIKLAPAGTKQHCDAELRKEISSVWANLPQKTLDL   1839

Qy  1869  GSPFLWPGVEGDSPDSPKPGALHPA------AHARSASH                      1907
Db  1840  LVP------PHKPDEMTVGKVYAALMIFDFYKQNKTTRDQTHQAPGGLSQMGPVSLFH   1891

Qy  1908  PTM------QPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKA 1963
Db  1892  PLKATLEQTQPAVLRGARVFLRQKSAT--SLSNGGAIQTQESGIKESL--SWGTQRT    1944

Qy  1964  QSGGSVLSVHSQPADTSYILQLPKDAPHLLQ--PHSAPTWG------TI           2003
Db  1945  Q--DVLYEARAPLERGHSAEIPVGQGALAVDVQMQNMTLRGPDGEPQPGLESQGRAASM  2002

Qy  2004  PKL----PPPGRSP------LAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGSPP    2051
Db  2003  PRLAAETQPAPNASPMKRSISTLAPRPHGTQ------LCNTVLDRPPP             2044

Qy  2052  LARAYSFWGQSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTE-- 2109
Db  2045  ------SQVSHHHHHCHRRRDK------KQRSLEKGP------SLSVDTEGA         2079
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Qy   537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTS  596
Db   431 ------------------------------------------------------------  430

Qy   597 PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK  656
Db   431 ----------------------------------AEGEDRFVDL----CAVGSPFAR     450

Qy   657 ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL  716
Db   451 ASLKSGKTESSSYFRR----------------------KEKMRFRF                473

Qy   717 GPDAEPSSVLAFWRLICDFFRKIVDSKYFRGRGIMIAILVNTLSMGIEYHQPEELTNALE  776
Db   474 ------FIRRMVKAQSFYWVLCVVALNTLCVAMVHYNQPQRLTTALY               515

Qy   777 ISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQ-----QGGGLS   831
Db   516 FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDPGVIVGSIFEVVWAAIKPGTSFGIS  575

Qy   832 VLRTFRLMRVLKLVRFLPALQRQLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKF   891
Db   576 VLRALRLLRIFKVTKYWNSLRNLVVSLLNSMKSIISLLFLFLFIVFALLGMQLFGGQF    635

Qy   892 ASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM----ASTSSWAALYFIA  946
Db   636 NFQDETPT--TIFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV    691

Qy   947 LMTFGNYVLFNLLVAILVEGF-QAEISK---REDASGQ                       986
Db   692 LTLFGNVTLLNVFLAIAVDNLANAQELTKDEEMEEAANQKLALQAKEVAEVSPMSAAN    751

Qy   987 LPVDSQGGGDANKSESEPPDFFSPSLDGDGDRKKCLAIVSLGE----HPELRK       1033
Db   752 ISIAAQQNSA-KARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRYASTRHVRPDMKT  810

Qy  1034 SLLPPLIIH---------------TAATPMS-LPK---------STSTGLGEALGPASR  1067
Db   811 HMDRPLVVEPGRDGLRGPVGSKSKPEGTEATESADLPRRHRHRDRDKTSATAPAGGEQD   870

Qy  1068 RTSSSGS------AEPGAAHEMKSPPS-----ARSSPHSPWSAASSWTSR----RSSR  1110
Db   871 RTESTETGPREERARPRRSHSKETPGADTQVRCERSRRHHRGSPEATERERPRCHRAHR   930

Qy  1111 NSL-----GRAPSLKRRSPSGERRSLLSGE---GQESQDEEESSEEERASPAGSDHHRG  1162
Db   931 HAQDSSKEGTVPVL--VPKGERRARHRGPRTGPREAENNEEPTRRHRA-----RHK-    979

Qy  1163 SLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPPLD   1220
Db   980 ------VPPTLQPP------EREAAEKESNPVEGD-----KETRNHQPKEPHCDLE    1018

Qy  1221 --------------------------GDDADDEGNLSK--------GE            1234
Db  1019 AIAVTDVGPLHMLPSTCLQKVDEQPEDADNQRNVTRMGSQPSTTVHPVVTLTGPGE    1078

Qy  1235 R------------------------VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLC  1269
Db  1079 TPVVPSGMNLEQAEGKKEAEADDVLRRGPRRPIVPYS------SMFCLSPTNLFRRFC   1131

Qy  1270 HRIITHKMPDHVVLVIFFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKM 1329
Db  1132 HYIVTMRXLEMVLVLVIALSSIALAAEDP-VRIDSFRRNALEYMDYIFFGVFCEMVKM   1190

Qy  1330 VALGWCFGQAYLRSSWNVIDGLLVLLSVIDIILVSMV-SDSGTKILGMIRVLRLLRTLRP 1388
Db  1191 FIVVSGALVAFASGSKGDINIIKSLRVLRVLRP                           1246

Qy  1389 LRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIFGLGVQLFKFFVCQGE----     1444
Db  1247 LKTIKRLPKLPKVFDSVVNSLKNVLNILIVYMLMFIFAVIAVQLFKGKFFYCTDESKEL  1306


Qy  2110 LSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRPTSWLDEQRRHSIAVSCLDSGS-  2168
Db  2080 PSTAAGSGLPHG--EGSTGCRRERKQERGRSQE-RRQPSSSSSEKQRF--YSCDRFGSR  2133

Qy  2169 -----QPHLGTDP----------SNLGGQPL------------GGPGSRPKKKLS     2196
Db  2134 EPPQKPFSLSSHPISPTAALEPGPHPQCSGGSVNGSPLMSTSGASTPGRGGRRQLPQTPLT 2193

Qy  2197 P-PSITIDPPES-------QGPRTPP--SPG-----------ICLRRRAPSDSKDPLASGPP 2238
Db  2194 FRPSITYKTANSSPVHFAEGQGSGLPAFSPGRLSRGLSEHNALIQKEPLS---QPLIASGSR 2250

Qy  2239 ---------DSMAASPKKDVLSL--------SGLSS                         2259
Db  2251 IGSDPYLGQRLDSEASAHNLPEDTITFEERAVATNSGRSS                      2289
```

RESULT 6
S41080
calcium channel alpha-1 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S41080
R;Coppola, T.; Waldmann, R.; Borsotto, M.; Heurteaux, C.; Romey, G.; Mattei, M.G.; Lazdu
FEBS Lett. 338, 1-5, 1994
A;Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Evidence
A;Reference number: S41080; MUID:94139884; PMID:8307146
A;Accession: S41080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2288 <COP>
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

```
Query Match        14.3%;  Score 1706;  DB 2;  Length 2288;
Best Local Similarity  24.5%;  Pred. No. 6.6e-96;
Matches   646;  Conservative 363;  Mismatches 802;  Indels 828;  Gaps 98;

Qy    27 GAGGRPGPGSAEKDPGSADSEAEGLPYALAPVVF----------FYLSQDSRP         70
Db    25 GAGGAGGPGQGGLPPGQRVLYKQSIAQRARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV  84

Qy    71 RSWCLRTVCNPWFERISMLVILLNCVTLGMERPCEDIACDSQRCRILQAFPD---FIFAF 127
Db    85 RKYAKRITEWPPFEYMILATTIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI  140

Qy   128 FAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR 183
Db   141 FCFEAGIKIIALGFVFHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR----TLRAVR  195

Qy   184 VLRPLRAINRVPSMRILVTILLDTLPMLGNVLLCCFFVFFIFGIVGVQLWAGLLRNRCFL 243
Db   196 VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFFAILMFGIIGLEFYMGKFHKACF- 254

Qy   244 PENFSLPLSVDLERYYQTENEDEDSPFICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYE 303
Db   255 ---PNSTDTE-------------------PV-------GDFPCGKDPP             273

Qy   304 AYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWITAIFQVITLEGWVDIMYFV 363
Db   274 ARQCDGDTEC----REYWP--------GPNFGITNFDNILFAILTVFQCITMEGWTDILYNT 323

Qy   364 MD-AHSFYNFYFILLIIVGSFFMINLCLVVIATQFSETKQRES-----QIMREQRVRF  416
Db   324 NDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRRQQQIE- 382

Qy   417 LSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET 476
Db   383 ----------RELNGYLEWIFKAEEVMLAEEDKNA------------------EEK     410

Qy   477 QPSSSCCRSHRRLSVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536
Db   411 SPIDVLKRAATKKKSRNDLIH-----------                              430
```

```
Query Match       14.3%;  Score 1697;  DB 2;  Length 2259;
Best Local Similarity  24.2%;  Pred. No. 2.3e-95;
Matches 619;  Conservative 362;  Mismatches 848;  Indels 730;  Gaps 84;

Qy   28 AGGRPGPGSAEKDPGSADSEAEGLPYPALA------------------PV------      59
         :       :        :::                              ||
Db    8 AAGRPASGEGDSDQG---RNLPGTPVPASGSAAAYKQSKAQRARTMALYNPIPVRQNCFT  64

Qy   60 ---VFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFR--PCEDIACDSQRC 114
            : ::  :: : :  ::   :  :::  ::: ::: ::::: :
Db   65 VNRSLFIFGEDNIVRKYAKKLLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR- 123

Qy  115 RILQAFDDFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN 173
          : :  :: :    :  : ::: :::  :   ::: ::: : :::::  : :: :
Db  124 -LEKTEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGNVMDFIVVLSGILATAGTHFN   181

Qy  174 --VSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQ 231
           : : ::: ::::::  ::  ::: :: :  :  :: ::  :::: : : :::: :
Db  182 THVDLRTIRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLE 241

Qy  232 LWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGD 291
            :  :: ::   :::    ::: :  :
Db  242 FYSGKLHRACFVNNSGVL--------------------EGFDP----PHPCGVQGC     273

Qy  292 GGGGPPCGLDYEAYNSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVI  351
                 :    ::                              ::   ::  ::::: :
Db  274 ------PAG--YE-----CKDW------------------IGPNDGITQFDNILFAVLTVFQCI 306

Qy  352 TLEGWVDIMYFVWDA-HSFYNFYFILLIIVGSFFMINLCLVVIATQPSETKQRESQLMR  410
          ::::  :  :      :::::  ::::::::::::::::: :: ::  :   :: ::
Db  307 TMEGWTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERV---   361

Qy  411 EQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAP 470
          : :::::                        ::::
Db  362 ENRRAFMK----------------------------LRRQQQI                  376

Qy  471 LGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSR  530
                                                            :::  ::::
Db  377 --------------------------------------ERELNGYR               384

Qy  531 RLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVY 590
           :
Db  385 AWI-----------------------------------------------          387

Qy  591 PTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKI 650
                       : : :  :  ::   ::
Db  388 ----------DKAEEVWLAEENKNSGTSALEVLRRAATIKRSRTEAMTRDSSDEHCVDISSV 438

Qy  651 SSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS 710
                : :::: ::                        :::
Db  439 GTPLARASIKSAKVDGASY------------------------FRHKE------       462

Qy  711 RRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEE  770
           :: ::   ::::: : :  :  ::::::  :::::::::::: :::::::   :
Db  463 ------------RLLRISVRHAVKSQVFYWIVLSLVALNTACVAIVHHNQPQW        503

Qy  771 LTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ----- 825
          ::  : ::  :  :::::::: :: ::::::::::: ::::: :: :::::::::
Db  504 LTHLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAIFRPG 563
```

```
Qy 1445 --DTRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAV 1499
            ::    :::: ::   ::   :::::: ::  :  ::  :::: :::: :::   ::
Db 1307 ERDCRGQYLDYEKEVEAQRPQWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDAT  1366

Qy 1500 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKR  1559
          : :  :       ::: : ::::: ::::: :::::::  :          :
Db 1367 YEEQGPSPGFRMELSILIVYVFVVPFFFVNIFVALIIITF------QBQGDKVMSE--   1417

Qy 1560 LRRLEKKRRKA----QCKPY-YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTM  1610
           :  ::          :       :       :            : : :::  ::
Db 1418 -CSLEKNERACIDFAISAKPLTRYMPQNKQSFQYKTWTFVVSPPFEYFIMAMIALNTVVL 1476

Qy 1611 AMEHYQQPQOILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIM 1670
              ::       ::    : ::::  : : :: :    :         ::::: :: :::
Db 1477 MMKFYDAPYEYELMLKCLNIVFTSMFSMECILKIIAFGVLNYFRDAWNVFDFVTVLGSIT  1536

Qy 1671 GITLEEI-EVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLG 1729
              ::    :        ::: ::: :: ::::::: :  :: ::  :
Db 1537 DILVTEIAETN----NFINLSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVC   1591

Qy 1730 LLFMLFFIFAALGVMLFLGDLECEDTHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGI 1789
          ::  :::: :: ::  :                       :  : ::::: :: :: :
Db 1592 LLIAMLFFIYAIIGMQVFGNSALDDD----TSINRHNNFRTFLQAIMLLFRSATGEAWHEI 1648

Qy 1790 MKDTL--RDCD---QESTCYNTVISPIYFVSFVITAQFVLVNVVIAVLMKHLEESNKEAK 1844
          :       :     :::  :   :  ::::::: :: ::  ::::: :::
Db 1649 MLSCLDNRACDPHANASEC-GSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS  1707

Qy 1845 ------EEAELEABLE-----------LEM-KTLSPQPHSPLGSPFLWPGVEGP----   1880
                                         :    ::   : :: :  ::
Db 1708 ILGPHLLDEFIRVWAEYDPAACCGRISYNDMFEMLKHMSP----PLGL----GKKCPARV 1758

Qy 1881 ----------PAAH---------                                      1896
                     :
Db 1759 AYKRLVRMNMPISNEDMTVHFTSTLMALIRTALEIKLAPADEMTVGKVYAALMIFDFYKQ 1818

Qy 1897 --ARSASH------------FSLEHPTM----QPHPTELPGPDLLTVRKSGVSRTHSLPN 1938
              ::                  :          :::  :: ::::: :::   ::
Db 1819 NKTTRDQTHQAPGGLSQMGPVSLFHPLKATLEQTQPAVLRGARVFLRQKSAT--SLSN    1874

Qy 1939 DSYM--CRHGSTAEGPIGHRGW------------GLPKAQSGSVL-SVHSQPADT      1978
                  :  :   :                     : :  ::   :    ::
Db 1875 GGAIQTQESGSRSRCPGGRRGTQDALYEGRAPLERDHSKEIPVGQSGTLLVDVQMQ---- 1930

Qy 1979 SYILQLPKDAPHLLQP--HSAPTWGTIPKL----PPPGRSPLAQRPLRRQAAIRTDSLD  2031
                ::   ::::      :::        ::    :  : :::     ::      :
Db 1931 NMTLRGPDGDP---QPGLESGQRAAASMLRLAAETQPAPNASPMKR---------S     1973

Qy 2032 VQGLGSRED----LLAEVSGPSPPLARAYSFWGQSSTOAQQHSRSHSKISKHMTPPAPCPG 2088
               ::       :                  :: :  ::  : ::
Db 1974 ISTLAPRPDGTQLCSTVLDRPPP--------SQASHHHHHRCHRRRDK--            2013

Qy 2089 PEPNWGKGPPETRSSLELDTELSWISGDLLP--PGGQEEPPSPRDLKKCYSVEAQSCQRR 2146
                 ::   ::     : :    :  ::      :  ::  ::  :         :  ::
Db 2014 KQRSLEKGP-----SLSVDPEGAPSTAAAGPGLPHGEGSTACRRDRKQ--ERGRSQERR   2065

Qy 2147 -PTSWLDEQRRHSIAVSC--LDSGS--QPHLGTDPS----------NLGGGQPL       2184
            :::      :        ::::    ::    ::          ::::  ::
Db 2066 QPSSSSEKQRF--YSCDRLGAGSPQLMPSLSSHPTSPAAALEPAPHPQGSGSVNGSPL   2122

Qy 2185 -------GGPGSRPKKKLSP-PSITIDPPES----QGPRTPP--SPG------        2217
               :: ::::  :    ::  :    :::     : : ::   ::
Db 2123 MSTSGAITPGRGGRRQLPQTPLTPRPSITYKTANGSPVHFAEGQSGLPAFSPGRLSRGLS 2182

Qy 2218 --ICLRRRAPSSD-------SKDPLASGPPDSMAASPSPKKDVLSL----SGLSS      2259
               : ::  ::        :::  :::    :::   ::  ::::       ::::
Db 2183 EHNALLQKEPLSQPLAPGSRIGSDPYLGQRLDSEASAHTLPEDTLFEEAVATNSGRSS   2241
```

RESULT 7
S29236
calcium channel protein BII-1, brain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)

```
Qy   826 QGGGLSVLRTFRLMRVLKLVRFLPALQRQLVLMKTDNVATFCMLLMLFIFIFSILGMH 885
          :||||| :|| :| .:| ||.|:  :: : :||| |:::  : ||.|||:|| ||.
Db   564 TSPGISVLRALRLLRIFKITKWASLRNLVVSLMSSMKSIISLLFLLFLFIVVFALLGMQ 623

Qy   886 LFGCKFASERDGDTLPDRKNFDSLLWAITVFQILTQEDWNKVLYNGM----ASTSSWA 940
          ||| :|.  ||  ||| :.| : ||  :|:|||||| |||| : |||    .:| ||
Db   624 LFGGRF-NFNDG--TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWS 679

Qy   941 ALYFIALMTFGNVLFNLLVAILVEGF-QAEEISK----REDASGQLSCIQLPVDSQGGD 995
          |:||| |:||||  .:||:|| :  : ||||.    ||:| :| :  ::
Db   680 AVYFIVLLTFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEAFNQKHALQKAKEV---- 735

Qy   996 ANKSESEPDFFSPSLDGDGRKKCLAL---------------------------VSL 1025
          .: :| : . :. :
Db   736 --SPMSAPNV--PSIERDRRRHHMSWMEPRSSHLRERRRRHHMSVWEQRTSQLRRHMQM 791

Qy  1026 GEHPELRKSLLPPLLIHTAATPMS--------------LPKSTSTCLGEALGPASRRTSSS 1072
          . : : . .: .: :   ||.
Db   792 SSQEALNKEEAPPMNPLNPLNPLSPLNPLNAHPSLYRRPRPME-GLALGLEKCEEEHVSR 850

Qy  1073 GSAEPGAAHEMKSPPS-ARSSPHSPWSA-------------ASSWT---------SRRS 1108
          | :     . .:| :|.   : .  |.|               ::|.         :||
Db   851 GGSLKGALDCQRSPLSLGRREP--PWLARPCHGNCEPALQETAGGETVVTFEDRARHRQS 908

Qy  1109 SRNSLGRAPSLKRRSPGERRSLLSGEGQESQDEEESSEEERASPAGSDHRHRGS----- 1163
          .|.| .| : :::|| ||||. |  | .|| |:|.| |||| :   :.| .
Db   909 QRRSRHRRVRTEAKRSSSASRS-RSVSQERSLDEGASTEGER------DHEARGSHGGKE 961

Qy  1164 --LEREAKSSFDLPDTLQVP--------GLHRTAS--------GRGSASEHQDCNGKS 1203
           | ::  .|| :. ||.               :|          |||
Db   962 PTIHEEERAQDLRRTDSIMVPKGSGLAGGLDEAGTPLVLSSPEGVGKEAAPTEQHADGSG 1021

Qy  1204 ASGRL-------ARALR---------------------------PDDPPL 1219
          | .             |:                             ||
Db  1022 EPALLGHGVQLDVGRAISQSEPDLSCVTATTDKVTTESTDVTVAIPDAEPLVDSTVVHIGN 1081

Qy  1220 --DGD-------DADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRL 1267
             |.       :| .| : | : :    : ::          :|     ::.|.|||
Db  1082 KTDGEASPFGQEAEMKEAEQETEKQKKKERPASGKAMVPHS-------SMFIFSTSNPIRR 1134

Qy  1268 LCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTV 1327
          .||.::  :. :.:| :.|| || || |.|.: || : ||:.::||.|||.||:||:|:
Db  1135 ACHYVVNLRYFEMCILLVIAASSIALAAEEDPVLTNSERNRV-LRYFDYVTFGVFTFEMVI 1193

Qy  1328 KVVALGWCFGEQAYLRSSWNVLDGLLVLLSVDI-LVSMVSDSGTKILGMLRVLRLLRTL 1386
          | :  |  ||:.||:| |.||||.|:|::||:  ||::|:|:| ||: ||||||:||.|
Db  1194 KMIDQGLILQDGSYFRDLWNILDFVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVL 1253

Qy  1387 RPLRVLSRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC--QGE 1444
          ||||.: |.: |||.| .::.||| :||:::: ||||:||||||||||||||| |  .
Db  1254 RPLKTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSK 1313

Qy  1445 DTRN-----ITNKSDCAEASYR--WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLD 1497
          ||:.     || :. |.: ::|   .|:::|:|| ::| ::||.:|: :|||  ::  .|
Db  1314 DTEKRCIGNYDVHEKNKMEVKGREWKRHEFHYDNIIWALLLTFTVSTGEGWPQVLQHSVD 1373

Qy  1498 AVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREE 1557
          .. :| .|  ::.| ||.::|:|:::|||||||:|||||::|||.||:||:: :.
Db  1374 VTEEDRGPSRSNRMEMSIFYVVYFVVFPFFFVNIFVALIIITF--------QEOGDKMMEE 1426

Qy  1558 KRLRRLEKKRRKA------QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTGVIGLNVV 1608
          ||| |  |::.        ||     : |.    || |.| | :.| |::: |:| ||.|
Db  1427 ---CSILEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTV 1483

Qy  1609 TMAMEHYQQPQILDEALKICNVIFTVIFLESVFKLVAFGFRFFQDRWNQLDLAIVLLS 1668
          . :: :| .| :|:|||||:|:||::||.|| :|::||||.:: ||||::||.||::|
Db  1484 VLMMKYYSAPCTYELALKYLNIAFTMVFSLECVLKVIAFGFVNYFRDTWNIFDFITVIGS 1543

Qy  1669 IMGITLEIEVNASLPINPTIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNL 1728
          |  : ||| :|:  ||| |:|| :|||:|.|||:||:..|:|| : .: ::| || ||
Db  1544 ITEIVLTDSKLVNTTGFNMSFLKLFRA--ARLIKLLRQGYTIRILLWTFVQSFKALPYV 1600
```

```
Qy  1729 GLLFMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLLFRVSTGDNWN 1787
          .|| .:||:|:|.:| ||||:   | || |||||.:  .|||| :|.|||||||| ||
Db  1601 CLLIAMLFFIYAIIGMQVFGNIRLDEESH---INRHNNPRSFFGSLMLLFRSATGEAWQ 1656

Qy  1788 GIMKDTL--RDCD-------QESTCYNTVISPIYFVSFVPLTAQFVLVNVIAVLMKHL 1836
          .||  .|  | ||       |||.||:|:||||:|.||:    ||.|.:::|.||::
Db  1657 EIMLSCLGEKGCEPDTTAPSGQQESERCGTDLAYVFVSFIFFCSFLMNLFVAVIMDNF 1716

Qy  1837 EESNKEAK---------EEAELEAELE----------LEMKTLSPQHPSPLGSPFLWPG 1876
          |.|.: ||         :|| :  .::          ||:.:..  .. |:
Db  1717 EYLTRDSSIIGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTLM-------SPPIGLG 1768

Qy  1877 VEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELRGPDLLTVRKSGVSRTHSL 1936
          .. |:||:|||.|.|  ||: ||::||:|||.| ||| .|| :.. ::   . : ::|
Db  1769 KRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD----IKIAKGGADRQQL- 1821

Qy  1937 PNDSYMCRHGSTAEGPLGHRGWGL---PKAQSGSVLSVHSQPADTSYI---------- 1981
           : .       ||.| ||.  .|:   |||.||:|||||||.|::|:
Db  1822 -DSELQKETLIAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMMIMDYYKQSKVKKQRRQ 1879

Qy  1982 LQLPKDAP--HLLQPHSAP-------------TWGTIPKLPP----PGRSPLAQRPLRRQ 2022
          |:.|..||  ::| | ..|             ||| |||:||    ||||| |:||||||
Db  1880 LEEQKNAPMFQRMEPSSLPQEIIANAKALPCLPQGPPAGLGGRSGCPAMSPLSPQIFQLT 1939

Qy  2023 AAIRTD-----------SLDVQGLGSREDLLAEVSGPSPPLARAYSFW-----GQSSTQ 2065
          .||.||           ||||.|| ||. :: .| |::|:|||.:|      ||:|:
Db  1940 CMDPADDDGQFQEQRSLVVTDPGSMRRSFSTIRD-----KRSSSSWLEEFSMERSSDNTY 1994

Qy  2066 AQQHSRSHS--KISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQ 2123
          .:: |||||  ||| : .           .       .|||.|:|: |||| ||||.
Db  1995 KSRRRSYHSSLRLSAHRL----------------NSDSGHKSDTHRS----------GGR 2028

Qy  2124 EEPPSPR----------DLKKCYSVEA--------QSCQRRPTSWLDEQRRHSIAVSCLDSGSQP 2170
          |..||.           ||::|.|.||        ||| |||.|:. ||||||  |.   ||.
Db  2029 ERGRSKEREHLLSADVSRCSSERGAQADWDSPERHPSRSPSEGRSQS------------- 2076

Qy  2171 HLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPES--QGPRTPPSPGICLRRRAPSSD 2228
          :.||.| .|||.|||||| ||::.| | |:.:||| |  || .  ||| ||:|||.
Db  2077 -----PSR-----QGTGSLSESSIPSVSDTSTPRHSRRQLPPVPPKPRPLL--SYSSL 2122

Qy  2229 SKDPLASGPP---------DSMAASPSPKKDVLSLSGLSSDP 2261
          ||.|:.|||||        |||.||||||||||||||||||
Db  2123 KQQPSNFSPPADGSQGGSLLASPALESAQVGLPESSDSP 2161
```

RESULT 8

T31092
probable voltage-gated sodium channel - Aiptasia pallida
C;Species: Aiptasia pallida
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T31092
R;White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.
submitted to the EMBL Data Library, January 1998
A;Description: Structure of a putative sodium channel from the sea anemone Aiptasia pal
A;Reference number: Z20975
A;Accession: T31092
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1810 <WHI>
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AAE
C;Genetics:
A;Gene: Na1
C;Superfamily: sodium channel protein

Query Match   14.2%;   Score 1689; DB 2; Length 1810;
Best Local Similarity 25.8%; Pred. No. 5.3e-95;
Matches 520; Conservative 343; Mismatches 721; Indels 428; Gaps 65;

```
Qy    78 VCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIP-AFFAVEMVKM 136
          : | :||.: ::::||: : |   |        .::|   |:.: .:| | ||.:.:|
Db   110 ITNQFFEFFILLTIIVNCIFLAL-----------RDAPEQPEYVFAAIYTFEMLLKI 155

Qy   137 VALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVP 195
```

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Db   156  ::|:|  ||||  ||||||  :||| |: | ||| |: : | |||||| ||                        : : |
          IAKGLVMHEYAYLRDFPWNWLDFVVVLGYVTLVPNVANL--SGIRIFRVLRALRTISAVE 213

Qy   196  SMRILVTLLLDTLPMLGNVLLCFFVFFIGVGVQLWAGLLRNRCFLPENFSLPLSVDL 255
          :::||  :  | ||| ||  :||::: ||  | |  :  : |:|  || ||||:
Db   214  GLKTMVNALLKSMKMLSDVLLLTTFFLCVFALVGMQLFVGSLRNKCVLKPPLNTTIDYDS 273

Qy   256  ----ERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNT 311
              :::||  |  :|| : :| || |   :| |   : ||| |: |:
Db   274  FVTNESHWYHHPDTDTPITC--------------GNSTSAGPCPLNY----------- 306

Qy   312  TCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFPVITLEGWGDIMYFVMDAHSFYN 371
          ::| ::|::  |: |  | |     : |||    |  |:||:|||::|:|:|: |::|
Db   307  TCL---ANIG-NNPNYGYTNLDNFGWAVITAFQLVTLDYWENVYNYVLSSMGSWY 357

Qy   372  FIYFILLIIVGSFFMINLCLVVIATQPSETKQRESQLMREQVRFLSNASTLIAS-FSEPG 430
          ||:|  ||:|:|| :  | | |   ::  |      : :| ||  | |:|||: |
Db   358  IFYFFMVIFFGSFYLLNLVLAVVAVSY-----QQEVLALQDRENYYNNLKGVASLYSFHG 412

Qy   431  SCYEELLKYLVVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLS 490
          || || | : ||:|::|  ||         : |                        ::
Db   413  CVPKLLRN---SKSKTKSLASKCK------MSFCVCPFSIGKQPE----------- 449

Qy   491  VHHLVHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGA 550
          |||:|::||::       :  |       :   :                   ::
Db   450  -HSNGHASDNESSHASTG-GTIRVDSTAIEMK------MLNDKNEVRTNG----- 491

Qy   551  ESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPETIK--EKALV 608
          |:|: |       |  |    |  |  || :: |  :   :  |   | ::  : |:|
Db   492  ---HSL--------PEPKTSSFFSVSSDNSIHIRMNSSTEVMPQISKFDDNILT 534

Qy   609  EVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCP 668
          || ::||||:|:||:||||  |:|: |:||: |  |:  | ||  |  |:| :|  :|
Db   535  K---------TLDVKSSFLRKLSAISEQSSTDGVDNNENINN-------TQPQKSVS 575

Qy   669  YCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL- 726
          | ||| :   ||   | | |    :   |: | |                   |   |
Db   576  FIARVLTPRGSLA------------------------RQTSGATHHKTITKQ 605

Qy   727  -AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSL 785
           | |||| ||||||||| ||:|  |  ||:|| |||  || ||    |  ||::: |:|
Db   606  DTKWNRIRRMISKIVLHGYMDTFITFCTMVNTLFLSLEYHNMDSNYLMVLEIGNKVFTMV 665

Qy   786  FALEMLKLLIVYGPFGYIKNPYNIFDGVIVVISVWE------IVGQQGGGLSVLRTFRLMR 840
          |  |:|| |::|: | |:|    ||  : |: | | :   :    |   |  |:|  |  :
Db   666  FLLEMLLKITAFGFKGYIKSRWNIFDGFIVISMVDLMVELLVDDHDSGLSVLRTFRLLR 725

Qy   841  VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
          ||:|:||| :|:|  |::: :: | ||| ||:| || | |::|||:||  |||:|| |
Db   726  VFKLAQSWQTMNMLLSTIARSVGQLGNLTIVLGIVIYMLAVVGVQLFDQYYTKNFNGDV 785

Qy   901  PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
          | |:||| || | |||||:|||:||:::  | |   |  | |:|:|: ||:|| |||:
Db   786  P-RWNFTDFWHSFMMIFRVLCGE-WIEPLYDCMRASTSWATLFLTTLVIGNFLVLNLFL 843

Qy   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
          :::  |  ::|:|:     |::
Db   844  ALLLNAFARESLEQ------------------------EAKKKTKKPSKFAQGVSKLSRALRFR 883

Qy   1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGAEPGAA 1080
               | :  |     |: | :
Db   884  STVS--------KTTQVLPTIRVHD-----------------GE------NATDGKAPTVQ 914

Qy   1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGE-----RRSLLSG 1134
          :  :::  |   |:|    | |   |: || :|  |     | |
Db   915  NGLLESKTSD-------SAIS--TSSNASNAMISAVTAFQQGNKGKLNRDTFRRLSLAI 964

Qy   1135 EGQESQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSAS 1194
          |
Db   965  E------------TANSDSNTSNVLAMAASST----------SIT 987

Qy   1195 EHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSW 1254
               ||       :  ::    ||  |   :
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Db   988  GRQD-HGTS--------DPPDPP----------MTEVDECCPWCMNKMTCGCITR--W 1024

Qy   1255 SAYI-FPFQSRFRLLCHLCHRIITHKMFDHVVLVIFPLNCITIAME------RPKIDPHSAER 1307
          ||:  ||:|||| ||::| ||:||||::||:||| :||:|  :|      |||:| || :
Db   1025 KASDGYRSWRNLRLAVKKFVEHKYFEWTILAIIMASSIALFEDINLPSRPKL------K 1078

Qy   1308 IFLTLSNYIFTAVFLAEMTVKVKVALGWCFGEQAYLRSSKNVLDGLLVLLSVIDIIVSMVS 1367
          |:| |||:|:|||:: || ::: || || |: |  :| | ||| |||:||:: ||::|||
Db   1079 EYLQYLNIFFAVTFSIEFLLKVIGLGL----GVVSYFRNCWNCLDVLIVFVPV----SSVIA 1130

Qy   1368 DSGTK- IlGMLRVLRLLRTLRPLRVISRAQGLKIVVETLMSSLKPIGNIVVICCAFFI 1425
          |::|  |::::|||:|||||||| | || |||::|::::|:| ||:||:||::| ||:
Db   1131 DSSNQDSSLSSLRSLRTLRALRPLRAISRWEGMRVVVNSLLFAIPGIGNVLLVCMVFWLI 1190

Qy   1426 FGIlGVQLFKGKFFVCQGEDTRN----ITNKSDCABASYRWVRHKYNFDNLGQALMSLF 1480
          |:| || |||::|| |   : |    | |:|| | :|:|  ||    ::||||:|||:|
Db   1191 FSIMGVQFFGGRFFKCVDNNKERLPISIVQNRSECIQKGYRWVNSDINFDNSLNGFMALF 1250

Qy   1481 VLASKDGWVDIMYDGLDAVGVDQQPIMNHPWMLLYFISFLLIVAFFVLNMFVGVVVENF 1540
          :|| :| | |:|::    :| |  ||||   |:|||: | |::  ||  :  |  :|:|
Db   1251 QVATFEGWIEVMRDAVDAREVDQQPSDGYNFSAYAYFVVFIIVGSFFTLNLFIGVIIDNF 1310

Qy   1541 HKCRQHQEE-----------EEARRREEKRLRR-LEKKRRKAQCKPYYSDYSRFRLLVHHLCT 1591
           |:| ::           :|||:||::|  |  ||:||:||   : : :|| | ||::| |
Db   1311 NRLKKQYEDFGALDVLLTPSQRAWFGTIRKAATKKPKKVISRPENS------FMAWLFDVIH 1366

Qy   1592 SHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFVFVLESVFKLVAFGFRR 1651
          :  :: | | |:  |  | : |:| :| ||:| |:| |||| : ||:||::|| ||::
Db   1367 SSRFETLIMFFICLNLVMIQHYGQKPAVEQALMINLVFTGLFTLEAILRIVLRL-H 1425

Qy   1652 FFQDRWNQLDLAIVILLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGM 1711
          : :|| :| | :|:|| ::: |:  :: :      : ||::|:::  |:|:|::|: ||:
Db   1426 YFREPWNVFDFVVVLSILGIIGIILEHLEYELFITPSPF---VARVFRIGRLLRFYKGAKGI 1482

Qy   1712 RALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFG 1771
          | ||   || ::   || | |::| |: | || :|  ::   | :     :
Db   1483 RRLLFALIISLPLALLNIGALLFLIMFYAIIGMSSFGYVK-----KTGALDSVVNFETFG 1537

Qy   1772 MAFLTLFRVSTGDNWNGIMKDTL--RDCDQE------STCYNTVISPIYFVSFVLTAQF 1822
          ::|:| |||| ||||:::|::|   |||:::    : | ||:  | |    :: |::|
Db   1538 NSMLLLFRLSTSAGWNDVLKPLLLIKPPDCDKKLWCIPNGNCSTPWLAVVYFTTFILFTFL 1597

Qy   1823 VLVNVVIAVLMKHLEESNKEAKEEAEALELEMKTLSPQHSPLGSPFLWPGVEGPDS 1882
          :  :|  ||:|:   | :   :|| |  |      :: |  |   ::
Db   1598 IINMYIAILLENLSQAH-EQEEVGVTDDLDMFY--------YHWERFD---- 1638

Qy   1883 PDSPKPGALHPAAHARSASHF--SLEHPTMOPHPTELPGPDLLTVRKSGVSRTHSLPNDS 1940
          |: | |   ::    |: :   : |:|   | |:| || ::: : : :|::
Db   1639 ----PGATQYIPHS-ALSDFVDGLDHPLRIPQPNKFACINLNIPIKQG-DRVHCFDVMQ 1691

Qy   1941 YMCRH--GSTAEGPLGHRGWGLPKAQSGGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAP 1998
          | || | || ||| | :|     :  ::::
Db   1692 ALVRRVLGDIEEDGLG----------------SSSV-----------AYTLMKSKMEQHCI----- 1725

Qy   1999 TWGTIPKLPPPGRSPLAQPRLRRQAAIRTDSL 2030
           : |:    |    |       :|| :| |
Db   1726 ----STFPK---RHRTKTBSTLKRTQEVRAATI 1752
```

RESULT 9

S29237

calcium channel protein BII-2, brain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29237
R;Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.
FEBS Lett. 308, 7-13, 1992
A;Title: Molecular cloning and characterization of a novel calcium channel from rabbit b₁
A;Reference number: S29236; MUID:92354772; PMID:1379552
A;Accession: S29237
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2178 <NII>

A;Cross-references: UNIPROT:Q02343; EMBL:X67856; NID:g1474; PIDN:CAA48041.1; PID:g1475
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

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Query Match             14.1%;    Score 1681; DB 2;   Length 2178;
Best Local Similarity   23.9%;    Pred. No. 2.1e-94;
Matches  605;  Conservative  366;  Mismatches  811;  Indels  752;  Gaps  83;

Qy    28 AGGRPGPGSAEKDPGSADSEAEGLPYPALA------------------------PV------   59
Db     8 AAGRPASGEGDSDQG---RNLPGTPVPASGSAAAYKQSKAQRARTMALYNPIPVRQNCFT    64

Qy    60 --VFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFR--PCEDIACDSQRC   114
Db    65 VNRSLFIFGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR-   123

Qy   115 RIILQAFDFDIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVLAGMLEYSLDLQN   173
Db   124 -LEKTEYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFN    181

Qy   174 --VSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQ    231
Db   182 THVDLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLE   241

Qy   232 LWAGLLRRNCFLPENFSLPLSVDLRERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGD   291
Db   242 FYSGKLHRACFVNNSGVL------EGFDP----FHPCGVQGC-                  273

Qy   292 GGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVI   351
Db   274 -PAG--YE----CKDW----------IGPNDGITTQFDNILFAVLTVFQCI          306

Qy   352 TLEGWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMR   410
Db   307 TMEGWTTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVLGVLSGEFAKERERV------   361

Qy   411 EQRVRFLSNASTLASFSEPGSCYEPLLKYIVYIIRKAARRLAQVSRAAGVRVGLLSSPAP   470
Db   362 ENRRAFMK------------------------LRRQQQI                      376

Qy   471 LGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSR   530
Db   377 -------------------ERELNGYR                                  384

Qy   531 RLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVY   590
Db   385 ------------------AWI                                        387

Qy   591 PTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKI   650
Db   388 ----------DKAEEVMLAAENKNSGTSALEVLRRATIKRSRTEAMTRDSSDEHCVDISSV  438

Qy   651 SSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS   710
Db   439 ------------------------FRHKE-                               462

Qy   711 RRQRSLGPDAEPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEE   770
Db   463 -----------RLLRISVRHAVKSQVFYWIVLSLVALNTACVAIVHHNQPQW          503

Qy   771 LTNALEISNIVFTSLFALEMLLKLLVYGPFGVIKNPYNIFDGVIVISVWEIVGQ------  825
Db   504 LTHLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAIFRPG  563

Qy   826 QGGGLSVLRTPRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMH  885
Db   564 TSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFLFIVFALLGMQ   623

Qy   886 LFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGM--ASTSSWA     940
Db   624 LFGGRF-NFNDG--TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWS  679

Qy   941 ALYFIALMTFGNYVLFNLLIVAIIVEGF-QAEEISK----REDASGQLSCIQLPVDSQGGD  995
Db   680 AVYFIVLTLFGNYILNVFLAIAVDNLANAQELTKDEQEEEAFNQKHALQKAKEV---     735

Qy   996 ANKSESEPDFFSPSLDGDGRKKCLAL-------------                     1025
Db   736 --SPMSAPNV--PSIERDRRRRHHMSWEPRSSHLRERRRHHMSVWEQRTSQLRRHMQM    791

Qy  1026 GEHPELRKSLLPLLIHTAATPMS---------------                      1072
Db   792 SSQEALNKEEAPPMNPLNPLNPLSLPNPLNAHPSLYRRPRPME-GLALGLEKCEEEHVSR  850

Qy  1073 GSAEPGAAHEMKSPPS-ARSSPHSPWSA----------                      1108
Db   851 GGSLKGALDCQRSPLSLGRREP--PWLARPCHGNCEPALQETAGGETVVTPEDRARHRQS  908

Qy  1109 SRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEERASPAGSDHRHRGS-----  1163
Db   909 QRRSRHRRVRTEAKESSSASRS-RSVSQERSLDEGASTEGER--------DHEARGSHGGKE 961

Qy  1164 ---LEREAKSSFDLPDTLQVP---------GLHRTAS-------GRGSASEHQDCNGKS   1203
Db   962 PTIHEEERAQDLRRTDSLMVPKGSGLAGLDEAGTPLVLSSPEGVGKEAAPTEQHADGSG  1021

Qy  1204 ASGRL----------ARALR-------PDDPPL-------                    1219
Db  1022 EPALLGHVQLDVGRAISQSEPDLSCVTATTDKVTTESTDVTVAIFDAEPLVDSTVVHIGN 1081

Qy  1220 --DGD-------------DADDEGNLSKGERVAWIRARLPACYLERDSWSAYIFPPQSRFRL 1267
Db  1082 KTDGEASPFQEAEMKEAEQETEKQKKKERPASGKAMVPHS--------SMFIFSTSNPIRR 1134

Qy  1268 LCHRIITHKMPFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTV 1327
Db  1135 ACHYVVNLRYFEMCILLVIAASSIALAAEDPVLTNSERNRV-LRYFDYVFTGVFTFEMVI  1193

Qy  1328 KVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTL  1386
Db  1194 KMIDQGLILQDGSYFRDLWNILDFVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVL   1253

Qy  1387 RPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGGILGVQLFKGKFFVC--QGE 1444
Db  1254 RPLKTKRLPLKLKAVFDCVVTSLKNVFNILIVYKLMFIFAVIAVQLFKGKFFYCTDSSK  1313

Qy  1445 DTRN-------------ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYGLD 1497
Db  1314 DTEKEICGNYVDHEKNKMEVKGREWKRHEFHYDNIIWALLLFTVSTGEGWPQVLQHSVD  1373

Qy  1498 AVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREE   1557
Db  1374 VTEEDRGPSRSNRMEMSIFYVVYFVVFPFFFVNIFVALIIITF-----QEQGDKMMEE   1426

Qy  1558 KRLRRLEKKRKA------QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVV   1608
Db  1427 ---CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTV  1483

Qy  1609 TMAMEHYQQPQIIDEALKICNVIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLS  1668
Db  1484 VLMMKYYSAPCTYELALKYLNIAFTMWFSLECVLKVIAFGFVNYFRDTWNIFDFITVIGS  1543

Qy  1669 IMGITLEEIEVNASLPINPTIIRMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNL   1728
Db  1544 ITEIVLTDSKLVNTTGFNMSFLKLFRA--ARLIKLLRQGYTIRILLWTFVQSFKALPYV   1600

Qy  1729 GLLFMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWN  1787
Db  1601 CLLIAMLFFIYAIIGMQVFGNIRLDEESH------INRHNNFRSFFGSLMLLFRSATGEAWQ 1656

Qy  1788 GIMKDTL-------RDCD--------QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMCHL 1836
Db  1657 EIMLSCLGEKGCEPDTAPSGQGGEESERCGTDLAYVYFVSFIFFCSFLMNLFVAVIMDNF  1716

Qy  1837 EESNKEAK-----------EEAELEABLE-------                         1876
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Db  1717 EYLTRDSSILGPHHLDEFVRVWAAEYDRAACGRIIHYTEMVEMLTIM------SPPLGLG 1768
Qy  1877 VEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLIVRKSGVSRTHSL 1936
Db  1769 KRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD----IKIAKGGADRQQL- 1821
Qy  1937 PNDSYMCRHGSTAEGPLGHRGWGL----PKAQSGSVLSVHSQPADTSYI----------- 1981
Db  1822 --DSELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMMIMDYYKQSKVKKQQRRQ 1879
Qy  1982 LQLPKDAP--HLLQPHSAP------TWGTIPKLP--PGGRSPLAQRPLRRQAAIRTDSLDV 2032
Db  1880 LEEQKNAPMFQRMEPSSLPQEIIANAKALPCLPQGPPA---------------------- 1917
Qy  2033 QGLGSREDLLAEVSGPSPPLARAYSFWGQSSTGAQQHSRSHSKISKHMTPPAP------C 2086
Db  1918 -GLGGGRSGCPA-----------------------------------MSPLSPQIFQLTC 1940
Qy  2087 PGPEPNWGKGPGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRR 2146
Db  1941 MDPADDDGQF--QEQRSLVVTD-----------------------PGSMRRSFSTIRD-KRS 1976
Qy  2147 PTSWLDE----------------QRHSIAVSC----------LDSGSQPHLGTDPSNLGGQPLGG 2186
Db  1977 SSSWLEEFSMERSSDNTYKSRRRSYHSSLRLSAHRLNSDSGH-----SDTHRSGGRRRG- 2031
Qy  2187 PGSRPKKKLSPSITIDPPESQ-----------PRTPPSPGICLRRRAPSSDSKDPLAS 2235
Db  2032 -RSKEREHLLSADVSRCSSEERGAQADWDSPERHPSRSPSEG---RSQSPSRQGTGSLSE 2087
Qy  2236 GPPDSMAASPSPKK 2249
Db  2088 SSIPSVSDTSTPRQ 2101
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Qy   234 AGLLRNRCFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGG 293
Db   245 SGKLHRACFMNNSGIL----------------------------EGFDP-----PHPCGVQGC 274
Qy   294 GGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITL 353
Db   275 ---PAG--YE------CKDW--------------IGPNDGITQFDNILFAVLTVFQCITM 309
Qy   354 EGWVDIMYFVMDA-HSFYNFIYFLILLIVGSSFMINLCLVVIATQFSETKQRESQLMREQ 412
Db   310 EGWTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKRERV-----EN 364
Qy   413 RVRFLSNASTLASFSEPGSCYEELLKLYVYILRKAARRLAQVSRAAGVRVGLLSSPAPLG 472
Db   365 RRAFMK-----------------------------------------------LRRQQQI 377
Qy   473 GQETQPSSSCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRL 532
Db   378 ----------------------------------------------------ERELNGYRAW 387
Qy   533 MLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPT 592
Db   388 I---------------------------------------------------------- 388
Qy   593 VHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISS 652
Db   389 ----------------DKAEEVMLAEENKNSGTSALEVLRRATIKRSTEAMTRDSSDEHCVDISSVGT 441
Qy   653 PCLKADSGACGPDSCPYCARAGAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRR 712
Db   442 PLARASIKSTKVDGASY------------------------------------FRHKE 463
Qy   713 QRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELT 772
Db   464 ----------------RLLRISIRHMVKSQVFYWIVILSVVALNTACVAIVHHNQPQWLT 506
Qy   773 NALEISNIVFTSLFALEMLLKLLLVGPGYIKNPYNIFDGVIVVISVWEIVGQ-----QG 827
Db   507 HLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVWAIFRPGTS 566
Qy   828 GGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFISILGMLF 887
Db   567 FGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFIVVFALLGMQLF 626
Qy   888 GCKFASBRDGDTLPDRKQNFDSLLWAIVTVFQILTQEDWNKVLYNGM----ASTSWAAL 942
Db   627 GGRF-NFNDG--TPSANFDTFPPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWSAI 682
Qy   943 YFIALMTFGNVLFNLLVAILVEGF-QAEEISK-------REDASGQLSCIQLPVDSQGGDAN 997
Db   683 YFIVLTLFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEAFNQKHALQKAKEV------ 736
Qy   998 KSESEPDFFSPSLDGDCDRKKCLAL--------------------------VSLGE 1027
Db   737 SPMSAPNM--PSIERDRRRRHHMSMWEPRSSHLRERRRRHHMSVWEQRTSQLRRHMQMSS 794
Qy  1028 HPELRKSLLPPLIIHTAATPMS--LPKSTSTGL-------GEALGPA----SRRTSSS 1072
Db   795 QEALNKEEAPMNPLNPLSPLNAHPSLYRRPRPIEGLALGLGLEKCEEERISRG 854
Qy  1073 GSAE------PGAAHEMKSPPS-ARSSPHSPWSAASSWTS----------------- 1105
Db   855 GSLKGDIGGLTSALDNQRSPLSLGKREP--PWLPRSCHGNCDPIQQEAGGGETVVTFEDR 912
Qy  1106 --RRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQOSQDEESSEEERASPAGSDHRHRG 1162
Db   913 ARHRQSQRRSRHRRVRTEGKDSASASRS-RSASQERSLDEGVSVEGEKEHEPHSSHRSKE 971
Qy  1163 SLERFAKSSFDL--PDTLQVP---GL------------HRTASGRGSASEHQDCNGK 1202
Db   972 PTIHEERTQDLRRTNSLMVPRGSLVGALDEAETPLVQPQPELEVGKDAALTEQEAEGS 1031
Qy  1203 SAS--------------------GRLARALRPD---------------------DPPLD 1220
```

RESULT 10
C54972
voltage-dependent calcium channel alpha 1E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: C54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: C54972
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2272 <WIL>
A;Cross-references: UNIPROT:Q61290; GB:L29346; NID:g522330; PIDN:AA59206.1; PID:g522331
A;Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

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Query Match       14.1%;   Score 1681;  DB 2;   Length 2272;
Best Local Similarity   23.7%;   Pred. No. 2.2e-94;
Matches  607;  Conservative  375;  Mismatches  844;  Indels  740;  Gaps  82;

Qy   30 GRPGPGSAEKDPGGSADSEAEGLPYPALAPVV---------------------------- 60
Db   11 GRPGSGGDGDSD--QSRNRQGTPVPASGPAAAYKQSKAQRARTMALYNPIPVRQNCFTVN 67
Qy   61 --FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFR--PCEDIACDSQRCRI 116
Db   68 RSLFIFGEDNIVRKYAKKLLDWPPEYMILATTIANCIVLALEQHLPEDDKTPMSRR--- 124
Qy  117 LQAFDDFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVAGMLEYSLDLQN-- 173
Db  125 LEKTEPYFIGIFCFEAGIKIVALGPIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFNTH 184
Qy  174 VSFSAVRTVRLPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLW 233
Db  185 VDLLRALRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFY 244
```

```
Db  2068 QADWESPERRQSRSPSEGRSQTPNRQGTGSLSLSESSIPSISDTSTPRRSRRQLPP---VP 2123
                                                                   ||
Qy  2127 PSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGG 2186
          ::     ::                                          :: ::  :
Db  2124 PKPRPLLSYSSL-----------------------------------MRHTGGISPPPDGSE- 2157

Qy  2187 PGSRPKKK-LSPPSITIDPPESQGPRTP---PSPGICLRRRAPSSD 2228
          :     : :.:   :  ::  ::       ::      : ::
Db  2158 QALESNSACLTESSNSLHPQQGQHPSPQHYISEPYLALHHDSHASD 2203


RESULT 11
A54972
voltage-dependent calcium channel alpha 1E-3 - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mi
 J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: A54972
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2270 <WIL>
A;Cross-references: UNIPROT:Q15878; GB:L29385; NID:g495869; PID:I29385; NID:g495587
A;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match         14.0%;  Score 1665;  DB 2;  Length 2270;
Best Local Similarity   24.2%;  Pred. No. 2.1e-93;
Matches  620;  Conservative  386;  Mismatches  814;  Indels 744;  Gaps  90;

Qy   31 RPGPGSGAEKDPGSADSEAEGLPYPALA-----------------------PV------- 59
         |||  : .: ||
Db   11 RPGSGDGDSD---QSRNRQGTPVPASGQAAAYKQTKAQRARTMALYNPIPVRQNCFVNR 67

Qy   60 VFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFR--PCEDIACDSQRCRIL 117
          ::  :  :      :           ::  :||:::|||  .   : :  : |   .|
Db   68 SLFIFGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR---L 124

Qy  118 QAFDDFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN--V 174
          .     |  || :|:| |:|||  |  : |  . |||:||| ::: |:|          :
Db  125 EKTEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFTVVLSGILATAGTHFNTHV 184

Qy  175 SFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWA 234
           :|||||||||||:   . |:: :::| : |  | |.|  ||| | |::||:|| ||
Db  185 DLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEYS 244

Qy  235 GLLRNRCPLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGG 294
         | | . | :  :                             :        ::
Db  245 GKLHRACFMNNSGIL-----------------EGFDP-------PHPCGVQGC- 273

Qy  295 GPPCGLDYEAYNSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLE 354
          |  ||                 |:  :   .       :.: ||| |    ||| |: |
Db  274 ---PAG----YE--------CKDW----------IGPNDGITQFDNILFAVLTVFQCITME 309

Qy  355 GWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES------Q 407
         |  :::| ::.     |: ||:: ||||||||::||  |||:.:      :: ||
Db  310 GWTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRAFMK 369

Qy  408 LMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSS 467
         | |:||:|                  ||  :    :         :.
Db  370 LRRQQQIE-------------------REINGYRAWIDKAEEVMLAEENKNAG------ 403

Qy  468 PAPLGGQETQPSSSCSRSHRRLSVHLVHHHHHHHYHLGNGTLRAPRASPEIQDRDAN 527
                          | ||| :    :
Db  404 ---------TSALEVLRRATI----------------------KRSRTEAMTRDS- 427

Qy  528 GSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSG 587
         ||                           ::
Db  428 --------------------------SDEH------------------------ 431

Qy  588 KVYPTVHTSPPPETLKEKALVEVAASSGPPTLTISINIPPGPYSSMHKLLETQSTGACQSS 647
```

```
Db  1032 SEQALLGDVQLDVGRGISQSEPDLSCMTANMDKATTESTSVTVAIPDVDPLVDSTVVNIS 1091
                  |||| |
Qy  1221 --------GDDADDEGNLSKGER----VRAWIRARLPACYLERDSWSAYIFPPQSR 1264

Db  1092 NKTDGEASPLKEAETKEEEEVEKKKKQKKEKRETGKAMVPHS-------SMFIFSTTNP 1144
                   : |:              .      . .         ||.||| :|
Qy  1265 FRLLCHRIITHKMFDHVVIVIFIFNCITIAMERPKIDPHSAERIFLTILSNYIFTAVFLAE 1324

Db  1145 IRRACHYIVNLRYFEMCILLVIAASSIALAAEDPVLTNSERNKV-LRYFDYVFTGVFTFE 1203
          :  |  |||  |||| |:|:|: |||:|| :: :| |: :| ||  ||||||||||||||
Qy  1325 MTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDI-LVSMVSDSGTKILGMLRVLRLL 1383

Db  1204 MVIKMIDQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGRDIKTIKSLRVL 1263
          ::: |:| |    :||| ||||||||| ||||::|||||||||| ||||||||||||:||
Qy  1384 RTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFYC-- 1441

Db  1264 RVLRPLKTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTD 1323
                                               .:|||:|: :|||||||||||||| :
Qy  1442 QGEDTRN------ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYD 1494

Db  1324 SSKDTEKECIGNVYDHEKNKMEVKGREWKREHEFHYDNIIWALLLFTTVSTGEGWPQVLQH 1383
          | |||  : ||   ||          |  .    :|||: ||   |:|| |:||| |:
Qy  1495 GLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEEARR 1554

Db  1384 SVDVTEEDRGPSRSNRMEMSIFYVVYFVVFPFFFVNIFVALIIITF--------QEQGDKM 1436
                                ||:| |||| || ||||| |||:||:|
Qy  1555 REEKRLRRLEKKRRKA------QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGL 1605

Db  1437 MEE------CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIAL 1493
                               :  :   | ||||  | ::|::|  ||::| ||| ||:| ||:
Qy  1606 NVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIV 1665

Db  1494 NTVLMMKYTAPCTYELALKYLNIAFTMVFSLECVIKVIAFGFLNYFRDTWNIFDFITV 1553
          | |:||||     ||||||| |||| |||| | |:|:||||| |:||||||:||| | |
Qy  1666 LLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQV 1725

Db  1554 IGSITEILITDSKLVNTSGFNMSFLKLFRA---ARLIKLLRQGYTIRILLWTFVQSFKAL 1610
           |:||| |:|   ||| | ||:|| ||||    ||:|||| |  ||||| ||||||| |
Qy  1726 GNLGLLFMLLFIFAIALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGD 1784

Db  1611 PYVCLLIAMLFFIYAIIGMQVFGNLKLDEESH---INRHNNFRSFFGGSLMLLFRSATGE 1666
              |||:|||||| ||:|:|:||| | ||         : :||  ||  |||||| :||:
Qy  1785 NWNGIMKDTL--RDCDQESTC----------YNTVLSPIYFVSFVLTAQFVLNVVIAVLM 1833

Db  1667 AWQEIMLSCLGEKGCEPDTTAPSGQNESERCGTDLAYVYFVSFIFFCSFLMLNLFVAVIM 1726
               :|                         :  :|:||||:: | |||:||:|||||:|
Qy  1834 KHLEESNKEAK-------------EEAELEAELE------LEMKTLSPQPHSPLGSPFL 1873

Db  1727 DNFEYLTRDSSILGPHHLDEFVRVWAFYDRAACGRIHYTEMYEMLTLM-------SPPL 1778
                                                         |:|:||        |||
Qy  1874 WPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTVRKSGGVSRT 1933

Db  1779 GLGKRCPSKVAYKRLVLMNNPVAEDMTVHFT--STLMALIRTALD----IKIAKGGADRQ 1832
           :|:         : :|:|  ||   :|  |   |::||:||: ||     |:| ||  ||
Qy  1934 HSLPNDSYMCRHGSTAEGPLGHRGWGL------PKAQSGGSVLSVHSQPADTSYI------ 1981

Db  1833 QL---DSELQKETLAIWPHLSQKMLDLLVPMFKASDLTVGKIYAAMMIMDYYKQSKVKKQ 1889
               :|                   |   ||   |:|:|| | |    :  :  .  | :
Qy  1982 --LQLPKDAP--HLIQPHSAP------TWGTIPKLPP---------PGRSPLAQRPL 2019

Db  1890 RQQLEEQKNAPMFQRMEPSSLPQEIIANAKALPYLQQDPVSGLSGRSGYPSMSPLSPQEI 1949
          :   :.  :|    :                  |       |  ||    ||| ||
Qy  2020 ----------------RRQAAIRTDSLDVQGLGSR------EDILAEVSGPSPPLA 2053

Db  1950 FQLACMDPADDGQFQEQQSLVVTDPSSMRRSFSTIRDKRSNSSWLEEFSMERSSENTYKS 2009
                           :|    | ::  ||| ||:   |      || |  .   |
Qy  2054 RAYSFWGQSSTQAQQH------SRSHSKISKHMTPP------ 2083

Db  2010 RRRSY--HSSLRLSAHRLNSDSGHKSDTHRSGGRERGRSKERKHLLSPDVSRCNSEERGT 2067
            ||:    ||                :: |  | :        | ||
Qy  2084 -APCPGPEPNWKGPPETRS---------------SLE-------LDTELSWISGDLLPPGGQEEP 2126
```

```
Db   1373 GWPQVLQHSVDTEEDRGPSRSNRMEMSIFYVVYFVFPFFFVNIFVALIIITF-----      1426
Qy   1547 QEEEARRREKRLRRLEKKRRKA------QCKPY--YSDYSR--FRLLVHHLCTSHYLDL   1597
             :.:                          ::                :. ::.:..::
Db   1427 -QEQGDKMME---CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPFEY    1482
Qy   1598 FITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVPKLVAFGFRRFFQDRW  1657
Db   1483 TIMAMIALNTVVLMKYYSAPCTYELALKYLNIAFTMVFSLECVLKVIAFGFLNYFRDTW   1542
Qy   1658 NQLDIAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVKLLKMAVGMRALLDT   1717
Db   1543 NIFDFITVIGSITEILILTDSKLVNTSGFNMSFLKLFRA----ARLIKLLRQGYTIRILLWT 1599
Qy   1718 VMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATERNFGMAFLT  1776
Db   1600 FVQSFKALPVCLLIAMLFFIYALIIGMQVFGNIKLDEESH---INRHNNFRSPFGSLML   1655
Qy   1777 LFRVSTGDNWNGIMKDTL--RDCDQESTC---------YNTVISPIYFVSFVLTAQFVLV  1825
Db   1656 LFRSATGEAWQEIMLSCLGEKGCEPDT-TAPSGQNENERCGTDLAYVVYVSFIFFCSFLML 1715
Qy   1826 NVVIAVLMKHLEESNKEAK---------EEAELEABLE----------LEMKTLSPQPH   1865
Db   1716 NLFVAVIMDNFEYLTRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTIM----  1771
Qy   1866 SPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTV  1925
Db   1772 ----SPPLGLGKRCPSKVAYKRLVLMNMPVAEDMTVHFT--STIMALIRTALD----IKI  1821
Qy   1926 RKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGL------PKAQSGSVLSVHSQPADTSYI 1981
Db   1822 AKGGADRQQL--DSELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMIMDYY    1878
Qy   1982 ----------LQLPKDAP--HLLQPHSAP--------------TWGTIPKLPP-------PGR 2011
Db   1879 KQSKVKKQRQQLEEQKNAPMFQRMEFSSLPQEIIANAKALPYLQQDPVSGLSGRSGYPSM  1938
Qy   2012 SPLAQRPLRRQAAIRTDSLDVQGLGREDLLAEVSGPSPPLARAYS---------       2057
Db   1939 SPLSPQDIFQLACM--DPADDGQFQERQSLV--VTDPS-SMRRSFSTIRDKRSNSSWLEE  1993
Qy   2058 FWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDT-ELSWISG-  2115
Db   1994 FSMERSSENTYKSRRRS------------------YHSSLRLSAHRLNSDSGH         2028
Qy   2116 --DLLPPGGQEEPPSPP---------DLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDS 2166
Db   2029 KSDTHPSGGRERRRSKERKHLLSPDVSRCNSEE------RGTQADWESPERRQSRSPS--EG 2082
Qy   2167 GSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPES--QGPRTPSPSPGICLR---  2221
Db   2083 RSQ------TPNR-------QGTGSLSESSIPSVSDTSTPRRSRRQLPVPPKPRPLLSYSS  2131
Qy   2222 --RRAPS---------SDSKDPLASGPPDSMAA------SPSPKK               2249
Db   2132 LIRHAGSISPPADGSEEGSPLTSQALESNNAWLTESSNSPHPQQ                 2175


RESULT 12
T43262
calcium channel alpha-1 chain, L-type - Stylophora pistillata
C;Species: Stylophora pistillata
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43262
R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J.
  Gene 227, 157-167, 1999
A;Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylo[
A;Reference number: Z22375; MUID:99148007; PMID:10023047
A;Accession: T43262
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1891 <ZOC>
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Db    432 ------------------------------------------------CVDI        435
Qy    648 CKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRD   707
Db    436 SSVGTPLARASIKSAKVDGVSY----------------------FRHKE---          462
Qy    708 PHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFPGRGIMIAILVNTLSMGIEYHEQ  767
Db    463 --------------RLLRISIRHHMVKSQVFFYWIVLSLVALNTACVAIVHHNQ        500
Qy    768 PEELTNALEISNIVFTSLFALEMLLKLLLVYGPPGYIKNPYNIFDGVIVVISVWEIVGQ--  825
Db    501 PQWLTHLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCDFGVTVGSIFEVWAIF     560
Qy    826 ---QGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSIL   882
Db    561 RPGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFLFIVFALL    620
Qy    883 GMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGM-----ASTS   937
Db    621 GMQLFGGRF-NFNDG--TPSANFDTFPAAIMTVFQIITGEDWNEVMYNGIRSQGGVSSG    676
Qy    938 SWAALYFIALMTFGNYVLFNLLVAILVEGF-QAEEISK----REDASGQLSCIQLPVDSQ   992
Db    677 MWSAIYFIVLTILFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEEAFNQKHALQKAKEV-  735
Qy    993 GGDANKSESEPDFFPSLDGDGDRKKCLAL-----------VSLGEH--PELRKS        1034
Db    736 ----SPMSAPNM--PSIERDRRRRHHMSWWEPRSSHLRERRRHHMSVWEQRTSQLRKH     788
Qy   1035 L---------------LPPLIIHTAATPM-----------SLPKSTSTGLGEALGPA------SR 1067
Db    789 MQMSSQEALNREEAPTMNPLNPLNPLSSLNPLNAHPSLYRRPRAIEGLALGLALEKFEE    848
Qy   1068 RTSSSGS---------AEPGAAHEMKSPPSARSSPHSPWSA-----------         1099
Db    849 RISRGGSLKGDGGDRSSALDNQRTPLSLGQREPPWLARPCHGNCDPTQQEAGGGRAVVTF   908
Qy   1100 -ASSWTSRRSSRNSLGR---------APSLKRRSPSGERRSL--LSGEGQESQD--------- 1141
Db    909 EDRARHRQSQRRSRHRVRTEGKESSSASRSRSASQERSLDEAMPTEGEKDHELRGNEHGA   968
Qy   1142 EEESSEEERASPAGSDHRHRGSLEREAKSSF---------DLPDTLQVPGLHRTASGRGSAS 1194
Db    969 KEPTIQEERA---QDLRRTNSLMVSRGSGLAGGLDEADTPLVLPHPELE---VGKHVVL    1021
Qy   1195 EHQDCNGKSAS-----------GRLARALRPD-------------------DPPL        1219
Db   1022 TEQEPEGSSEQALLGNVQLDMGRVVISQSEPDLSCITANTDKATTESTSVTVAIPVDPLV   1081
Qy   1220 DG------------------DDADDEGNLSKGERVRAWIRARLPACYLERDSWSA       1256
Db   1082 DSTVVHISNKTDGEASPLKEAEIREDEEEVEKKKQKKEK-RETGKAMVPHS------SM    1133
Qy   1257 YIFPPQSRFLLCHRIITHHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYI   1316
Db   1134 FIFSTTNPIRRACHYIVNLRYFEMCILLVIAASSIALAAEDPVLTNSERNKV-LRYFDYV   1192
Qy   1317 FTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDI-LVSMVSDSGTKILG   1375
Db   1193 FTGVFTFEMVIKMIDQGLIIQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGRDIK   1252
Qy   1376 MLRVLRLLRTLRPLRVISRAQGLKLVVETIMSSLKPIGNIVVICCAFFIIFGIILGVQLFK  1435
Db   1253 TIKSLRVLRPLKTIKRLPKLKAVFDCVVTSLKNVFNILIVYMLFMFIFAVIAVQLFK     1312
Qy   1436 GKFPVC--QGEDIRN-----ITNKSDCAEEASYR-WVRHKYNFDNLGQALMSLFVLASKD   1486
Db   1313 GKFFYCTDSSKDTEKECIGNYVDHEKNKMEVKGREWKRHEFHYDNIIWALLTLFTVSTGE   1372
Qy   1487 GWDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQH   1546
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A;Cross-references: UNIPROT:O97017; EMBL:U64465; NID:g4204977; PID:g4204978; PIDN:AAD114
C;Genetics:
A;Gene: CACH1
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match     14.0%;  Score 1664.5; DB 2;  Length 1891;
Best Local Similarity   25.2%;  Pred. No. 1.8e-93;
Matches  486;  Conservative 316;  Mismatches 510;  Indels 617;  Gaps 55;

Qy    11  EESGQPRSFMRLND----------------------------------LSGAGGRPGPGSAEKDPGSADSEAEGLPYP  54
              |:  ||:
Db     2  EQNGYPRANFTQGSKIFWPNGTDLMQTRARLNGHGGKYAKSVAAKRQKKSGNTVR--PKR  59

Qy    55  ALAPVFVFYLSQDSRPRSWCLRTVCNPW--FERISMLVILLNCVTLGMRPCEDIACDSQ  112
                                           :: ||||  :||||::  |:
Db    60  AL-----LCLSLGNPIRSAAINLV--EWKPFDVMILITIFANCAALAAFEPLPE--KDSS  110

Qy   113  RCRILQAFDDFIF-AFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAG---MLE  166
                  :  ||| ||:  |:  |||| ::::|:  ||   ||  :
Db   111  EINDNLEVAEYVFLAVFTMEAVLKIIIAYGFLFHPGAYLRNGWNILDFVIVVVGLATILVK  170

Qy   167  YSLDLQNVSFSAVRTVRLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFG  226
                 |:  :  |||:  ||||:  |   :::: |:  ||::  |||||
Db   171  ATLSSGSFDVKALRAFRVLRPLRLRVSGVPSLQVVLNSIIKALIPLFHIALLVVFVVIYA  230

Qy   227  IVGVQLWAGLLRNRCFLPENFSLPLSVDLRERYYQTENEDESPFICSQPRENGMRSCRSVP  286
              ||| |       : |::    |:  :  :  |   :     ::
Db   231  IIGVELFMGRLHKTCY--DNVT-----GAESF-------EEPHPCS-------  262

Qy   287  TLRGDGGGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIA  346
                                            :  ::|
Db   263  ---SGSSGFQC-----------DKAAGQV--CEGGWKGPNHGITNFDNIGLACWT  301

Qy   347  IFQVITLEGWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIIATQFSETKQR-  404
              |:  |||| |:  ::   :  |:|  :|:|:||||| :||:|:  |:||||:|:  |   |
Db   302  VFQCITLEGWTDVLYWVNDAVGNSWPWVYFVTLIIWGSFFVLNLVLGVLSGEFAKEKARR  361

Qy   405  --ESQLMREQR----------VRFLSNASTLASFSEPGSCYEBLLKYLVYILRKAARL  451
              :   |::|                         :: |||
Db   362  QKSGEFQKFREKQQVEDAYNGYLDWITQAEDIEGDSESESGDES---------KASKKT  411

Qy   452  AQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGNGT  511
               :
Db   412  S--SRQS----------RTEDIEMIDRNERQDSI------SQHDTHHY-  441

Qy   512  LRAPRASPEIQDRDANGSRRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAP  571
              ||
Db   442  -------------------QSEGREEFKGCELDKNQRQCIEFALKAKPLKRYIPENRLQFH  441

Qy   442  -------------------------------------------  441

Db   572  PPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSS  631

Qy   442  -----------------------------------------------------  441

Db   632  MHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGAVELADREMPDSDSE  691

Qy   451  -----------------LKKWHHRRQTEL-------  477
                               |||
Db   692  AVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMI  751

Qy   478  VVFLNSLTLALEHYDQPDWLTKFLDIANKLFGIFTIEMIVKMYCLGHGYFASLFNRFD  537

Db   752  AILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVFGPGFYIKNPYNIFD  811

Qy   538  CLVVISSLLELAITEALKQPPIGISVLRCIRLLRIFKVTRYMSSLSNLVASLLNSMRSIA  597

Db   812  GVIVV----ISVWEIVGQQGGGLSVLRTFRLMRVLKLVKFLPALQRQLVVLMKTMDNVA  866

Qy   598  GLLILLSLFMLICSLLGMQIFGGKF--NTDDDEIP-RSNFDSFWRALITVFQLLTGEDWN  654

Db   867  TFCMLIMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLLTQEDWN  926

Qy   927  KVLYNGMAS----------------TSSWAALYFIALMTFGNYVLFNLLVALLVEGF----QAEE  971

Db   655  AVMYDGIRAWGIGEGGSAIAILYFIFLVVVGNYILLNVFLAIAVDNLADAENLTEMEE  714

Qy   972  ISKREDASQOLSCIQL-PVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHP  1029

Db   715  KKKKKEKAREKEALKMKGSVDSQG----------RIDQDG  744

Qy  1030  ELRKSLLPPLLIHTAA--TPMSLPKSTSTGLGEALGPASRTSSSGSAEPGAAHEMKSPP  1087

Db   745  ----AIVPN--HSSASRSNVTLDKST-----QELHSTGT-  772

Qy  1088  SARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEG---QESQDEEE  1144

Db   773  LNGNGVARTASHDDVE  788

Qy  1145  SSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCNGKSA  1204

Db   789  AQSTDISEIVGS----------------KSAVSNNNESASASS  815

Qy  1205  SGRLARALARPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSGAYIPPQSR  1264

Db   816  SDDIDRAPMPPESAL--------------FIFSPTNI  838

Qy  1265  FRLLCHRIITHKMFDHVLVLIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAE  1324

Db   839  FRVVCYKIAINTYFVNFILCLIIVSSILLAAEDP-LNASAKRNQVLNYFDYFFTSVFTFE  897

Qy  1325  MTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRVLRLLR  1384

Db   898  ILVKFISYGLIIHKGSFCRSAFNLLDLLVVSVSISLSR----TSQFSVVRILRVLR  951

Qy  1385  TLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIFGILGVLFGKFVCQGE  1444

Db   952  VLRPLRAINRAKGLKHVVQSVFVAVKTIGNIKLVTMLFQFLFAVIGVQLFKGTFFSCNDE  1011

Qy  1445  DTRNITNKSDCAEASY---------------RWVRHKYNFDNLGQALMSLFVLASKDGW  1488

Db  1012  ---KILTAEBC-QGNYIDFKGPGLSNPVVKEREWRRHDFNFDNVGNAMLTFTVMTFEGW  1067

Qy  1489  VDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQE  1548

Db  1068  PGILENSIDSTEVDKGPQNQNRPWVAIYYIIYIIIIAFFMVNIFVGFVIVTF-  1119

Qy  1549  EEEARRREEKRIRLEKKRRKA------QCKPY-YSDYSRFLLVHHLCTSHYLDLFITG  1601

Db  1120  -QSEGREEFKGCELDKNQRQCIEFALKAKPLKRYIPENRLQFHIWPVTVSQAFEYLFFA  1177

Qy  1602  VLGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFPRRFQDRWNQLD  1661

Db  1178  FIVCNTVVLMQYYQEPKLYTRVLDGFNIGFTAVFLLECILKLIAFKPKNYFTDRWNLFD  1237

Qy  1662  LAIVLLSIMGTTLEEIEVNASLPINPTIIRIMRVLRIARVLKLKMAVGMRALLDTVM-  1719

Db  1238  FFRLFRALRLVKLLKLLNQGSGIKTLLWTFIKS  1292

Qy  1720  -QALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLF  1778

Db  1293  ----ALLIVMMFFIYAVIGMQMFGRIAINSD--TAINRNNFQTFPQSLMVLF  1346

Qy  1779  RVSTGDNWNGIM-KDTLRD---CDQE------STCYNTVISPIYFVSFVLTAQFVLNVV  1828

Db  1347  RSATGENWQQIMLACTHRDDVKCDQNADPQEPSCLCGSDFAYFYFVSFYSICSFLIINLF  1406

Qy  1829  IAVLMKHLE  1837

Db  1407  VAVIMDNFD  1415
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RESULT 13
B54972
voltage-dependent calcium channel alpha 1E-1 - human
C;Species: Homo sapiens (man)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Accession: B54972
R;Williams, M.E.; Marrubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J;Biol. Chem. 269, 22347-22357; 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: B54972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2251 <WIL>
A;Cross-references: GB:L29384; NID:g495867; PIDN:AAA59204.1; PID:g495868
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1663.5; DB 2; Length 2251;
Best Local Similarity 24.2%; Pred. No. 2.6e-93;
Matches 617; Conservative 383; Mismatches 815; Indels 735; Gaps 89;

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Qy    31 RPGPGSAEKDPDGSADSEAEGLPYPALA----------------------PV---- 59
Db    11 RPGSGDGSD--QSRNRQGTPVPASGQAAAYKQTKAQRARTMALYNPIPVRQNCFTVNR 67

Qy    60 VFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFR--PCEDIACDSQRCRIL 117
Db    68 SLFIFGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVLALEQHLPEDDKTPMSRR--L 124

Qy   118 QAFDDFIFAFFAVEMVVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN--V 174
Db   125 EKTEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGLLATAGTHFNVTHV 184

Qy   175 SFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWA 234
Db   185 DLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYS 244

Qy   235 GLLRNRCFLPENFSLPLSVDLLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGG 294
Db   245 GKLHRACFMNNSGIL-----EGFDP-----PHPCGVQGC 273

Qy   295 GPPCGLDYEAXNSSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLE 354
Db   274 --PAG--YE-----CKDW--------IGPNDGITQDFNILFAVLTVFQCITME 309

Qy   355 GWVDIMYFVMDA-HSFYNFYFILLIIVGSFFMINLCLVVIATQFSETKQRES------Q 407
Db   310 GWTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLSGEFAKERERVENRRAFMK 369

Qy   408 LMREQRVRFLSNASTLASFSEPGSCYEELLKYLVILVILRKAARRLAQVSRAAGVRVGLLSS 467
Db   370 LRRQQQIE----------RELNGYRAWIDKAEEVMLAEENKNAG--------- 403

Qy   468 PAPLGGQETQPSSSCSRSHRRLSVHHLVHHLVHHHHHHYHLGNGTLRAPRASPEIQDRDAN 527
Db   404 --------TSALEVLRRATI----------KRSRTEAMTRDS- 427

Qy   528 GSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSG 587
Db   428 --------SDEH---------------------- 431

Qy   588 KVPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSS 647
Db   432 ---------------------------------CVDI 435

Qy   648 CKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDACHSDLRD 707
Db   436 SSVGTPLARASIKSAKVDGVSY----------FRHKE--- 462

Qy   708 PHSRRQRSLGPDAEPSSVLAFWRLICDTFPKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ 767
Db   463 ----RLLRISIRHHMVKSQVFWIVLSLVALNTACVAIVHHNQ 500

Qy   768 PEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQ-- 825
Db   501 PQWTHLLYYAEFLFLGLFLLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAIF 560


Qy   826 --QGGGLSVLRTFRLMRVLKLVRFLPALQRQLJVLMKTMDNVATFCMLMLFIFIFSIL 882
Db   561 RPGTSFGISVLRALRLLRIFKITKYWASLRNLVVSLMSSMKSIISLLFLLFLFIVFALL 620

Qy   883 GMHLPGCKFASERDGDTLPDRKNFDSLLWAIVTVFQLTQEDWNKVLYNGM----ASTS 937
Db   621 GMQLFGGRF NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSG 676

Qy   938 SWAALYFIALMTFGNYVLFNLLVAILVEGF-QAEEISK---REDASGQLSCIQLPVDSQ 992
Db   677 MWSAIYFIVLTLFGNYTLLNVFLAIAVDNLANAQPLTKDEQEEEAFNQKHALQKAKEV- 735

Qy   993 GGDANKSESEPDFFSPSLDGDGDRKKCLAJ------VSLGEHPELRK--------- 1033
Db   736 -----SPMSAPNM--PSIERERRRHHMSVWEQRTSQLRKHQMSSQEALNREEAPTMNP 788

Qy  1034 ------SLLPPLIIHTAATPMSLLPKSTSTGLGEALGPA-----SRRTSSSGS----AE 1076
Db   789 LNPLNPLSSLNPLNAHP-----SLYRRPRAIEGLALGLALEKFEEERISRGGSLKGDGGD 843

Qy  1077 PGAAHEMKSPPSARSSPHSPWSA----------------------ASSWTSRRSSR 1110
Db   844 RSSALDNQRTPLSLGQREPPWLARPCHGNCDPTQQEAGGGEAVVTFEDRARHRQSQRRSR 903

Qy  1111 NSLGR------APSLKRRSPSGERRSL--LSGEGQESQD---------EEESSEERASPAG 1155
Db   904 HRRVRTEGKESSSASRSRSASQERSLDEAMPTEGEKDHELRGNHGAKEPTIQEERA----- 959

Qy  1156 SDHRHRGSLEREAKSSF------DLPDTLQVPGLHRTASGRGSASEHQDCNGKSAS--- 1205
Db   960 QDLRRTNSLMVSRGSGLAGGLDEADTPLVLPHPELE---VGKHVVLTEQEPEGSSEQALL 1016

Qy  1206 -------GRLARALRPD--------------------DPPLDG----- 1221
Db  1017 GNVQLDMGRVISQSEPDLSCITANTDKATTESTSVTVAIPDVPLVDSTVVHISNKTDGE 1076

Qy  1222 --------------DDADDEGNLSKGERVRAWIRARLPACYLERDSWSAVIFPPQSRFRLLCH 1270
Db  1077 ASPLKAEAIREDEEEVEKKKQKKEK-RETGKAMVPHS-------SMFIFSTTNPIRRACH 1128

Qy  1271 RIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVVV 1330
Db  1129 YIVNLRYFEMCLLLVIAASSIALAAEDPVLTNSERNKV-LRYFDYVFTGVFTFEMVIKMI 1187

Qy  1331 ALGWCFGEQAYLRSSWNVLDGLLVLLSVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPL 1389
Db  1188 DQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVLRPL 1247

Qy  1390 RVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKFFVC--QGEDTR 1447
Db  1248 KTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDTE 1307

Qy  1448 N------ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
Db  1308 KECIGNYVDHEKNKMEVKGREWKRHEFHYDNIIWALLTLFVSTGEGWPQVILQHSVDVTE 1367

Qy  1501 VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARREEKRL 1560
Db  1368 EDRGFSRSNRMEMSIFYVVVFVVFPFFVNIFVALLIITF--------QEQGDKMMEE--- 1417

Qy  1561 RRLEKKRRA----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1611
Db  1418 CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTVLLM 1477

Qy  1612 MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG 1671
Db  1478 MKYYSAPCTYELALKYLNIAFTMVFSLECVLKVIAFGFLNVFRDTWNIFDFITVIGSITE 1537

Qy  1672 ITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLL 1731
Db  1538 IILTDSKLVNTSGFNMSFLKLFRA---ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLL 1594

Qy  1732 FMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIM 1790
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```
Db  1595 IAMLFFYAIIGMQVFGNIKLDEESH----INRHNNRSFFGSLMLLFRSATGEAWQEIM 1650
Qy  1791 KDTL--RDCDQBSTC------YNTVISPIYFVSVFLTAQFVLNVVIAVLMKHLEES 1839

Db  1651 LSCLGEKGCEPDTTAPSGQENERCGTDLAYVYFVSFIFFCSFLMLNLFVAVIMDNFEYL 1710
Qy  1840 NKEAK------EEAELEABLE-----------LEMKTLSPQPHSPLGSPPLWPGVEG 1879

Db  1711 TRDSSIIGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTLM-------SPPLGLGKRC 1762
Qy  1880 PDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPND 1939

Db  1763 PSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD----IKIAKGGADRQQL--D 1813
Qy  1940 SYMCRHGSTAEGPLGHRGWGL---PKAQGSGVLSVHSQPADTSYI------LQL 1984

Db  1814 SELQKEFLAIWPHLSQKMDLLVPMPKASDLTVGKIYAAMMIMDYYKQSKVKKQRQQLEE 1873
Qy  1985 PKDAP--HLLQPHSAP----TWGTIPKLPP----------PGRSPLAQRPLRRQAAI 2025

Db  1874 QKNAPMFQRMEPSSLPQEIIANAKALPYLQQDPVSGLSGRSGYPSMSPLSPQDIFQLACM 1933
Qy  2026 RTDSLDVQGLGSREDLLAEVSGPSPPLARAYS-----------FWGQSSTQAQQHSR 2071

Db  1934 --DPADDGQFQERQSLV--VTDPS-SMRRSFSTIRDKRSNSSWLEEFSMERSSENTYKSR 1988
Qy  2072 SHSKISKHMTTPPAPCPGPPENWGKGPPETRSSLELDT-ELSWISG---DLLPPGGQEEPP 2127

Db  1989 RRS-------------YHSSLRLLSAHRLNSDSGHKSDTHPSGGRERRR 2023
Qy  2128 SPR---------DLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLLDSGSQPHLGTDPSNLG 2180

Db  2024 SKERKHLLSPDVSRCNSEE----RGTQADWESPERRQSRSPS--EGRSQ----TPNR-- 2070
Qy  2181 GQPLGGPGPGRPKKKLSPPSITIDPPES--QGPRTPPSPGICLR---RRAPS--- 2226

Db  2071 ----QGTGSLSESSIPSVSDTSTPRRSRRQLPPVPKPRPLLSYSSLIRHAGSISPPADG 2126
Qy  2227 SDSKDPLASCPPDSMAA---------SPSPKK 2249

Db  2127 SEEGSPLITSQALESNNAWLTESSNSPHPQQ 2156
```

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Db   141 -IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRI 199
Qy   161 FVFHKGSYIRNGWNVMDFIVVLSGLL--ATAATHFNLRTLRAVRVLRPLKLVSGIPSLQI 218

Qy   200 LVTLLLDTLPMLGNVLLLCFFVFFIGVGVQLWAGLLRNRCFLPENFSLPLSVDLERYY 259
Db   219 VLKSIMKAMVPLLIQIGLLLFFAIIMFAIIGLEFYYGKLHRTCYTDDAAAELDLQF--- 274

Qy   260 QTENEDESPICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNTTCVNWNQY 319
Db   275 ----------------------------PCGTQEPTRLCPNGTVCSYW--- 294

Qy   320 YTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDA-HSFYNPIYFILL 378
Db   295 --------IGPNDGITQFDNILFALLTVFQCITMEGWTTILYNTDDALGAMWNWLYFIPL 346

Qy   379 IIVGSFFMINLCLVVIATQFSETKQRES-------QLMREQRVRFLSNASTLASFSEPGSC 432
Db   347 IIIGSFFVLNLVLGVLSGEFAKERERVENRRSFLKIRRQQQIE--- 389

Qy   433 YEELLKYLVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVH 492
Db   390 -RELNGYRAWIDKAEEVMLLEENKNAGEKSAL--- 420

Qy   493 HLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSPTPALSGAPPGGAES 552
Db   421 ----------------HVLRRATIKKGR 432

Qy   553 VHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAA 612
Db   433 ----------------MEMIQTES--- 450

Qy   613 SSGPPTLTSLNIPPGYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR 672
Db   451 ------------VGSPLARASI--------KSTKLLEGSS 470

Qy   673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVLAFWRLI 732
Db   471 ---------------------------YFRRKE- 479

Qy   733 CDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLL 792
Db   480 RISIRHMVKSHAFYWIVLGLVALNTCVAVVHYDQPLWLSNFLYYAEFTFLGLFSSEMFL 539

Qy   793 KLLIVGPFGYIKNPYNIFDGVIVVISWEIV----GQQGGGLSVLRTFRLMRVLKLVRF 847
Db   540 KMYGCGPRLYFHSSFNCFDCGVIIGSIFDVVWTIIRPETSFGISVLRALRLLRIFKITKY 599

Qy   848 LPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFD 907
Db   600 WASLRNLVVSLMSSMKSIISLLFLLFIVFALLGMQLFGGQFNFEE--GTPP--TNFD 655

Qy   908 SLLWAIVTVFQIITQEDWNKVLYNGMAS------TSSWWAALYFIALMTFGNYVLFNLLVAI 962
Db   656 TPPAAIITVFQIITGEDWNEVMYNGIKSQGGVNSGMWSSVYFIVLTLFGNYTLLNVFLAI 715

Qy   963 LVEGF-QAEEISK----REDASGQLSCIQ----LPVDSQGGDANKSE- 1000
Db   716 AVDNLANAQELTKEQEEEAINQKHALQKAKEVSPMSAPGFSTEREFRRHKHMSIWEA 775

Qy  1001 ------------------SEPDFFSPSLDG-DGDRKK----CLAIVSLGEHPELRKSLLPPL 1039
Db   776 RTSQLRRRMQMSREALFTDALQGLEGSGRYRRHRSRIFEAESLRRLAEQQAAESHQLGEV 835

Qy  1040 IIHTAATPMSLPKSTGLGEALGPASRRTS------SSGSAFPGAAHEMKSPPSA 1089
Db   836 GRREAFKSRSLRNS------WQPAGPDKRSSSIKVNGEQGRALGRSVEAGASFRMAEPIRA 890

Qy  1090 RSSPHSPW--------SAASSWTSRRSRNSLGR-APSLKRRSPG--- 1137
Db   891 RRRYRSLYKEAKMGLEESAETSLSRRPGKNKEGRLLQQLCEEQESGQLTQTPEVMDAQGQ 950
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RESULT 14

A47447

calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)

C;Species: Discopyge ommata
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47447
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
   Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Disc
A;Reference number: A47447; MUID:93248175; PMID:7683405
A;Accession: A47447
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2223 <HOR>
A;Cross-references: UNIPROT:P56699
A;Note: sequence extracted from NCBI backbone (NCBIP:130671)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   13.9%; Score 1656; DB 2; Length 2223;
Best Local Similarity   24.2%; Pred. No. 7.3e-9;
Matches 595; Conservative 385; Mismatches 811; Indels 668; Gaps 89;

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Qy    35 GSAEKDPGSADSBEARGLPYPAL--APV------VFFYLSQDSRPRSWCLRTVCNPW 82
Db    44 GAAQGSAGFKQTRAQRARTMALYNPIPVRHNCLTANRSLFLFGEDNIVRKSARRVIEWPP 103

Qy    83 FERISMLVILLNCVTLGMFR--PCEDIACDSQRCRIIQAFDDFEIFAFFAVEMVVKMVALG 140
Db   104 FEYMILATIIANCVVLALEQHLPNGD----KTPMAKSLEQTEPYFIGIFCFEAAGIKIVALG 160
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Db   1953 AANHSNS-TWLNEYSLERA---GPEDLYKWRSRRPLRPPSRSS------------N 1992

Qy   2121 GGQEEPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLG 2180

Db   1993 AGSRERGRSRERKHLLSPERSVCS------TGQCAH------------------------ 2034

Qy   2181 GQPLGGPGPGSRPKKKLSPPSITIDDPPESQGPRTPPSPGICLRRRAPSSDSKD-PLASGPP 2238

Db   2035 RSPSPGYSHRPREQVN-SSVSESPVPSSSGTSPPKQG--QRQLPQTPSKPRPLVSYSP 2089

RESULT 15
A37490
voltage-dependent calcium channel alpha 1E - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A37490
R;Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A;Title: Structure and functional expression of a member of the low voltage-activated ca
A;Reference number: A37490; MUID:93262464; PMID:8388125
A;Accession: A37490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2222 <SOO>
A;Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:132101)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match   13.9%; Score 1651.5; DB 2; Length 2222;
Best Local Similarity 23.6%; Pred. No. 1.4e-92;
Matches 591; Conservative 374; Mismatches 831; Indels 707; Gaps 77;

Qy   62 FYILSQDSRPRSWCLRTVCNPWFERISMLVILLNCVLGMFR--PCEDIACDSQRCRILQA 119
Db   21 FIFGEDNIVRKYAKKLIDWPPFEYMILATIIANCIVALEQHLPEDDKTPMSRR--LEK 77

Qy   120 FDDFIFAFFAVEMVKMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDIQN--VSF 176
Db   78 TEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFNTHVDL 137

Qy   177 SAVRTVRVLRPLRAINRVPSMRILVTLLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGL 236
Db   138 RTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYSGK 197

Qy   237 LRNRCPLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGP 296
Db   198 LHRACFMNNSGIL---------------EGFDP------PHPCGVQGC-- 224

Qy   297 PCGLDYEAYNSSSNTTCVWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGW 356
Db   225 PAG--YE-------CKDW-----IGPNDGITQFDNLLFAVLTVFQCITMEGW 262

Qy   357 VDIMYFVMDA-HSFVNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESLMREQRVR 415
Db   263 TTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVLGIVLVLSGEFAKERERV----ENRRA 317

Qy   416 FLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQE 475
Db   318 FMK-----------LRRQQQI-- 327

Qy   476 TQPSSSCSRSHRRLSVHHLVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLP 535
Db   328 ----------------------ERELNGYRAWI-- 338

Qy   536 PPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKYYPTVHT 595
Db   339 ------------------------ 338

Qy   596 SPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCL 655

Qy   1138 ES-----QDEEESSEERASPAGSDHRHRGSLERE-----------------AKSSFDLPD------ 1176
Db   951 MKAFSWQGEPHSSSMTRTPDVDTD-PSSGNLEKESGRTPENGKEESANTSEQVNEQSNWL 1009

Qy   1177 TLQV------PGLHRTASGRGSASEHQ--------------DCNGKSASGRLARALRPDDPPLD-- 1220
Db   1010 NLQLNQQATPGDRELTTGTRDTKQDKTQEOTEIDVDCEN------------------TETPMDSL 1056

Qy   1221 --GDDADEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFLLCHRIITHKM 1277
Db   1057 VTPGNAYSSSSSVKEDEKKS---KAIIPYT-----SMFLFRKTNPIRRVCHFIVNLRY 1106

Qy   1278 FDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFG 1337
Db   1107 FEMCILLVIAASSVALAAEDP-IHKDSARNQVLRYFDYVFTGVFTFEMVIKMIDIGLVFH 1165

Qy   1338 EQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQ 1396
Db   1166 EGSYFRDVWNILDFIVVSGALVAFAFTNLIGGSSGKDINTIKSLRVLRVLRPLKTIKRLP 1225

Qy   1397 GLKLIVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCA 1456
Db   1226 KLKAVEFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYC--TDSSKMT-KQDC- 1281

Qy   1457 EASYRWVRHK----------------YNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQ 1504
Db   1282 RGQFVLYRQRTKLSIENGNVTTFHYDNVVWALLTLFVSTGEGWPQVLQHSVDVTEADQG 1341

Qy   1505 PIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLE 1564
Db   1342 PIPGNRMEMSIFYIVYFVFPFFFVNIFVALIIITF------QEQGDKMLEES---SLE 1391

Qy   1565 KKRRKA--------QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHY 1615
Db   1392 KNERACIDFAISAKPLTRYMPQNRQTFQYRVWQFVVSPSFEYTILTMIALNTVVLMMKHH 1451

Qy   1616 QQPQILDEALKICNYIFTVLFVLESVFKLIVAFGRRRFFQDRWNQLDLAIVLLSIMGITLE 1675
Db   1452 SPPPGFASVVLKMNIAFTITFTLECILKLIAFGFLNYFRDSWNVFDFVTVVGSSEIIVT 1511

Qy   1676 EIE--VNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLF 1732
Db   1512 ECNLKFVNLS--------FLKLFRAARLIKLLRQGITIRILLWTFVQSFKALPYVCLLI 1562

Qy   1733 MLFFIFAAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD 1792
Db   1563 AMLFFIYAIIGMQLFGNIGLDDHTP--INRHNNFHTFFNALMLLFRSATGESWQEIMLA 1619

Qy   1793 TL--RDCD--QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAK---- 1844
Db   1620 CLSGKECEGTREPSC--GTDVAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGP 1678

Qy   1845 ---EEAELEAELE---------LEMKTL-SPQHSPLGSPFLWPG-------VE 1878
Db   1679 HHLDEFVRVWAEYDRAACGRIHYTDMYQMLTLMSP-----PLGLGKKCPSKVAYKRLVLMN 1734

Qy   1879 GPDSPD-------SPKPGALHPAAHARSA---------SHFSLEHPTMQPHPTELPGPDL 1922
Db   1735 MPVTEDKTVHFTSTLMGLIRTALQIKLARGGADKQQLDAELRKEIMTIWPHLSQ-KTLDL 1793

Qy   1923 L------TVRKSGVSRTHSL----------PNDSVMCRHGSTAEGPLGHR--------- 1956
Db   1794 LVPMHTYSDLTVGKIYAAMMIDYYKQSKNKKYQKLQEEQSRTPMFQRMEASSLPPQIIS 1853

Qy   1957 -GWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWG-TIPKLPPPGRSPL 2014
Db   1854 STKGLPYLQTGTGPDVDSR-SEFTPLVPLP--PVMFQQGRTSSQGEBIHKQRPKELKKI 1909

Qy   2015 AQR--------PLRRQA-AIRTDSLDVGLGSREDLLAEVSGPPLLARAYSFWGQSTQ 2065
Db   1910 KLEYPHYGHYLPIENQGRAVSMPRLEIE--SAED--------TSPLKRSL----STF 1952

Qy   2066 AQQHSRSHSKISKGHMTPPAPCPGPE---PNWGKGP--PETRSSLEDTELSWISGDLLPP 2120

```
Db 1558 KRLRRLEKKRRKA------QCKPY--YSDYSR--FRLLVIHLCTSHYLDLFITGVIGLNVV 1608
             :  :              :  :         ||:| || |: |||| ||:||:| |
Qy 1389 ---CSLEKNERACIDPAISAKPLTRYMPQNRHTFQYRVWHFVVSPSFEYTIMAMIALNTV 1445

Db 1609 TMAMEHYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRRWNQLDLAIVLLS 1668
            :    |:||| ||| | | |||: |  |||:||| ||||| |::|| |||::|| |
Qy 1446 VLMKKYYSAPWTYELALKYLNIAFTMVFSLECVLKVIAFGFLNYFRDTWNIFDFITVIGS 1505

Qy 1669 IMGITLEBIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNL 1728
            |:|    :  ::    ::| |:||||:|| | :|:||:| :||:|  :|:|| || |:
Db 1506 ITEIILTDSKLVATSGFNMSFLKLFRA--ARLIKLLRQGYTIRILLWTFVQSFKALPYV 1562

Qy 1729 GLLFMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWN 1787
            ||::|| |:: |: | |||  ::|   : | |:| | | :| |:|:||||:||||:|
Db 1563 CLLIAMLFFIYAIIGMQVFGNIKLDEESH---INRHNNFRSFFGSLMLLFRSATGEAWQ 1618

Qy 1788 GIMKDTL--RDCDQESTC------YNTVISPIYFVSFVLTAQFVLNVVIAVLMKHL 1836
            || |    |:|  |         ||:||| ||| ||::  ||:|| ||||:|:::
Db 1619 EIMLSCLGEKGCEPDTTAPSGQNESERCGTDLAYVYFVSFIFFCSFLMLNLFVAVIMDNF 1678

Qy 1837 EESNKEAK--------EEAELEAELE-----------LEMKTLSPQPHSPLGSPFLWPG 1876
            ||:|: |         |  | | |               : |||:  ||:| ||
Db 1679 EYLTRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTLM-------SPPLGLG 1730

Qy 1877 VEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSL 1936
                     |  |  |   |   |  :: ||| :    | :|   |:| : |  |:
Db 1731 KRCFSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD----IKIAKGGADRQQL- 1783

Qy 1937 PNDSYMCRHGSTAEGPLGHRGWGL-----PKAQSGSVLSVHSQPADTSYI- 1981
              ||    :   |  ||           |||:  |:|  :||:
Db 1784 --DSELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMMIMDYYKQSKVKKQRQQ 1841

Qy 1982 LQLPKDAP--HLLQPHSAP------TWGTIPKLPP----------PGRSPLAQRPI-- 2019
            |: |     |  || :|         | ||:|            ||  | ::|
Db 1842 LEEQKNAPMFQRMEPSSLPQEIISNAKALPYLQQDPVSGLSGRSGYPSMSPLSPQEIFQL 1901

Qy 2020 --------------RRQAAIRTDSLDVQCLGSR-------EDLLAEVSGPSPPLARAY 2056
                          ||:|   ||:    | |          :| :|||| |
Db 1902 ACMDPADDGQFQEQQSLVVTDPSSMRRSFSTIRDKRSNSSWLEEFSMERSSENTYKSRRR 1961

Qy 2057 SFWGQSSTQAQQH------------SRSHSKISKHMTPP---------------AP 2085
             :   || |             ||||::|| | :
Db 1962 SY--HSSLRLSAHRLNSDSGHKSDTHRSGGRERGRSKERKHLLSPDVSRCNSEERGTQAD 2019

Qy 2086 CPGPEPNWGKGPPETRS-------SLE-----LDTELSWISGDLLPPGGQEEPSP 2129
             | |    | | |:      || ||     |||| ||:|| |||  |  ||: |
Db 2020 WESPERRQSRSPSEGRSQTPNRQGTGSLSESSIPSISDTSTPRRSRRQLPP----VPPKP 2075

Qy 2130 RDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLLDSGSQPHLGTDPSNLGGPLGPGPGS 2189
             ::  ||:::   ||||  || :|| |     |  |  ||| |  ::|:| |||||  ||
Db 2076 RPLLSYSSL--------MRHTGGISPPPDGSE--------------GGSPLASQAL 2109

Qy 2190 RPKKK-LSPPSITIDPPBSQGPRTP--PSPGICLRRRAPSSD 2228
            ||::  ||| |: ||| ||: | |   || |:|||| |: |
Db 2110 ESNSACLTESSNSLHPQOGQHFSPQHYISEPYIALHEDSHASD 2152
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Search completed: November 18, 2004, 13:35:23
Job time = 97.2671 secs

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Db  339 ----DKAEEVMLAEENKNSGTSALEVLRRATIKRSTEAMTRDSSDEHCVDISSVGTPLA 394
             ||: ::  ||: |||||| |  |::| |:  || |   ||||  :|| |::|   ||
Qy  656 KADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS 715

Db  395 RASIKSTKVDGASY-------FRHKE-------------- 413
            ||:||| || ||         |  :
Qy  716 LGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL 775

Qy  414 ----RLLRISIRHMVKSQVFTWIVLSVVALNTPACVAIVHHNQPWLTHLL 459
              |:|:|| || |: ||:|  || |  ::| | : |: :|: | | ||:
Db  776 EISNIVFTSLFALEMLLKLLVGPFGYIKNPYNIFDGVIVLSWELVGQ----QGGGL 830

Qy  460 YYAEFLFIGLFILLEMSLKMYGMGPRLYFHSSFNCFDFGVTVGSIFEVVWAIFRPGTSFGI 519
             | |||| || | :|:|||:   ||||| |  ||| || |:|| || |||| || |: ||
Db  831 SVLRTFFLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCK 890

Db  520 SVIRALRLLRIFPKITKYWASLRNIVVSIMSSMKSIISLLFLLFLFIVVFALLGMQLFGGR 579
            |:|| || || ||| ||: |:|:||| |:  ||| ||||||||| |:||||||| |||| |
Qy  891 FASERDGDTLPDRKNFDSLLWAIVTVFQILTQSDWNKYLYNGM-----ASTSSWAALYFI 945

Db  580 F-NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFI 635
              :|||     |||||| | ||:||||||| |||||: :|||  |  |  | | |||||
Qy  946 ALMTFGNVLFNLLVAILVEGF-QAEEISK----REDASGQLSCIQLFVDSQGQDANKSE 1000

Db  636 VLTIFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEEAFNQKHALQKAKEV-----SPM 689
            |:| |||  || |||||||||| |||||||||| |||:| ||| |:||:|      |
Qy 1001 SEPDFFGSPSLDGDGDRKKCIAL--------------------VSLGEHPE 1030

Db  690 SAPNM--PSIERDRRRHHMSMWEPRSSHLRERRRHHMSVWEQRTSQLRRHMQMSSQEA 747
                    |: ||||||||| |||  ||| ||||||||| ||| ||| ||:  | :
Qy 1031 LRKSLLPPLIIHTAATPMS---------LPKS-TSTGLGEALGPASRRTSSSGSAE 1076

Qy  748 LNKEEAPPMNPLNPLNPLSPLNPLNAHPSLYRRPRPIEGLALGLGLEKCEEERISRGGSL 807
               |  |  |  |    ||  ||         || | ||  || | |  ||| || ||
Db 1077 PGAAHEMKSPPSARRSPHS---------PW---------------SAASSWT 1104

Qy  808 KGDIGGLTSVLDNQRSPLSLGKREPPWLPRSCHGNCDPTQQETGGGETVVTFEDRARHRQ 867
            : | | | |:|:| || | |   | |  |  | |  |  ||| | ||   :|::| |||
Db 1105 SRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEERASPAGSDHRHRGSL 1164

Qy  868 SQRRSRHRRRVRTEGKESASASRSR---SASQERSLDEGVSIDGEKEHEPQSSHRSKEPT 923
            |:|||||||||||  |||||||||    || |||| | |:| || | |||||||||||
Db 1165 EREAKSSFDL--PDTLQVP---GL---------HRTASGRGSASEHQDCNGKSA 1204

Db  924 IHEEERTQDLRRTNSLMVPRGSGLVGALDEAETPLVQPQPELEVGKDAALTEQEAEGSSE 983
            |  ||| ||| || |:|  | | | ||||| | || | |||| |||||||| |||||||
Qy 1205 SGRLA-------RALRPDDPPL------------------SAASSWT 1219

Db  984 QALLADVQLLDVGRGLSQOSEPDLSCMTTNMDKATTESTSVTVAIPDVPLVDSTVVNISNK 1043
            |||||| ||||| |||| |||||||||||||||||| || |||| ||||||||| ||||
Qy 1220 -DGDDA-------DDEGNLSKGER---VRAWIRARLPACYLERDSWSAYIFPPQSRFRL 1267

Db 1044 TDGEASPLKEAETKEEEEVEVKKKQKKEKRETGKAMVPHS--------SMFIFSTNNPIRK 1096
            ||| |||| || ||||| | |||| ||| ||||||||||          |:||||||||
Qy 1268 LCHRIITHKMFDHVULVIIFLNCITTAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTV 1327

Db 1097 ACHYIVNLRYFEMCILLVIAASSIALAAEDPVLTNSERNKV-LRYFDYVFTGVFTFEMVI 1155
            | | |:| ||||| ||| || ||||||||||| |||||||  |||| |||||||||||
Qy 1328 KVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTL 1386

Db 1156 KMIDQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGRDIKTIKSLRVLRVL 1215
            ||||| ||| ||| |||| ||||| |||| | |||| ||| |||||||| ||||||||
Qy 1387 RPLRVISRAQGLKLVVETLMSSLKPIGNIVIICCAFFIFGILGVQLFKGKFPVC--QGE 1444

Db 1216 RPLKTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSK 1275
            ||| |:| | ||||||| ||||||| ||| :||||| |||| |||||||||| || ||
Qy 1445 DTRN-----TTNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLD 1497

Db 1276 DTEKECIGNYVDHEKNCKEVKGREWKRHEFHYDNIIWALLLTLFTVSTGEGWPVLQHSVD 1335
            || || ||| ||| | | |||| | ||| |||||| |||||||| | |||| |||| |
Qy 1498 AVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREE 1557

Db 1336 VTEEDRGPSRSNRMEMSIFYVVYFVVFPFFFVNIFVALIIITF------QEQGDKMMEE 1388
            | |||||| | | |||||||| || ||| |||| |||||||||      ||:||:| |
```

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                    GenCore version 5.1.6
      Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    November 18, 2004, 13:06:30 ; Search time 251.833 Seconds
                                          (without alignments)
                                5177.235 Million cell updates/sec

Title:          US-09-611-257A-37
Perfect score:  11904
Sequence:    1 MDEEEDGAGAEESGQPRSFM.........PKKDVLSLSGLSSDPADLDP 2266

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:       1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      UniProt 02:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                 SUMMARIES

                %       Query
Result          Match   Length  DB  ID
No.    Score                                Description
-----  -------  -----   ------  --  ------- -----------
  1 11815.5     99.3    2377     1  CCAG_HUMAN    O43497 homo sapien
  2 11133.5     93.5    2295     2  Q9WUT2        Q9wut2 mus musculu
  3 11111       93.3    2288     2  Q9WUB8        Q9wub8 rattus norv
  4 10945       91.9    2254     1  CCAG_RAT      O54898 rattus norv
  5 10945       91.9    2254     2  AAG35186      Aag35186 rattus no
  6 10913       91.7    2248     2  Q6PFV8        Q6pfv8 mus musculu
  7 10913       91.7    2248     2  AAH57399      Aah57399 mus muscu
  8  6573       55.2    1389     2  Q6ZPX4        Q6zpx4 mus musculu
  9  6573       55.2    1389     2  BAC98104      Bac98104 mus muscu
 10  6217.5     52.2    2359     1  CCAH_RAT      Q9eq60 rattus norv
 11  6210       52.2    2353     1  CCAH_HUMAN    O95180 homo sapien
 12  6176.5     51.9    2365     2  CCAH_MOUSE    O88427 mus musculu
 13  5496.5     46.2    2223     1  CCAI_HUMAN    Q9p0x4 homo sapien
 14  5383       40.6    1835     1  CCAI_RAT      Q9z0y8 rattus norv
 15  4836       40.6    1994     2  Q7Z6S8        Q7z6s8 homo sapien
 16  4200.5     35.3    1762     2  Q7PQV4        Q7pqv4 anopheles g
 17  4180       35.1    2893     2  Q9W433        Q9w433 drosophila
 18  3855       32.4    1837     2  Q967R4        Q967r4 caenorhabdi
 19  3845.5     32.3    1852     2  Q7Z002        Q7z002 caenorhabdi
 20  3845.5     32.2    1852     2  AAR25651      Aar25651 caenorhab
 21  3828.5     32.2    1844     2  Q7YZR6        Q7yzr6 caenorhabdi
 22  3828.5     32.2    1844     2  AAR25653      Aar25653 caenorhab
 23  3823       32.1    1885     2  Q7Z003        Q7z003 caenorhabdi
 24  3823       32.1    1885     2  AAR25652      Aar25652 caenorhab
 25  3683.5     30.9    1460     2  Q80TU2        Q80tj2 mus musculu
 26  2925.5     24.6    1418     2  Q7JPB4        Q7jpb4 caenorhabdi
 27  2925.5     24.6    1418     2  AAR30210      Aar30210 caenorha
 28  2866       24.1    1942     2  Q869H0        Q869h0 lymnaea sta
 29  2089       17.5    1211     2  Q8MQ95        Q8mq95 caenorhabdi
 30  1746.5     14.7    2339     1  CCAB_HUMAN    Q00975 homo sapien
 31  1740.5     14.6    2333     2  O89089        O89089 rattus norv
```

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 32  1732.5     14.6    2327     1  CCAB_MOUSE    O55017 mus musculu
 33  1729.5     14.5    2331     2  Q9TTA4        Q9tta4 bos taurus
 34  1722       14.5    2336     1  CCAB_RAT      Q02294 rattus norv
 35  1712.5     14.4    541      2  Q6PE92        Q6pe92 mus musculu
 36  1712.5     14.4    541      2  AAH58206      Aah58206 mus muscu
 37  1710       14.4    2339     1  CCAB_RABIT    Q05152 oryctolagus
 38  1697.5     14.3    2357     2  Q9PUM6        Q9pum6 gallus gall
 39  1697       14.3    2259     1  CCAE_RABIT    Q02343 oryctolagus
 40  1689       14.2    1810     2  O44930        O44930 aiptasia pa
 41  1688.5     14.2    2295     2  Q923K6        Q923k6 rattus norv
 42  1685       14.2    2346     2  Q9PW47        Q9pw47 gallus gall
 43  1683       14.1    2332     2  Q9PW45        Q9pw45 gallus gall
 44  1681       14.1    2272     1  CCAE_MOUSE    Q61290 mus musculu
 45  1666.5     14.0    2312     1  CCAE_HUMAN    Q15878 homo sapien
```

```
                                 ALIGNMENTS

RESULT 1
CCAG_HUMAN
ID   CCAG_HUMAN     STANDARD;      PRT;   2377 AA.
AC   O43497; O43498; O94770; Q9NYU4; Q9NYU6; Q9NYU7; Q9NYU8;
AC   Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;
AC   Q9Y5T3;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).
GN   Name=CACNA1G; Synonyms=KIAA1123;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
RC   TISSUE=Brain;
RX   MEDLINE=20014446; PubMed=10548410;
RA   Mittman S., Guo J., Agnew W.S.;
RT   "Structure and alternative splicing of the gene encoding alpha1G, a
RT   human brain T calcium channel alpha1 subunit.";
RL   Neurosci. Lett. 274:143-146(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=20115462; PubMed=10648811;
RA   Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;
RT   "Molecular cloning and functional expression of ca(v)3.1c, a T-type
RT   calcium channel from human brain.";
RL   FEBS Lett. 466:54-58(2000).
RN   [3]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
RC   TISSUE=Brain;
RX   MEDLINE=20158909; PubMed=10692398;
RA   Monteil A., Chemin J., Bourinet E., Mennessier G., Lory P.,
RA   Nargeot J.;
RT   "Molecular and functional properties of the human alpha1G subunit that
RT   forms T-type calcium channels.";
RL   J. Biol. Chem. 275:6090-6100(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 14).
RA   Kishi F.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).
RC   TISSUE=Brain;
RX   MEDLINE=22158633; PubMed=12168954;
RA   Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT   "Construction of expression-ready cDNA clones for KIAA genes: manual
RT   curation of 330 KIAA cDNA clones.";
RL   DNA Res. 9:99-106(2002).
RN   [6]
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RP   SEQUENCE OF 750-2377 FROM N.A. (ISOFORM 13).
RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA   Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 3), AND GENE STRUCTURE.
RC   TISSUE=Prostatic carcinoma;
RX   MEDLINE=99421245; PubMed=10493502;
RA   Toyota M., Ho C., Ohe-Toyota M., Baylin S.B., Issa J.-P.J.;
RT   "Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant
RT   methylation of its 5' CpG island in human tumors.";
RL   Cancer Res. 59:4535-4541(1999).
RN   [8]
RP   SEQUENCE OF 1126-1444, 1778-1927 AND 2021-2312 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98154730; PubMed=9495342;
RA   Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
RA   Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT   "Molecular characterization of a neuronal low-voltage-activated T-type
RT   calcium channel.";
RL   Nature 391:896-900(1998).
-!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC   entry of calcium ions into excitable cells and are also involved
CC   in a variety of calcium-dependent processes, including muscle
CC   contraction, hormone or neurotransmitter release, gene expression,
CC   cell motility, cell division and cell death. The isoform alpha-1G
CC   gives rise to T-type calcium currents. T-type calcium channels
CC   belong to the "low-voltage activated (LVA)" group and are strongly
CC   blocked by mibefradil. A particularity of this type of channels is
CC   an opening at quite negative potentials and a voltage-dependent
CC   inactivation. T-type channels serve pacemaking functions in both
CC   central neurons and cardiac nodal cells and support calcium
CC   signaling in secretory cells and vascular smooth muscle. They may
CC   also be involved in the modulation of firing patterns of neurons
CC   which is important for information processing as well as in cell
CC   growth processes.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=14;
CC   Comment=Additional isoforms seem to exist;
CC   Name=5;
CC     IsoId=O43497-1; Sequence=Displayed;
CC   Name=1;
CC     IsoId=O43497-2; Sequence=VSP_000940, VSP_000943, VSP_000946;
CC   Name=2;
CC     IsoId=O43497-3; Sequence=VSP_000940, VSP_000944, VSP_000946;
CC   Name=3;
CC     IsoId=O43497-4; Sequence=VSP_000940;
CC   Name=4;
CC     IsoId=O43497-5; Sequence=VSP_000940, VSP_000943, VSP_000946,
CC                             VSP_000948;
CC   Name=6;
CC     IsoId=O43497-6; Sequence=VSP_000943, VSP_000946;
CC   Name=7;
CC     IsoId=O43497-7; Sequence=VSP_000943, VSP_000947;
CC   Name=8;
CC     IsoId=O43497-8; Sequence=VSP_000940, VSP_000943, VSP_000947;
CC   Name=9;
CC     IsoId=O43497-9; Sequence=VSP_000940, VSP_000946;
CC   Name=10;
CC     IsoId=O43497-10; Sequence=VSP_000940, VSP_000945;
CC   Name=11;
CC     IsoId=O43497-11; Sequence=VSP_000946;
CC   Name=12;
CC     IsoId=O43497-12; Sequence=VSP_000947;
CC   Name=13;
CC     IsoId=O43497-13; Sequence=VSP_000944, VSP_000946;
CC   Name=14;
CC     IsoId=O43497-14; Sequence=VSP_000941, VSP_000942;
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CC   -!- TISSUE SPECIFICITY: Highly expressed in brain, in particular in
CC       the amygdala, subthalamic nuclei, cerebellum and thalamus.
CC       Moderate expression in heart; low expression in placenta, kidney
CC       and lung. Also expressed in colon and bone marrow and in tumoral
CC       cells to a lesser extent. Highly expressed in fetal brain, but
CC       also in peripheral fetal tissues as heart, kidney and lung,
CC       suggesting a developmentally regulated expression.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- DOMAIN: The linker region between repeat III and IV probably play
CC       a role in the inactivation of the channel. The C-terminal part may
CC       be implicated in the anchoring of the protein to the membrane,
CC       this by interfering/restricting its lateral diffusion.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF134986; AAF19347.1; -.
DR   EMBL; AF134985; AAF19346.1; -.
DR   EMBL; AF227744; AAF37689.1; -.
DR   EMBL; AF227745; AAF37690.1; -.
DR   EMBL; AF227746; AAF37691.1; -.
DR   EMBL; AF227747; AAF37692.1; -.
DR   EMBL; AF227748; AAF37693.1; -.
DR   EMBL; AF227749; AAF37694.1; -.
DR   EMBL; AF227750; AAF37695.1; -.
DR   EMBL; AF227751; AAF37696.1; -.
DR   EMBL; AF124351; AAD34352.1; -.
DR   EMBL; AB032949; BAA86437.2; -.
DR   EMBL; AB012043; BAA36409.1; -.
DR   EMBL; AF126965; AAD29400.1; -.
DR   EMBL; AF126966; AAD29401.1; -.
DR   EMBL; AF190860; AAF35287.1; -.
DR   EMBL; AF029228; AAD12731.1; -.
DR   EMBL; AF029229; AAD12732.1; -.
DR   Genew; HGNC:1394; CACNA1G.
DR   MIM; 604065; -.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.
DR   GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.
DR   GO; GO:0006810; P:transport; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Repeat; Transmembrane; Voltage-gated channel.
FT   REPEAT         68     398       I.
FT   REPEAT        729     967       II.
FT   REPEAT       1263    1540       III.
FT   REPEAT       1596    1854       IV.
FT   DOMAIN         81     101       S1 of repeat I (Potential).
FT   DOMAIN          1      80       Cytoplasmic (Potential).
FT   TRANSMEM      102     119       Extracellular (Potential).
FT   DOMAIN        120     141       S2 of repeat I (Potential).
FT   TRANSMEM      142     150       Cytoplasmic (Potential).
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FT   TRANSMEM    151    170     S3 of repeat I (Potential).
FT   DOMAIN      171    175     Extracellular (Potential).

Query Match           99.3%;    Score 11815.5;   DB 1;   Length 2377;
Best Local Similarity 95.2%;    Pred. No. 0;
Matches 2264;  Conservative 1;  Mismatches 1;  Indels 111;  Gaps 2;

Qy     1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV   60

Qy    61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVIILNCVTLGMFRPCEDIACDSQRCRIILQAF  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVIILNCVTLGMFRPCEDIACDSQRCRIILQAF  120

Qy   121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180

Qy   181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR  240

Qy   241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL  300

Qy   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360

Qy   361  YFVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  YFVMDAHSFYNFIYFILLIIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420

Qy   421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRGLLSSPAPLGGQETQPSS  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRGLLSSPAPLGGQETQPSS  480

Qy   481  SCSRSRHRLSVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  SCSRSRHRLSVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP  540

Qy   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600

Qy   601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG  660

Qy   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720

Qy   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780

Qy   781  VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQQGGGLSVLRTFRLMR  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQQGGGLSVLRTFRLMR  840

Qy   841  VLKLVRFLPQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  VLKLVRFLPQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL  900

Qy   901  PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  PDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960

Qy   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL  1020

Qy  1021  ALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  ALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA  1080

Qy  1081  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ  1140

Qy  1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN  1200

Qy  1201  GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACCLLERDSWSAYIFP  1260

Qy  1261  PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV  1320

Qy  1321  FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLRVL  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLISVIDILVSMVSDSGTKILGMLRVL  1380

Qy  1381  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGIIGVQLFKGKFFV  1440

Qy  1441  CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG  1500

Qy  1501  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  VDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRL  1560

Qy  1561  RRLEKKKR--------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGV  1602
          ||||||||              ||||||||||||||||||||||||||||||||||
Db  1561  RRLEKKKRRNLMLDDVIASGSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGV  1620

Qy  1603  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDL  1662
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  IGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDL  1680

Qy  1663  ATVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQAL  1722
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQAL  1740

Qy  1723  PQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST  1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  PQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVST  1800

Qy  1783  GDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE  1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE  1860

Qy  1843  AKEEAELEAELELEMKTLSPQHSPLGSFLWPGVEGPDSPSPKPGALHPAAHARSASH  1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  AKEEAELEAELELEMKTLSPQHSPLGSFLWPGVEGPDSPSPKPGALHPAAHARSASH  1920

Qy  1903  FSLEHPT-------  1909
          |||||||
Db  1921  FSLEHPTDRQLFDTISLLIQQSLEWELKMDELAGPGGQPSAFPSAPSLGGSDPQIPLAE  1980

Qy  1910  -----------------MQPHPTELPGDLLTVRKSG  1929
                           |||||||||||||||||||
Db  1981  MEALSLTSEIVSEPSCSLALTDDSLPDDMTLLLSALESNMQPHPTELPGDLLTVRKSG  2040

Qy  1930  VSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLLPKAQSGSVLSVHSQPADTSYILQLPKDAP  1989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  VSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLLPKAQSGSVLSVHSQPADTSYILQLPKDAP  2100
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Qy   1990  HLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPS  2049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  HLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPS  2160

Qy   2050  PPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTE  2109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  PPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTE  2220

Qy   2110  LSWISGDLLPPGGQEEPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQ  2169
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  LSWISGDLLPPGGQEEPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQ  2280

Qy   2170  PHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITITDPPESQGPRTPPSPGICLRRRAPSSDS  2229
           ||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||
Db   2281  PHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITITDPPESQGPRTPPSPGICLRRRAPSSDS  2340

Qy   2230  KDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP  2266
           ||||||||||||||||||||||||||||||||||||
Db   2341  KDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP  2377
```

RESULT 2

```
Q9WUT2
ID   Q9WUT2                PRELIMINARY;      PRT;    2295 AA.
AC   Q9WUT2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Voltage-gated calcium channel, alpha-1-G subunit.
GN   Name=Cacna1g;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99189326; PubMed=10087148;
RA   Klugbauer N., Marais E., Lacinova L., Hofmann F.;
RT   "A T-type calcium channel from mouse brain.";
RL   Pflugers Arch. 437:710-715(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
DR   EMBL; AJ012569; CAB40793.1; -.
DR   MGD; MGI:1201678; Cacna1g.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
SQ   SEQUENCE   2295 AA;  253957 MW;  FEB17D054ED269984 CRC64;
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Query Match   93.5%; Score 11133.5; DB 2; Length 2295;
Best Local Similarity   93.3%; Pred. No. 0;
Matches 2142; Conservative 32; Mismatches 91; Indels 31; Gaps 5;

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Qy     1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPCPGSAEKDPGSADSEAEGLPYPALAPVV  60
          ||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||
Db     1  MDEEEDGAGAEESGQPRSFTQLNDLSGAGRGRQSPGSTEKDPGSADSEAEGLPYPALAPVV  60

Qy    61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVIILNCVTLGMFRPCEDIACDSQRCRIILQAF  120
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    61  FFYLSQDSRPRSWCLRTVCNPWFERVSMIVIILNCVTLGMFRPCEDIACDSQRCRIILQAF  120
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Qy   121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR  180

Qy   181  TVRVLRPLAINRYPSMRILVTLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TVRVLRPLAINRYPSMRILVTLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR  240

Qy   241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCGL  300

Qy   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM  360

Qy   361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA  420

Qy   421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAVGVRAGLLSSPVARGGQEPQPSG  480

Qy   481  SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP  540
          ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db   481  SCSRSHRRLSVHHLVHHHHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRWLMLPPSTP  540

Qy   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPTVHTSPPPE  600
          |: |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVGSGKVYPFVHTSPPPE  600

Qy   601  TLKEKALVEVAASSGPPTLTSLNIPGPGYSSMHKLLETQSTGACQQSCKISSPCLKADSG  660
          :||:||||||||||||||||||||| |||:|||||||||||||| ||||||||||||||
Db   601  MLKDKALVEVAPSPGPPTLTTFNIPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG  660

Qy   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA  720
          ||||||||||||||||||||||||||||||||||||||||||||||| ||:|||||||||
Db   661  ACGPDSCPYCARTGAGEPESADHEMPDSDSEAVYEFTQDAQHSDLRDPHRRRPSLGPDA  720

Qy   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI  780

Qy   781  VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRIMR  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  VFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRIMR  840

Qy   841  VLKIVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDTL  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  VLKIVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFSILGMHLFGCKFASERDGDTL  900

Qy   901  PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV  960

Qy   961  AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEEPDFFSPSLDGDDRKKCL  1020
          ||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||||
Db   961  AILVEGFQAEEIGKREDTSGQLSCIQLPVNSQGGDATKSESEEPDFFSFSVDGDGDRKKRL  1020

Qy  1021  ALVSLGEHPELRKSLLPLIIHTAATPMSLPKSSTGLGEALGPASRRTSSSGSAEPGTA  1080
          || |||||||||||| ||||||||||||||||:|||||||| |||||||||||:||||||
Db  1021  ALVALGEHSELRKSLLPLIIHTAATPMSLPKSSTGVGEALGSGSRRTSSSGSAEHQDC  1080

Qy  1081  -HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQES  1139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  HHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQES  1140

Qy  1140  QDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSASEHQDC  1199
          |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  QDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSASEHQDC  1200
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Db        2280 ALSLSGLSSDPTDLDP 2295
               |||||||||| ||||
Db             2280 ALSLSGLSSDPTDLDP 2295

RESULT 3
Q9WUB8
ID   Q9WUB8;                   PRELIMINARY;      PRT;   2288 AA.
AC   Q9WUB8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   T-type calcium channel isoform.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=20081696; PubMed=10615950;
RA   Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
RA   Wu S., Berggren P.O., Li M.;
RT   "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
RT   cells.";
RL   Diabetes 49:59-64(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
DR   EMBL; AF125161; AAD26858.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
SQ   SEQUENCE   2288 AA;  253476 MW;  B89DBB5A1D81757F CRC64;

Query Match             93.3%;  Score 11111;  DB 2;  Length 2288;
Best Local Similarity   93.3%;  Pred. No. 0;
Matches 2135;  Conservative 35;  Mismatches 95;  Indels 24;  Gaps 5;
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Qy    1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MDEEEDGAGAEESGQPRSFTQLNDLSGAGRPGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
         |||||||||||||||||||||||||::||||||||||||||||||||||||||||||||
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy  121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy  181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy  241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
         ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL 300

Qy  301 DYEAYNSSSNTTCVWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
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Qy    1200 NGKSASGRLARALRPDDPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIF 1259
            |||||||||||||||      |||||||||||||||    ||||||||||||||||||
Db    1201 NGKSASGRLARTLRADDPPLDGDGDGDDEGNLSKGERLRAWVRARLPACCRERDSWSAYIF 1260

Qy    1260 PPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1319
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 PPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1320

Qy    1320 VFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRV 1379
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 VFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRV 1380

Qy    1380 LRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFF 1439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 LRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFF 1440

Qy    1440 VCQGEDTRNITNKSDCAEASYRWVRHKXNFDNLGQALMSLFVLASKDGWVDIMYDGLDAV 1499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 VCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAV 1500

Qy    1500 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMVGVVVENFHKCRQHQEEEARRREEKR 1559
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMVGVVVENFHKCRQHQEEEARRREEKR 1560

Qy    1560 LRRLEKKRR-------------------------KAQCKPYYSDYSRFRLLVHHLCTSHY 1594
            |||||||||                         :  |||||||||||||||||||||||
Db    1561 LKRLEKKRRSSKEKQMADLMLDDVIASGSSASAAASEAQCKPYYSDYSRFRLLVHHLCTSHY 1620

Qy    1595 LDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQ 1654
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 LDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQ 1680

Qy    1655 DRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAL 1714
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 DRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAL 1740

Qy    1715 LDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLLECDETHPCEGLGRHATFRNFGMAF 1774
            :|||||||||||||||||||||||||||:|||::|||||||||||||||||||||||||
Db    1741 LDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLLECDETHPCEGLGRHATFRNFGMAF 1800

Qy    1775 LTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMK 1834
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 LTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMK 1860

Qy    1835 HLEESNKEAKEAELEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGPDSPDSPKPGALHPA 1894
            |||||||||||||||||||||||||||||||||||||||||::|||| |||:|||:|||
Db    1861 HLEESNKEAKEAELEAELEAELELEMKTISPQHSPLGSPFLWPGVEGVNSPDSPKPGAPHTT 1920

Qy    1895 AHARSASH-FSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAE 1950
            ||:|:|:   ||||| | |:|  ||   ||||||||||||||||||||||||:||||||
Db    1921 AHIGAASSGFSLEHPTMVPHTEEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAE 1980

Qy    1951 GPLGHRGWGLPKAQSGSSVLSVHSQPADTSYLQLPKDAPHLLQPHSAPTWGTIPKLPPPG 2010
            |||:||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    1981 RSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTWGAIPKLPPPG 2040

Qy    2011 RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPLARAYSFWGQSSTQAQQHS 2070
            |||||||||||||||||||||||||||||||||||:|||||||||||||||:||||||
Db    2041 RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRS 2100

Qy    2071 RSHSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPR 2130
            |:|| :|:       | | ||||||||:::||||||:|||||||||||||:|:|||||||
Db    2101 GSQSKVSKHIRLPAPCPGLEPSWAXDPQETRSSLELDTELSWISGDLL-PSSQEEPLSPR 2159

Qy    2131 DLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSR 2190
            ||||||||||||| ||:|||||:|||||||||||||||||||:||:||||||||||||||
Db    2160 DLKKCYSVEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSR 2219

Qy    2191 PKKKLSPPSITIDDPPESQGPRTPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKD 2250
            ||||||||||:||||||||||  :|||||:|||||||||||||:|||:||||||||||||
Db    2220 PKKKLSPPSISIDDPPESQGPRPPCSPGVCLRRRAPASDSKDPSASSPLDSTAASPSPKKD 2279

Qy    2251 VLSLSGLSSDPADLDP 2266
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Db   301 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| DYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
Qy   361 YFVMDAHSFYNFYFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 YFVMDAHSFYNFYFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
Qy   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
         |||||||||||||||||||||||||||||| || | || || ||| : | | :
Db   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG 480
Qy   481 SCSRSHRRLSVHHLVHHHHHHHYHLGNGTLRAPRASPEIQRDANGSRRLMLPPPSTP 540
         || :|||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   481 SCTRSHRRLSVHHLVHHHHHHHYHLGNGTLRVPRASPEIQRDANGSRRLMLPPPSTP 540
Qy   541 ALSGAPPGGAESVHSFYHADCHLEPVRCCAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
         : | || |||||||||||||||||||| |||||| ||||||||||||||||||||||||
Db   541 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPE 600
Qy   601 TLKEKALVEVAASSGPPTLTSLNIIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
         :|:||||||||| | ||||||| ||||||:||||||||||||||| ||||||||| |||||
Db   601 ILKDKALVEVAPSPGPPTLTSFNIIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 660
Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RQQRSLGPD 719
         ||||||||||| ||||| || :|||||||||||||||||||||||||| | ||||||||
Db   661 ACGPDSCPYCCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPD 720
Qy   720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPELTNALEISN 779
         |||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db   721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISN 780
Qy   780 IVFTSLFALEMLLKLLVYGFPGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLM 839
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 IVFTSLFALEMLLKLLVYGFPGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLM 840
Qy   840 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 899
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 900
Qy   900 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 960
Qy   960 VAILVEGFQAEEISKKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGDRKKC 1019
         |||||||||||||| ||||||||||||||||::|| | ||:|||||||||::||||||||
Db   961 VAILVEGFQAEEIGKREDASGQLSCIQLPVNSQGGDATKSSESEPDFFSPSVDGDGDRKKR 1020
Qy 1020 LALVSLGEHPELRKSLLPPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
         ||||:|||| |||||||||||||||||||||||||:||:||||| |:|||||||||||||||
Db 1021 LALVALGEHAELRKSLLPPLLIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGA 1080
Qy 1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
         | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 AHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1140
Qy 1139 SQDEEESSEEERRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD 1198
         ||||||||||: |||||||||||||||||||||||||||||||||||||||||| ||||||
Db 1141 SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD 1200
Qy 1199 CNGKSASGRLARALRPDDFPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
         |||||||||||: ||.|| || |||::|||||||||::| :||:|||| | ||||||||||
Db 1201 CNGKSASGRLARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1260
Qy 1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNVIFT 1318
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNVIFT 1320
Qy 1319 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLR 1378
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLR 1380
Qy 1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438

Db 1381 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1439 FVCCGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 FVCCGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1500
Qy 1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMPVGVVVENFHKCRQHQEEEARRREEK 1558
         |||||||||||||||||||||||||||||||||.|||||||||||||||||||||||||||
Db 1501 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEEARRREEK 1560
Qy 1559 RLRRLEKKR----------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT 1600
         ||||||||| |||||||||||||||||||||||||||||||||
Db 1561 RLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT 1620
Qy 1601 GVIGLNVVIMAMEHYQQPQLLDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQL 1660
         |||||||||||||||||||||||||||||||||||||.||||||||||||||||||||||||
Db 1621 GVIGLNVVIMAMEHYQQPQLLDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQL 1680
Qy 1661 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ 1720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ 1740
Qy 1721 ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1800
Qy 1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN 1840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN 1860
Qy 1841 KEAKEEAELEAELEMKTLSPQPHSPLGSPFLWPGVEGPDSPKPGALHPAAHARSA 1900
         ||||||||||||||||||||||||||||||||||||||.|||||||| || |: | :|
Db 1861 KEAKEEAELEAELEMKTLSPQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAA 1920
Qy 1901 SHFSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
         |.|||||||| ||| |:| |||||||||||||||||||||||||||:||||| :|||||
Db 1921 SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRG 1980
Qy 1958 WGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQR 2017
         |||||||||| :|||||||||| ||||||||.| |||||.|||| |||||||||||||||||
Db 1981 WGLPKAQSGSIISVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR 2040
Qy 2018 PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKIS 2077
         |||||||||||||||||||||||||:|||||| |.|||||| |.||:|.|||.|| || |
Db 2041 PLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVS 2100
Qy 2078 KHMTPPAPCPCGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRDLKKCYS 2137
         ||: | || || |||.|||.|||||||||||||||||||||||.||||| ||||||||||
Db 2101 KHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLL-PSSQEEPLSPRDLKKCYS 2159
Qy 2138 VEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP 2197
         ||:|||:||| ||||||||||||||||||||||: | ||:||||||||||||||||||||||
Db 2160 VETQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSSSLGGQPLGGPGSRPKKKLSP 2219
Qy 2198 PSITIDDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL 2257
         |||:||||||||| || | |||||||||:||||||| ||||:| || ||||||||||||
Db 2220 PSISIDDPPESQGSRPPCCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGL 2279
Qy 2258 SSDPADLDP 2266
         ||||:| |||
Db 2280 SSDPTDMDP 2288

RESULT 4
CCAG_RAT
ID   CCAG_RAT   STANDARD;   PRT;   2254 AA.
AC   O54898;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1G subunit (voltage-
DE   gated calcium channel alpha subunit Cav3.1).
GN   Name=Cacna1g;

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OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=98154730; PubMed=9495342;
RA   Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
RA   Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT   "Molecular characterization of a neuronal low-voltage-activated T-type
RT   calcium channel.";
RL   Nature 391:896-900(1998).
-!-  FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1G
CC       gives rise to the "T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials and a voltage-
CC       dependent inactivation. T-type channels serve pacemaking functions
CC       in both central neurons and cardiac nodal cells and support
CC       calcium signaling in secretory cells and vascular smooth muscle.
CC       They may also be involved in the modulation of firing patterns of
CC       neurons which is important for information processing as well as
CC       in cell growth processes.
-!-  SUBCELLULAR LOCATION: Integral membrane protein.
-!-  TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression
CC       in heart; low expression in placenta, kidney and lung.
-!-  DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
-!-  PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
-!-  SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
--------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
--------------------------------------------------------------------------
DR   EMBL; AF027984; AAC67372.1; -.
DR   PIR; T09053; T09053.
DR   RGD; 68942; Cacna1g.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M-channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW   Ionic channel; Multigene family; Phosphorylation; Repeat;
KW   Transmembrane; Voltage-gated channel.
FT   REPEAT        68     398       I.
FT   REPEAT       730     968       II.
FT   REPEAT      1242    1519       III.
FT   REPEAT      1564    1822       IV.
FT   DOMAIN         1      80       Cytoplasmic (Potential).
FT   TRANSMEM      81     101       S1 of repeat I.
FT   DOMAIN       102     119       Extracellular (Potential).
FT   TRANSMEM     120     141       S2 of repeat I (Potential).
FT   DOMAIN       142     150       Cytoplasmic (Potential).
FT   TRANSMEM     151     170       S3 of repeat I.
FT   DOMAIN       171     175       Extracellular (Potential).
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FT   TRANSMEM     176     193       S4 of repeat I.
FT   DOMAIN       194     213       Cytoplasmic (Potential).
FT   TRANSMEM     214     234       S5 of repeat I (Potential).
FT   DOMAIN       235     370       Extracellular (Potential).
FT   TRANSMEM     371     395       S6 of repeat I.
FT   DOMAIN       396     744       Cytoplasmic (Potential).
FT   TRANSMEM     745     765       S1 of repeat II (Potential).
FT   DOMAIN       766     778       Extracellular (Potential).
FT   TRANSMEM     779     800       S2 of repeat II (Potential).
FT   DOMAIN       801     806       Cytoplasmic (Potential).
FT   TRANSMEM     807     825       S3 of repeat II (Potential).
FT   DOMAIN       826     833       Extracellular (Potential).
FT   TRANSMEM     834     857       S4 of repeat II (Potential).
FT   DOMAIN       858     868       Cytoplasmic (Potential).
FT   TRANSMEM     869     889       S5 of repeat II (Potential).
FT   DOMAIN       890     940       Extracellular (Potential).
FT   TRANSMEM     941     965       S6 of repeat II (Potential).
FT   DOMAIN       966    1251       Cytoplasmic (Potential).
FT   TRANSMEM    1252    1274       S1 of repeat III (Potential).
FT   DOMAIN      1275    1292       Extracellular (Potential).
FT   TRANSMEM    1293    1313       S2 of repeat III (Potential).
FT   DOMAIN      1314    1323       Cytoplasmic (Potential).
FT   TRANSMEM    1324    1343       S3 of repeat III (Potential).
FT   DOMAIN      1344    1357       Extracellular (Potential).
FT   TRANSMEM    1358    1379       S4 of repeat III (Potential).
FT   DOMAIN      1380    1389       Cytoplasmic (Potential).
FT   TRANSMEM    1390    1413       S5 of repeat III (Potential).
FT   DOMAIN      1414    1490       Extracellular (Potential).
FT   TRANSMEM    1491    1516       S6 of repeat III (Potential).
FT   DOMAIN      1517    1578       Cytoplasmic (Potential).
FT   TRANSMEM    1579    1599       S1 of repeat IV (Potential).
FT   DOMAIN      1600    1613       Extracellular (Potential).
FT   TRANSMEM    1614    1635       S2 of repeat IV (Potential).
FT   DOMAIN      1636    1642       Cytoplasmic (Potential).
FT   TRANSMEM    1643    1661       S3 of repeat IV (Potential).
FT   DOMAIN      1662    1675       Extracellular (Potential).
FT   TRANSMEM    1676    1699       S4 of repeat IV (Potential).
FT   DOMAIN      1700    1713       Cytoplasmic (Potential).
FT   TRANSMEM    1714    1734       S5 of repeat IV (Potential).
FT   DOMAIN      1735    1794       Extracellular (Potential).
FT   TRANSMEM    1795    1822       S6 of repeat IV (Potential).
FT   DOMAIN      1823    2254       Cytoplasmic (Potential).
FT   DOMAIN       290     295       Poly-His.
FT   DOMAIN       496     506       Poly-Gly.
FT   DOMAIN      1527    1530       Poly-Glu.
FT   SITE         354     354       Calcium ion selectivity and permeability
FT                                  (By similarity).
FT   SITE         924     924       Calcium ion selectivity and permeability
FT                                  (By similarity).
FT   SITE        1465    1465       Calcium ion selectivity and permeability
FT                                  (By similarity).
FT   SITE        1770    1770       Calcium ion selectivity and permeability
FT                                  (By similarity).
FT   CARBOHYD     173     173       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     246     246       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     306     306       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     310     310       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     322     322       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    1427    1427       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    1430    1430       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    1666    1666       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   2254 AA;  250405 MW;  697BBE0636OCF0F6 CRC64;
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Query Match             91.9%;  Score 10945;  DB 1;  Length 2254;
Best Local Similarity   92.5%;  Pred. No. 0;
Matches 2107;  Conservative  34;  Mismatches 101;  Indels 36;  Gaps  6;

Qy      1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
            ||||||||||||||||||  ||| |||:| ||||| |:|||||||||||||||||||||
Db      1 MDEEEDGAGAEESGQPRSFTQLNDLSGAGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
           |||||||||||   |||||||||||||||||   ||||||||       |||    ||||
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Qy  1199 CNGKSASGRLIARALRLPDDPPLDGDDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
Db  1178 CNGKSASGRLIARTLRTDDPQLDGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1237

Qy  1259 FPPQSRFRLLCHRIITHKMFDHVVLIVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db  1238 FPPQSRFRLLCHRIITHKMFDHVVLIVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297

Qy  1319 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1378
Db  1298 AVFLAEMTVKVVALGWCFGQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1357

Qy  1379 VLRLLRTLRPLRVISRAQGLKLVVETIMSSLKPIGNIVICCAFFIIFGILGVQLFKGKF 1438
Db  1358 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVICCAFFIIFGILGVQLFKGKF 1417

Qy  1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
Db  1418 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1477

Qy  1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK 1558
Db  1478 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK 1537

Qy  1559 RLRRLEKKR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1611
Db  1538 RLRRLEKKRRSREKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1597

Qy  1612 MEHYQQPQILDEALKICNYIFTVIFVFVFESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG 1671
Db  1598 MEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMG 1657

Qy  1672 ITLBEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLL 1731
Db  1658 ITLBEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLL 1717

Qy  1732 FMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791
Db  1718 FMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1777

Qy  1792 DTLRDCDQESTCYNTVISPIYFVSFVITAQFVLVNVVIAVLMKHLEESNKEAKEEAELEA 1851
Db  1778 DTLRDCDQESTCYNTVISPIYFVSFVITAQFVLVNVVIAVLMKHLEESNKEAKEEAELEA 1837

Qy  1852 ELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQ 1911
Db  1838 ELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV 1897

Qy  1912 PHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSV 1968
Db  1898 PHPEEVPVLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI 1957

Qy  1969 LSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTD 2028
Db  1958 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD 2017

Qy  2029 SLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKLSKHMTPPAPCPG 2088
Db  2018 SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVVQRSGIQSKVSKHIRLPAPCPG 2077

Qy  2089 PEPNWGKGPPETRSSLELDTELSWISGDLLPPGQEEPPSPRDLKKCYSVEAQSCQRRPT 2148
Db  2078 LEPSWAKDPPETRSSLELDTELSWISGDLL--PSSQEEPIFPRDLKKCYSVETQSCRRRPG 2136

Qy  2149 SWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPSGSRPKKKLSPPSIITIDPPESQ 2208
Db  2137 FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPSGSRPKKKLSPPSISIDPPESQ 2196

Qy  2209 GPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAAASPSPKKDVLSLSGLSSDPADLDP 2266
Db  2197 GSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2254


Db   61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAF 120

Qy  121 DDFIFAFFAVEMVVKMVALGIFGKKCYIGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
Db  121 DDFIFAFFAVEMVVKMVALGIFGKKCYIGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy  181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
Db  181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy  241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
Db  241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCSL 300

Qy  301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLLEGWVDIM 360
Db  301 DYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLLEGWVDIM 360

Qy  361 YFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
Db  361 YFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy  421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
Db  421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEPQPSG 480

Qy  481 SCSRSHRRLSVHHLVHHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
Db  481 SCTRSHRRLSVHHLVHHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy  541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
Db  541 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy  601 TLKEKAIVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db  601 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 660

Qy  661 ACGPDSCPYCARAGAGEVELADAREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSLGPD 719
Db  661 ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 720

Qy  720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISN 779
Db  721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISN 780

Qy  780 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLM 839
Db  781 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLM 840

Qy  840 RVLKLVRFLPALQRQLVLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 899
Db  841 RVLKLVRFLPALQRQLVLVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDT 900

Qy  900 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959
Db  901 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 960

Qy  960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSRSEPDFFSPSLDGDGDRKKC 1019
Db  961 VAILVEGFQAE------------GDATKSESSEPDFFSPSVDGDGDRKKR 997

Qy 1020 LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEAIGPASRRTSSSGSAEPGA 1079
Db  998 LAIVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGRRTSSSGSAEPGA 1057

Qy 1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPGSERRSLLSGEGQE 1138
Db 1058 AHHEMKCCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPGSERRSLLSGEGQE 1117

Qy 1139 SQDEERSSEEERASPAGSDHRHRGSLERRAKSSFDLPDTLQVPGLHRTASGRGSASEHQD 1198
Db 1118 SQDEEESSEEDRASPAGSDHRHRGSLERRAKSSFDLPDTLQVPGLHRTASGRSSASEHQD 1177
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RESULT 5
AAG35186
ID   AAG35186;            PRELIMINARY;       PRT;   2254 AA.
AC   AAG35186;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Calcium channel alpha-1-G subunit.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=brain;
RX   PubMed=11073957;
RA   McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA   Baillie D.L., Stea A., Snutch T.P.;
RT   "Molecular and functional characterization of a family of rat brain T-
RT   type calcium channels.";
RL   J. Biol. Chem. 276:3999-4011(2001).
DR   EMBL; AF290212; AAG35186.2; -.
SQ   SEQUENCE   2254 AA;  250405 MW;  697BBE06360CF0F6 CRC64;

Query Match             91.9%;  Score 10945;  DB 2;  Length 2254;
Best Local Similarity   92.5%;  Pred. No. 0;
Matches 2107;  Conservative   34;  Mismatches 101;  Indels 36;  Gaps   6;

Qy      1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAAKDPGSADSEAEGLPYPALAPVV 60
            |||||||||||||||||||||||| |||||||  |||| ||||||||||||||||||||
Db      1 MDEEEDGAGAEESGQPRSFTQNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy     61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMRFPCEDIACDSQRCRIIQAF 120
            |||||||||||||||| ||||||||| || |||||||||| |||||||||||||||||||
Db     61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMRFPCEDIACDSQRCRIIQAF 120

Qy    121 DDFIFAFFAVEMVVKMVVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DDFIFAFFAVEMVVKMVVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy    181 TVRVLRPLRAINRVPSMRIILVTLLDDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    181 TVRVLRPLRAINRVPSMRIILVTLLDDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy    241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGBGGGGPPCSL 300

Qy    301 DYEAYNSSSNNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
            |||  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DYETYNSSSNNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy    361 YFVMDAHSFYNFIYFLLLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YFVMDAHSFYNFIYFLLLIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
            ||||||||||||||||||||||||||||||||||| |||||||||| |||| |||| |||
Db    421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQPQPSG 480

Qy    481 SCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
            | |||||||||||||||||||||||||| |||||||||| |||||||||||||||||||
Db    481 SCTRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy    541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKYPTVHTSPPPE 600
            | |||| ||||||||||||||||||| ||||||||||||||||||||| |||||| |||
Db    541 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKYPTVHTSPPPE 600

Qy    601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSSPCLKADSG 660
            |||||||||| | |||| || ||||| ||||||||||||||| ||||||||||| |||||
Db    601 ILKDKALVEVAPSPGPPTLTSFNIPPGPFSSMKLLETQSTGACHSSCKISSPCSKADSG 660

Qy   1732 FMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791
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Qy    661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVEFTQDAQHSDLRDPHS-RRQRSLGPD 719
            ||||||||||  || || || || |||||||| ||||||||||||||||  |||| |||
Db    661 ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVEFTQDAQHSDLRDPHSRRRQRSLGPD 720

Qy    720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISN 779
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISN 780

Qy    780 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLM 839
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    781 IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLM 840

Qy    840 RVLKLVRFLPALQRLVVLMKTMNVATFCMLMLFIFIFSILGMHLFGCKFASERDGDT 899
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    841 RVLKLVRFLPALQRLVVLMKTMNVATFCMLMLFIFIFSILGMHLFGCKFASERDGDT 900

Qy    900 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 960

Qy    960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC 1019
            |||||||||||                            ||||||||||| || |||| |
Db    961 VAILVEGFQAE------------------------------GDATKSESEPDFFSPSVDGDGDRKKR 997

Qy   1020 LAIVSLGEHPELRKSLLPPLIIHTAATEMSLPKSTSTGLGEAIGPASRRTSSSGSAEPGA 1079
            ||| | || ||||||||||||||||||||| ||  |||| || |||| ||| |||||||
Db    998 LAIVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEAIGSGRRTSPSGERRSLLSGEGE 1057

Qy   1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGE 1138
            | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 AAHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGE 1117

Qy   1139 SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD 1198
            |||||||||||||||||||||||||||||||||||||||||||||||| ||| || |||
Db   1118 SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD 1177

Qy   1199 CNGKSASGRLARALRPDDPPLGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
            ||||||||||  |||  ||| |||| | ||||||  | || |  |||  |||||| |||||
Db   1178 CNGKSASGRLARTLRTDDPQLGDGDDDNDEGNLSKGERIQAWTVRSRLPACCRERDSWSAYI 1237

Qy   1259 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297

Qy   1319 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLR 1378
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1298 AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLR 1357

Qy   1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
            ||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db   1358 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417

Qy   1439 FVCQGEDTRNITNKSDCAEASYRWRWHKCRQHQEEEARRREEK 1498
            ||||||||||||||||| ||||||||||||||||| |||||||
Db   1418 FVCQGEDTRNITNKSDCAEASYRWRWHKCRQHQEEEARRREEK 1477

Qy   1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGGVVENFHKCRQHQEEEARRREEK 1558
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGGVVENFHKCRQHQEEEARRREEK 1537

Qy   1559 RLRRLEKKR------KACKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1611
            |||||        :||::  |:||||||||||||||||||||||||||||||||||
Db   1538 RLRRLEKKRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMA 1597

Qy   1612 MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDIAIVLLSIMG 1671
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1598 MEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDIAIVLLSIMG 1657

Qy   1672 ITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLL 1731
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 ITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNLGLL 1717
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Db   1718  FMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK  1777
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1792  DTLRDCDQESTCVNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEA  1851
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778  DTLRDCDQESTCVNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEA  1837

Qy   1852  ELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQ  1911
           |||||||||||||||||||||||| :| :::|||||||||||  :|:|||||||||||||
Db   1838  ELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV  1897

Qy   1912  PHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCREGSTAEGPLGHRGWGLPKAQSGSV  1968
           || |:|     |||||||||||||||||||||||||  ||| | | ||||||||||||:|
Db   1898  PHPEVPVPLGPDILLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSI  1957

Qy   1969  LSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTD  2028
           |||||||||||:|||||||||||||||:|||| ||||||||||||||||||||||||||
Db   1958  LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTD  2017

Qy   2029  SLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTOAQHSRSHSKISKHMTPPAPCPG  2088
           |||||||||||||:|:|||||||||::||||||:|::||:||||||||:|||:||||:|
Db   2018  SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPG  2077

Qy   2089  PEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPI  2148
           |||:|:|  ||||||||||||||||||||||  :  ::|||||||||||:|::||||| |
Db   2078  LEPSWAKDPPETRSSLELDTELSWISGDLL-PSSOEEPLFPRDLKKCYSVETQSCRRRPG  2136

Qy   2149  SWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQ  2208
           :||||||||||||||||||||||||||:||||||||||||||||||||||:|||||||||
Db   2137  FWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPPESQ  2196

Qy   2209  GPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLLSSDPADLDP  2266
           | | |||||:||||||| ||||||| |  ||  ||:|||||  | ||| |||||  ||
Db   2197  GSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLLSSDPTDMDP  2254

Query Match                    91.7%;   Score 10913;   DB 2;   Length 2248;
Best Local Similarity         92.0%;    Pred. No. 0;
Matches 2106;  Conservative   30; Mismatches  89; Indels  64; Gaps    7;

Qy     1  MDEEEDGAGAEESGQPRSFMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MDEEEDGAGAEESGQPRSFTQLNDLSGAGRQGPGSTEKDPGSADSEAEGLPYPALAPVV    60

Qy    61  FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRIILQAF   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMERPCEDIACDSQRCRIILQAF   120

Qy   121  DDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR   180

Qy   181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR   240

Qy   241  CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPCGL   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGQPCGL   300

Qy   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM   360

Qy   361  YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATCFSETKQRESQLMREQRVRFLSNA   420
          |||||||||||||||||| ||||||||
Db   361  YFVMDAHSFYNFIYFILLII--------------FSETKQRESQLMREQRVRFLSNA   403

Qy   421  STIASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   404  STIASFSEPGSCYEELLKYLVVILRKAARRLAQVSRAVGVRAGLLSSPVVRGGQEPQPSG   463

Qy   481  SCSRSHRRLSVHHLVHHHHHHYHLGNGTLRAPRASPEIQRDANGSRRLMLPPPSTP   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464  SCSRSHRRLSVHHLVHHHHHHYHLGNGTLRVPRASPEIQRDANGSRWLMLPPPSTP   523

Qy   541  ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524  TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE   583

Qy   601  TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   584  MLKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG   643

Qy   661  ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA   720
          |||||||||||||||| || ||||| | | | ||||||||||||:||||||||:||||||
Db   644  ACGPDSCPYCARTGAGEPESADHEMPDSDSEAVYEFTQDAQHSDLRDPHRRRRPSLGPDA   703

Qy   721  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNI   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   704  EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNI   763
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RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC057399; AAH57399.1; -.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M-channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE 2248 AA; 248888 MW; 332C5A8D9115A64F CRC64;

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RESULT 6
Q6PV8
ID   Q6PV8               PRELIMINARY;   PRT;   2248 AA.
AC   Q6PV8;
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DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cacnalg protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]

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Qy   781 VFTSLFALEMLLKLLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQOGGLSVLRTFRLMR 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   764 VFTSLFALEMLLKLLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQOGGLSVLRTFRLMR 823

Qy   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   824 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 883

Qy   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   884 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 943

Qy   961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
                ::|||||                  :|||||||||| ||||||||| |
Db   944 -------GDATKSESEPDFFSPSVDGDGDRKKRL 980

Qy  1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
         |||:||||:|||||||||||||||||||||||| :|||:|||: ||||||||||||||:|
Db   981 ALVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGTA 1040

Qy  1081 -HEMKSPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPSGERRSLLSGEGQES 1139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041 HHEMKSPPSARSSPHSPWSAASSWTSRRSSRRNSLGRAPSLKRRSPSGERRSLLSGEGQES 1100

Qy  1140 QDEEESSEEERASPAGSDHRHRGSLEREEAKSSFDLPDTLQVPGLHRTASGRGSASEHQDC 1199
         |||||||||:|||||||||||||||||||||||||||||||||||||||||||:|||||||
Db  1101 QDEEESSEEDRASPAGSDHRHRGSLEREEAKSSFDLPDTLQVPGLHRTASGRSSASEHQDC 1160

Qy  1200 NGKSASGRLAARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIF 1259
         ||||||||||:|||:|||||||||: ||||||||||| | ||:||||||  ||||||||||
Db  1161 NGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLLRAWVRARLPACCRERDSWSAYIF 1220

Qy  1260 PPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1221 PPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1280

Qy  1320 VFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRV 1379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1281 VFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRV 1340

Qy  1380 LRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGILGVQLFKGKFF 1439
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341 LRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGILGVQLFKGKFF 1400

Qy  1440 VCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQAIMSLFVLASKDGWVDIMYDGLDAV 1499
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1401 VCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQAIMSLFVLASKDGWVDIMYDGLDAV 1460

Qy  1500 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKR 1559
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1461 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKR 1520

Qy  1560 ----------KAQCKPYYSDYSRPFLLVHHLCTSHYLDLFITG 1601
                 :|| |:|||||||||||||||||||||||||||||||
Db  1521 LKRLEKKRRNLMLDDVIASGGSASAASEAQCKPYYSDYSRPFLLVHHLCTSHYLDLFITG 1580

Qy  1602 VIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFLESVFKLIARVLRIARVLKLLKM 1661
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1581 VIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFLESVFKLIARVLRIARVLKLLKM 1640

Qy  1662 LAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIARVLKLLKMAVGMRALLDTVMQA 1721
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1641 LAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIARVLKLLKMAVGMRALLDTVMQA 1700

Qy  1722 LPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVS 1781
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1701 LPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVS 1760

Qy  1782 TGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNK 1841
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1761 TGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNK 1820

Qy  1842 EAKEEAELAELAELEMKTLSPQHHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSAS 1901
         |||||||||||||||||||||||||||||||||||||:|||||||||||  |:| :||:|
Db  1821 EAKEEAELAELAELEMKTLSPQHHSPLGSPFLWPGVEGVNSPDSPKPGAPHTAHIGAAS 1880

Qy  1902 H-FSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
           |||||||:  ||  |     |||||||||||||||||||||||||||:||||: ||||
Db  1881 SGFSLEHPIMVPHTEEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRG 1940

Qy  1958 WGLPKAQGSGVLSVHSQPADTSYIIQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQR 2017
         ||||||||||:|||||||||||  |||||||:|||||| |||| |||||||||||||||||
Db  1941 WGLPKAQGSGILSVHSQPADTSCIIQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPLAQR 2000

Qy  2018 PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKIS 2077
         ||||||||||||||||||||||||||:||||| ||:|  |||| ||||||:| |:|||:|
Db  2001 PLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQRSGGSQSKVS 2060

Qy  2078 KHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPSPSRDLKKCYS 2137
         ||: | ||||| |||  |: |||||||||||||||||||| ||  |:|||||||||||||
Db  2061 KHIRLPAPCPGLEPSWAKDPQETRSSLELDTELSWISGDLL-PSSQEEPLSPRDLKKCYS 2119

Qy  2138 VEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP 2197
         ||||||:|||:||||||||||||||||||||||:| ||:||||||||||||||||||||||
Db  2120 VEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP 2179

Qy  2198 PSTTIDPPESQGRPTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL 2257
         ||: ||||||||||  | ||:||||||| |||||| ||||  | |||||||||| |||||
Db  2180 PSISIDPPESQGRPRPCSPGVCLRRRAPASDSKDPSASSPLDSTAASPSPKKDALSLSGL 2239

Qy  2258 SSDPADLDP 2266
         |||| ||||
Db  2240 SSDPTDLDP 2248
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RESULT 7
AAH57399
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ID   AAH57399;    PRELIMINARY;     PRT;   2248 AA.
AC   AAH57399;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cacna1g protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; BC057399; AAH57399.1; -.
SQ   SEQUENCE   2248 AA;  248888 MW;  332C5A8D9115A64F CRC64;

Query Match         91.7%;  Score 10913;  DB 2;  Length 2248;
Best Local Similarity  92.0%;  Pred. No. 0;
Matches 2106;  Conservative 30;  Mismatches 30;  Indels 89;  Gaps 64;  Indels 7;

Qy     1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
           ||||||||||||||||||: |||||||||||:|||||||||||||||||||||||||||
Db     1 MDEEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVV 60

Qy    61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
           |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db    61 FFYLSQDSRPRSWCLRTVCNPWFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy   121 DDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
           ||||||||||||||:|||||||||||||||||||||||||||||||||:||::||||||
Db   241 CFLPENFSLPLSVDLEPYYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPCGL 300

Qy   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Qy   361 YFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
           |||||||||||||||||||            |||||||||||||||||||||
Db   361 YFVMDAHSFYNFIYFILLII------------FSETKQRESQLMREQRVRFLSNA 403

Qy   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSS 480
           |||||||||||||||||||||||||||||||||||:||||:|||||||: ||::|:||:
Db   404 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAVGVRAGLLSSPVVRGGQEPQPSG 463

Qy   481 SCSRSHRRLSVHHLVIHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
           |||||||||||||| |||||||||||||||| |||||||||||||||:||||||||||
Db   464 SCSRSHRRLSVHHLVHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRWLMLPPPSTP 523

Qy   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRPSEASGRTVGSGKVYPTVHTSPPPE 600
           : ||.||.|:|||||||||||||||||||||||.||||||||||||||||||||||||
Db   524 TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 583

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACOQSSCKISSPCLKADSG 660
           .||:|||||| :.|||||||:|||||| :||||||||||||||.|:||||||||| ||||
Db   584 MLKDKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSG 643

Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
           |||||||||||:|||| |:|| ||||||||||||||||||||||||||: || ||||||
Db   644 ACGPDSCPYCARTGAGEPESADHEMPDSDSEAVYEFTQDAQHSDLRDPHRRRPSLGPDA 703

Qy   721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   704 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 763

Qy   781 VFTSLFALEMLLKLLVYGPFGVIKNPVNIFDGVIVVISWEIVGQQGGGGLSVLRTFRLMR 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   764 VFTSLFALEMLLKLLVYGPFGVIKNPVNIFDGVIVVISWEIVGQQGGGGLSVLRTFRLMR 823

Qy   841 VLKLVRFLPALORQLVVLIMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERDGTL 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   824 VLKLVRFLPALORQLVVLIMKTMDNVATFCMLLMLFIFIFSIIGMHLFGCKFASERDGTL 883

Qy   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   884 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 943

Qy   961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
           |||||||||                           |||||||||||||.||||||||:|
Db   944 AILVEGFQAE------------------------GDATKSESEPDFFSPSVDGDGDRKKRL 980

Qy  1021 ALVSLGEHEPLRKSLLPPLLIHTRATPMSLPKSTSTGLGEALGPASRRTSSSGSARPGAA 1080
           ||.:|||.||||||||||||||||:||||||||:||.|||||| .|||||||||||.||:
Db   981 ALVALGEHSELRKSLLPPLLIHTATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGTA 1040

Qy  1081 -HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQES 1139
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041 HHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQES 1100

Qy  1140 QDEEESSEEPRASPAGSDHHRRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDC 1199
           |||||||||.|||||||||||||||||||||||||||||||||||||||||| ||||||
Db  1101 QDEEESSEEDRASPAGSDHHRRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQDC 1160

Qy  1200 NGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIF 1259
           ||||||||||.:|.|||||||||| :||||||||||:||||:||||| .:||||||||||
Db  1161 NGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLRAWVRARLPACCRERDSWSAYIF 1220

Qy  1260 PPQSRRFLLCHRIITHKMFDHVVLVLIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1319
           ||||.|||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db  1221 PPQSRFFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1280

Qy  1320 VFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRV 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1281 VFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRV 1340

Qy  1380 LRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFF 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341 LRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFF 1400

Qy  1440 VCQGEDTRNIINKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAV 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1401 VCQGEDTRNIINKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAV 1460

Qy  1500 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRRREKR 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1461 GVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRRREKR 1520

Qy  1560 LRRLEKKRR-----------------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITG 1601
           |:||||||||
Db  1521 LKRLEKKRRNLMLDDVIASGSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITG 1580

Qy  1602 VIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNOLD 1661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1581 VIGLNVVTMAMEHYQQPOILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLD 1640

Qy  1662 LAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIARVLRLLKLLKMAVGMRALLDTVMQA 1721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1641 LAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIARVLRLLKLLKMAVGMRALLDTVMQA 1700

Qy  1722 LPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVS 1781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1701 LPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVS 1760

Qy  1782 TGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNK 1841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1761 TGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNK 1820

Qy  1842 EAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGPDSPKPGALHPAAHARSAS 1901
           ||||||||||||||||||||||||||||||||||||| :||||||:|.||:.|:|
Db  1821 EAKEEAELEAELELEMKTLSPQHSPLGSPFLWPGVEGNSPDSPKPGAPHTAHIGAAS 1880

Qy  1902 H-FSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
            ||||||||.||:.   ||||||||||||||||||||||||||||.||||| .||||
Db  1881 SGFSLEHPTMVPHTEEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRG 1940

Qy  1958 WGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQR 2017
           |||||||||.:|||||||||| ||| |||| .||||| |||||.||||||||||||||||
Db  1941 WGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPLAQR 2000

Qy  2018 PLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPLARAYSFWGQSSTQAQQHGRSHSKIS 2077
           ||||||||||||||||||||||||||:|||||. |.:::|||.||:|.||:.|||.||:|
Db  2001 PLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGSGQSKVS 2060
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Qy    2078  KHMTPPAPCPGEPENWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYS  2137
             ||:  ||||| ||||||||||||||||||||||||||||||||| :||||||||||||||
Db    2061  KHIRLPAPCPGLEPSWAKDPQETRSSLELDTELSWISGDLL-PSSQEEPLSPRDLKKCYS  2119

Qy    2138  VEAQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSP  2197
            ||||||||||| ||||||||||||||||||||  ||||| :|| || ||||| ||||||
Db    2120  VEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSP  2179

Qy    2198  PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLSLSGL  2257
            ||:|||||||||||| |  ||| ||| ||||||  ||||||||  |||||||| ||||||
Db    2180  PSISIDPPESQGPRPPCSPGVCLRRRAPASDSKDPSASSPLDSTAASPSPKKDALSLSGL  2239

Qy    2258  SSDPADLDP  2266
            |||| |||
Db    2240  SSDPTDLDP  2248
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RESULT 8
Q6ZPX4
ID   Q6ZPX4          PRELIMINARY;       PRT;   1389 AA.
AC   Q6ZPX4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA1123 protein (Fragment).
GN   Name=mKIAA1123;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=14621295;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:167-180(2003).
CC   -!-  SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!-  SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC        family.
DR   EMBL; AK129294; BAC98104.1; -.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 2.
DR   PRINTS; PR00167; CACHANNEL.
KW   Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW   Transmembrane; Transport; Voltage-gated channel.
FT   NON_TER        1
SQ   SEQUENCE   1389 AA;  153067 MW;  DA31535CA3C03B10 CRC64;

Query Match             55.2%;  Score 6573;  DB 2;  Length 1389;
Best Local Similarity   92.0%;  Pred. No. 1.2e-294;
  Matches 1279;  Conservative   25;  Mismatches   62;  Indels   24;  Gaps   5;
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Qy    121   LALVALGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGT  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1080  A-HEMKSPPSARSSPHSPWSAAASWTSRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE   1138

Qy    181   AHHEMKSPPSARSSPHSPWSAAASWTSRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1139  SQDEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD  1198

Qy    241   SQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRSSASEHQD  300
            |||||||||:||||||||||||||||||||||||||||||||||||||||||:||||||
Db    1199  CNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI  1258

Qy    301   CNGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLRAWVRARLPACCRERDSWSAYI  360
            |||||||||||| ||:||||||| ||||||||||||| ||:||||||  |||||||||
Db    1259  FPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  1318

Qy    361   FPPQSRFRLLCHRIITHKMFDHVVLVIIFLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT  420
            ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    1319  AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  1378

Qy    421   AVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1379  VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF  1438

Qy    481   VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1439  FVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA   1498

Qy    541   FVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1499  VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK  1558

Qy    601   VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK  660
            ||||||||||||||||||||||||||||||                             
Db    1559  RLRRLEKKRR-----------------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  1600

Qy    661   RLKRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT  720
                                   ||||||||||||||||||||||||||||||||||||||
Db    1601  GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVPKLVAPGFRRFFQDRWNQL  1660

Qy    721   GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVPKLVAPGFRRFFQDRWNQL  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1661  DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ  1720

Qy    781   DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1721  ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRV  1780

Qy    841   ALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATPRNFGMAFLTLFRV  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1781  STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFYVSFVLTAQFVLNVNVIAVLMKHLEESN  1840

Qy    901   STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFYVSFVLTAQFVLNVNVIAVLMKHLEESN  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1841  KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSA  1900

Qy    961   KEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAA  1020
            |||||||||||||||||||||||||||||||||||||||       :||||||  ::||
Db    1901  SH-FSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHR  1956

Qy    1021  SSGFSLEHPTMVPHTEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR  1080
            ||  |||||||  |::|||  ||||||||||||||||||||||||||| |||||  |||
Db    1957  GWGLPKAQSGSVLSVHSQPADTSYIILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQ  2016

Qy    1081  GWGLPKAQSGSILSVHSQPADTSCIIQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPLAQ  1140
            ||||||||||| |||||||||:| ||:|||||: |||||.||||| |||||||||||||
Db    2017  RPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSTQAQHSRSHSKI  2076

Qy    1141  RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQORSGGSQSKV  1200
            |||||||||||||||||||||||||||:|||| ||  | |||||:||:|  ||| | ||:
Db    2077  SKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCY  2136
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Qy    900   LPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVLVFNLL  959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1     LPDRKNFDSLLWAIVTVFQLLTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVLVFNLL  60

Qy    960   VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC  1019
            ||||||||||||||||||||||||||||||| ||||:|||||||||||  |||||||:|
Db    61    VAILVEGFQAEEIGKCREDTSGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGDRKKR  120

Qy    1020  LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA  1079
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Db 1319 AVFLAEMTVKVVALGWCFEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 AVFLAEMTVKVVALGWCFEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR   480

Db 1379 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 VLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF   540

Db 1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA   600

Db 1499 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK 1558
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601 VGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEK   660

Db 1559 RLRRLEKKRR-----------------------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTT 1600
          ||:||:|||| :|||||||||||||||||||||||||||
Qy   661 RLKRLEKKKRRNLMLDDVIASGSSASAAAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFIT   720

Db 1601 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFPQDRWNQL 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFPQDRWNQL   780

Db 1661 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   781 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQ   840

Db 1721 ALPQVGNLGLLFLMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 ALPQVGNLGLLFLMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV   900

Db 1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESN 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESN   960

Db 1841 KEAKEEABLEABLEABLEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSA 1900
          :|||||:|||:||||||||||||||||||||::||||||||||||| : :
Qy   961 KEAKEEARLEARLEARLEMKTLSPQPHSPLGSPFLWPGVEGVNSPDSPKPGAPHTTAHIGAA 1020

Db 1901 SH-FSLEHPTMQPHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHR 1956
          |: || ||:|| :| | ||||||||||||||||||||:|||||| || ::|
Qy 1021 SSGFSLEHPTMVPHTEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR 1080

Db 1957 GWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQ 2016
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Qy 1081 GWGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTWGAIPKLPPPGRSPIAQ 1140

Db 2017 RPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKI 2076
          ||||||||||||||||||||||||||||||||||||:::||||||||:||| |:|:|:|
Qy 1141 RPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGSQSKV 1200

Db 2077 SKHMTPAPCPGPEPNWGKGPPETRSSLEDTELSWISGDLLPPGGQEPPSPRDLKKCY 2136
          |||:|||||||||||||||||||||||||||||||||| ||| :||||||||||||
Qy 1201 SKHIRLPAPCGLEPSWAKDPQETRSSLELDTELSWISGDLL-PSSQEPLSPRDLKKCY 1259

Db 2137 SVEAQSCCRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLS 2196
          ||||||| ||||:||||||||||||||||||:|||| :||||||||||||||||||||||
Qy 1260 SVEAQSCRRRPGSWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLS 1319

Db 2197 PPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSG 2256
          |||||:|||||||| :|||| ||||||||||||:|||:|||||||||||||||||||||||
Qy 1320 PPSISIDPPESQGPRPFCSPGVCLRRRAPASDSKDPSASSPLDSTAASPSPKKDALSLSG 1379

Db 2257 LSSDPADLDP 2266
          |||| |||||
Qy 1380 LSSDPTDLDP 1389

RESULT 9
BAC98104
ID BAC98104;   PRELIMINARY;   PRT; 1389 AA.
AC BAC98104;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update).
DE MKIAA1123 protein (Fragment).
GN MKIAA1123.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-fractionated Libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129294; BAC98104.1; -.
FT NON_TER   1   1
SQ SEQUENCE   1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match   55.2%; Score 6573; DB 2; Length 1389;
Best Local Similarity   92.0%; Pred. No. 1.2e-294;
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;

Qy   900 LPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL   959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 LPDRKNFDSLLWAIVTVFQIITQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL   60

Qy   960 VAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLLDGDGDRKKC 1019
          |||||||||||||||||||||||||||||||||||||||||||:|||:|||||||||||||
Db   61 VAILVEGFQAEEIGKREDTSGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGDRKKR   120

Qy 1020 LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
          ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LALVAIGEHSELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGT   180

Qy 1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
          | |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db   181 AHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQK   240

Qy 1139 SQDEERSSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD 1198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 SQDEERSSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQD   300

Qy 1199 CNGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
          ||||||||||||||||||||||||||:|||||||||||||||||||||||::|||||||
Db   301 CNGKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLRAWVRARLPACCRERDSWSAYI   360

Qy 1259 FPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 FPPQSRFLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT   420

RESULT 10
CCAH_RAT
ID CCAH_RAT   STANDARD;   PRT;   2359 AA.

```
AC   Q9EQ60;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.2).
GN   Name=Cacna1h;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA   McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA   Baillie D.L., Stea A., Snutch T.P.;
RT   "Molecular and functional characterization of a family of rat brain T-
RT   type calcium channels.";
RL   J. Biol. Chem. 276:3999-4011(2001).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1H
CC       gives rise to the "low-voltage activated (LVA)" group and are strongly
CC       belong to the "T-type calcium currents. T-type calcium channels
CC       blocked by nickel and mibefradil. A particularly of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in brain.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF290213; AAG35187.1; -.
DR   RGD; 68943; Cacna1h.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Phosphorylation; Repeat; Transmembrane;
KW   Voltage-gated channel.
FT   REPEAT         87     422       I.
FT   REPEAT        776    1015       II.
FT   REPEAT       1292    1569       III.
FT   REPEAT       1607    1868       IV.
FT   DOMAIN          1     100       Cytoplasmic (Potential).
FT   TRANSMEM      101     119       S1 of repeat I (Potential).
FT   DOMAIN        120     139       Extracellular (Potential).
FT   TRANSMEM      140     160       S2 of repeat I (Potential).
FT   DOMAIN        161     169       Cytoplasmic (Potential).
FT   TRANSMEM      170     184       S3 of repeat I (Potential).
FT   DOMAIN        185     193       Extracellular (Potential).
FT   TRANSMEM      194     212       S4 of repeat I (Potential).
FT   DOMAIN        213     232       Cytoplasmic (Potential).
FT   TRANSMEM      233     253       S5 of repeat I (Potential).
FT   DOMAIN        254     394       Extracellular (Potential).
FT   TRANSMEM      395     419       S6 of repeat I (Potential).
FT   DOMAIN        420     790       Cytoplasmic (Potential).
FT   TRANSMEM      791     811       S1 of repeat II (Potential).
FT   DOMAIN        812     824       Extracellular (Potential).
FT   TRANSMEM      825     846       S2 of repeat II (Potential).
FT   DOMAIN        847     852       Cytoplasmic (Potential).
FT   TRANSMEM      853     871       S3 of repeat II (Potential).
FT   DOMAIN        872     879       Extracellular (Potential).
FT   TRANSMEM      880     903       S4 of repeat II (Potential).
FT   DOMAIN        904     914       Cytoplasmic (Potential).
FT   TRANSMEM      915     935       S5 of repeat II (Potential).
FT   DOMAIN        936     987       Extracellular (Potential).
FT   TRANSMEM      988    1012       S6 of repeat II (Potential).
FT   DOMAIN       1013    1301       Cytoplasmic (Potential).
FT   TRANSMEM     1302    1324       S1 of repeat III (Potential).
FT   DOMAIN       1325    1342       Extracellular (Potential).
FT   TRANSMEM     1343    1363       S2 of repeat III (Potential).
FT   DOMAIN       1364    1373       Cytoplasmic (Potential).
FT   TRANSMEM     1374    1393       S3 of repeat III (Potential).
FT   DOMAIN       1394    1407       Extracellular (Potential).
FT   TRANSMEM     1408    1429       S4 of repeat III (Potential).
FT   DOMAIN       1430    1439       Cytoplasmic (Potential).
FT   TRANSMEM     1440    1463       S5 of repeat III (Potential).
FT   DOMAIN       1464    1540       Extracellular (Potential).
FT   TRANSMEM     1541    1566       S6 of repeat III (Potential).
FT   DOMAIN       1567    1621       Cytoplasmic (Potential).
FT   TRANSMEM     1622    1642       S1 of repeat IV (Potential).
FT   DOMAIN       1643    1656       Extracellular (Potential).
FT   TRANSMEM     1657    1678       S2 of repeat IV (Potential).
FT   DOMAIN       1679    1685       Cytoplasmic (Potential).
FT   TRANSMEM     1686    1704       S3 of repeat IV (Potential).
FT   DOMAIN       1705    1718       Extracellular (Potential).
FT   TRANSMEM     1719    1742       S4 of repeat IV (Potential).
FT   DOMAIN       1743    1756       Cytoplasmic (Potential).
FT   TRANSMEM     1757    1777       S5 of repeat IV (Potential).
FT   DOMAIN       1778    1840       Extracellular (Potential).
FT   TRANSMEM     1841    1868       S6 of repeat IV (Potential).
FT   DOMAIN       1869    2359       Cytoplasmic (Potential).
FT   DOMAIN        521     531       Poly-His.
FT   DOMAIN       1594    1597       Poly-Arg.
FT   SITE          378     378       Calcium ion selectivity and permeability
FT                                   (By similarity).
FT   SITE          971     971       Calcium ion selectivity and permeability
FT                                   (By similarity).
FT   SITE         1515    1515       Calcium ion selectivity and permeability
FT                                   (By similarity).
FT   SITE         1813    1813       Calcium ion selectivity and permeability
FT                                   (By similarity).
FT   CARBOHYD      192     192       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD      271     271       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     1477    1477       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   2359 AA;  261138 MW;  F73B083E94180081 CRC64;
```

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Query Match             52.2%;  Score 6217.5;  DB 1;  Length 2359;
Best Local Similarity   56.4%;  Pred. No. 5.2e-278;
Matches 1369;  Conservative 228;  Mismatches 512;  Indels 317;  Gaps  62;

Qy      2 DEEEDGAGAEESGQPRSFMRLNDLS-GAGGRP---GPGS---AEKDPGS---AD---SEA  48
            ||||||||||||||||||||||||| |||||   ||||   ||||||   ||   |||
Db      9 DEVRVPLGASPPA-PAAPVRASPASPGAPGREEQGSGSGVLAPESPGTECGADLGADEE  67

Qy     49 EGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIA 108
          :||||||||||||||||||||||||||||||||||:||||:||:||||||||||||||:
Db     68 QPVPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVE 127
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Qy   109  CDSQRCRILQAFDFIFAFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYS  168
          |||  |  | | || |||||||| |  |||||| |||||||||||||||||| |||| ||
Db   128  CRSERCSLEAFDDFIFAFFAVEMVIKMVALGLPGQKCYLGDTWNRLDFFIVMAGMMEYS  187

Qy   169  LDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIV  228
          ||  ||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   188  LDGHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIV  247

Qy   229  GVQLWAGLLRNRCFLPENFSLPLSVD-LERYYQTENEDRSPFICSQPRENGMRSCRSVPT  287
          |||||||||||||||      |  ||  ||::|:||  : |:||| : : |  |   :| :
Db   248  GVQLWAGLLRNRCFLDSAFVRNNNLITFLRPYYQTEBGEENPFICSSRRDNGMQKCSHIPS  307

Qy   288  ---LRGDGGGGPPCGLDYEAY------NSSSNTTCVNWNQYYTNCSAGEHNPFKGAINF  337
             :    |     | ||:  |       :: |:| ||||||||: || |||||| ||||
Db   308  RRELR------VQCTLGWEAYGQPQABDGGAGRNACINWNQYYNVCRSGEFNPHNGAINF  361

Qy   338  DNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINLCLVVIATQ  397
          |||||||||||||||||||||||| ||||||||||||||||:|:||||||||||||||||
Db   362  DNIGYAWIAIFQVITLEGWVDIMYVMDAHSFYNFIYFILLIMGSFFMINLCLVVIATQ  421

Qy   398  FSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVVILRKAARRLAQVSRA  457
          |||||||| |||:|:| |||||:||:|||||||||||||||||  |:||  ||  : | :
Db   422  FSETKQRENQLMRQRARYLSNDSTIASFSEPGSCYEELLKYVGHIFRKVKRRSLRLYAR  481

Qy   458  AGVRVGLLSSP-APLGGQETQPSSSCSRSHRR-LSVHHIV-HHHHHHHHYHLGNGTLRA  514
           | : | : |    ||:|  ||  | || :   :|||:|| |||||||||:|| :| ||
Db   482  WQSRWRKKVDPSSTVHGQ-GPGRPRRAGRTASVHHLVHHHHHHHHHHYHFSHGGPRR  539

Qy   515  PRASPEIQDRDANGSRRLM-LPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPP  572
                 |  |  :| ||::|  || ||| :||| ||| |:||| ||||||| ||:|:|| |
Db   540  P--SPE----PGAGDNRLIVRACAPPSPPSPGHGPP-DSESVHSIYHADCHVEGPQERARV  592

Qy   573  PRSPSEASGRTVGSG---KVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIP----  625
            || :|   : |:    ||||       :| : ||    |  ||| :| :||
Db   593  AHSIATPAASLKLASGLGTMNYPTI--LPSGTVNSKG-----GTSSRPKGLRGAGAPGAAV  645

Qy   626  --------PGPYSSMHKLLETQSTGACQS----------SCKISSPCLKADSGACGPDSCPYC  670
                   | | ||:||||||||  |: |            |||||||| ||:| |||||||
Db   646  HSPLSLGSPRPYEKIQDVVGEQGLGRASSHLSGLSVPCPLPSP-QAGTLTCELKSCPYC  703

Qy   671  ARA-GAGEVELADREMPDSDSEAVFFTQDAQHSDLRDP----HS-RRQRSL  716
          |:|  :||| ||| |  ||| |||||||| :| | ||| ||  | :|||:|||
Db   704  ASALEDPEFFFSGSESGDSDAHGVVFFTQDVRHGDCRDPVQQPHBVGTPGHSNERRRTPL  763

Qy   717  GPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALE  776
          | ||: ||| ||| | ||||||||||||| ||||:|||||||||| |||||||||:|||||
Db   764  RKASQPGGIGHLWASFSGKLRRIVDSKYFNRGIMAAILVNTLSMGVEYHEQPEELTNALE  823

Qy   777  ISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTF  836
          ||||||||:|||||||||| | ||||||||||||||||:|||||||||| | | ||||||
Db   824  ISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGVVVVISVWEIVGQADGGQSVLRTF  883

Qy   837  RLMRVLKLVRFLPALORQLVVLMKMDNVATFCMLLMLFIFSILGMHLFGCKFASERD  896
          || ||||||||||| ||||||||: ||||||||||||||||||||||||||||   :|
Db   884  RLLRVLKLVRFLPALRRQLVVLMRTMDNVATFCMLMLFIFSILGMHLFGCKFSLKTD  943

Qy   897  -GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVL  955
           |||:||||||||||||||||||||||||||:|||||||||||||||||:|||||||||||
Db   944  SGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGNYVL  1003

Qy   956  FNLLVAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPPDFFSPSLDGDGD  1015
          |||||||||||||||       |  |     |||  ||
Db  1004  FNLLVAILVEGFQAE------GDATRSDTDEDKTSTQLEGDFD  1040

Qy  1016  RKKCL------ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPAS  1066
          : |   |||||::| | | :|:|:| |||||||||||||| | | |   |     ||
Db  1041  KLRDLRATEMKMYSLAVTPNGHLEGRGSLPPLITHTAATPMPTPKS-SPNLDVAHALLD  1099

Qy  1067  RRTSSSGSSAEPGAAHEMKSPPSARSSPHSPWSAASWTSRRSSRNSLGRAPSLKRRSPSG  1126
           || |:| : |  :  |  |||| || |||| ||  |: |||:| |||||||||||| : |
Db  1100  SRRSSSGSVDPQLG-DQKSLASLRSSPCTPWGPNSAGSSRRASSWNSLGRAPSLKRRNQCG  1158

Qy  1127  ERRSLLSGEGQESQDEESSEEERAS-----------PAGSDHRURGSLEREAKSSFDL--  1174
          || ||||| |: | ::: : :   ||            || ||    | || :  |
Db  1159  ERESLLSGEGKGSTDDE--AEDSRPSTGTHPGASPGPRA1PLRRABSLDH--RSTLDLCP  1214

Qy  1175  --PDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDADDGNLSK  1232
                 :|   |  |                  |:    : : || | |||| | ||:|||
Db  1215  --------DCNGQMVALPSEFFLRIDSHKEDAAEFDDDIEDSC  1261

Qy  1233  GERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMPDHVVLVIIFLNCIT  1292
           | |:  | || || : ::::||| |||||:||| || ::| |||| |||||||:|||||||
Db  1262  CFRLHKVLEPYAPQWCRSRESWALYLFPPQNRLRVSCQKVIAHKMFDHVVLVFIFLNCIT  1321

Qy  1293  IAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGL  1352
          || ||| |||  :||:|| | ||||||:| |||:|||||| | | || | | ||||||||
Db  1322  IALERPDIDPGSTERAFLSVSNYIFTAIFVVEMMVKVVALLWGEHAYLQSSWNVLDGL  1381

Qy  1353  LVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPI  1412
          || :|::||::|:    | ||||:|||||||||||||||||||| ||||||||:|||:||
Db  1382  LVIVSLVDIIVAMASAGGAKILGVLRVRLLRTLRPLRVISRAPGLKLVVETLISSLRPI  1441

Qy  1413  GNIVIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNL  1472
          |||:::|||||||||||||||||||||:|| | |||||| |::| | :|||||:||||||
Db  1442  GNIVLICCAFFIIFGILGVQLFKGKFYYCEGTDTRNITTKAECHAAHYRWVRRKYNFDNL  1501

Qy  1473  GQALMSLFVLASKDGWVDIMYDGLDAVGVDGQQPIMNHNPWMLLYFISFLLIVAFFVLNMF  1532
          |||||||||| |||||::|||||||||| |||||: | ||||||||||||||| ||||||||
Db  1502  GQALMSLFVLSSKDGWVNIMYDGLDAVGIDGQQPVQNPNPWMLLYFISFLLIVSFFVLNMF  1561

Qy  1533  VGVVVENFHKCRQHQEEEARRREEKRLRILEKKRRKAQCRKPYYSDYSRFRLLVHHLCTS  1592
          ||||||||||||||||: ||||||||||||| :|||||  |:|||:||: |||:|||||||
Db  1562  VGVVVENFHKCRQHQEAEAARRREEKRLRILERRRRKAQRRPYYADYSHTRRSIHSLCTS  1621

Qy  1593  HYLDLFITGVIGLNVVTMAMEHYQQPILDEALKICNYIFTVIFVLESVFKLVAFGFRRF  1652
          ||:||||| :| |||| |:||||:||  ||||| ||| ||:|||:|  |||||||||||
Db  1622  HYIDLFITFIICLNVVITMSMEHYNQPKSLDEALKYCNYVFTIVFVFEAALKLVAFGFRRF  1681

Qy  1653  FQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMR  1712
          | |||||||||||||||||| |||||:|| ||||||||||||||||||||||||||:|||
Db  1682  FKDRWNQLDLAIVLLSIMGIALEEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATGMR  1741

Qy  1713  ALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGCLEDCDETHPCEGLGRHATFRNFGM  1772
          ||||||:||||||||||||||||||| ||||||||| :|  || ||||| |||||| ||||
Db  1742  ALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPCEGLSRHATFTNFGM  1801

Qy  1773  AFLTLFRVSTGDNWNGIMKDTLRDC---DQESTCYNTVISPYIYFVSFVLTAQFVLVNVVI  1829
          |||||||||||||||||||||||:|    | |  | ::::|  |||:||::|||||||||:
Db  1802  AFLTLFRVSTGDNWNGIMKDTLRECTREDKHCLSYLPALSPVYFVTFMLVAQFVLVNVVV  1861

Qy  1830  AVLMKHLEESNKEAKEEABLEAELELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPG  1889
          |||||||||||||| ||  ::|| : :||
Db  1862  AVLMKHLEESNKEAREDAEMDAEIELEM  1889

Qy  1890  ALHPAAHARSASHFSLEHPTMQPHPT--ELPG---PDLLTVRKSGVSRTHSLPNDSYM  1942
                   : :   |  |   ||  | | || :||| ||||
Db  1890  ------AQGSTAQPPTAQESQGTQPDTPNLLVVRKVSVSRMLSLPNDSYM  1934

Qy  1943  CRHGSTAEGPLGHRGWGLP----KAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHS  1996
            |  :  |  |  |  |  |    : | : :  |:: : :      |:
Db  1935  FRPVAPAAAPHSH-----PLQEVEMETYTGPVTSAHSPPLEPRASFQVPSAA------S  1982

Qy  1997  APTWGTIP--KLPPPG--RSPLAQRPLRRQAAIRTDSLD--VQGLGSREDLLAEVSGPSP  2050
              :  |       |   | :  :|   :|:  : | |      ::       :|   |
Db  1983  SPARVSDPLCALSPRGTPRSLSLSRILCRQEAMHSESLRGKVDDVGG--DSIPDYTEPAE  2040

Qy  2051  PLARAYSFWG------QSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPET  2100
                   |:        | | :|  : ::|   :     |  |  |        :
Db  2041  NMGSTSQASTGAPRSPPCSPRPASVRTRKHTFGGQRCISSR--PPT------LGGDEA  2088

Qy  2101  RSSLELDTELSWISGDLLP-------PGGGQEPP------SPRDLKKCCYSVEAQSCQR  2145
           ::  :|    | :: | |         || :| |       |    |||| |||| | :
Db  2089  EAADPADEEVSHITSSAHPWPATEPHSPEASPTASPVKGTMGSGRDPRRFCSVDAQSFLD  2148

Qy  2146  RPTSWLDEQRRHSIAVSCLDSGSGQPHLGTDPSNLGGQPLG------GPGSRPKKKLSPP  2198
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Db    2149  KP-GRPDAQRWSSVE---LDNG-ESHLES------GEVRGRASELEPALGSRRKKKMSPP 2197
             :|   |||  |  |    |||:|  |  :||  | ||      ||| |:|| |||:|||:||
Qy    2199  SITIDPP-ESQGPRTPPSP--GICLRRRAPSSDSK------------DPLASGPP 2238
             |:|:||:|: :||  :|:  |: ||      ||:|| ||       |:|| |
Db    2198  CISIEPPTKDEGSSRPPAAEGGNTTLRRRTPSCEAALHRDCPEPTEGPGTGGDPVAKGER 2257
                               |||:|  ||||| |  ::  |
Qy    2239  DSMAASPSPKKDVLSLSGLSSDPADL 2264
             : |   | :|||  : |: |: |
Db    2258  WGQA---SCRAEHITVPNFAFEPIDM 2280


RESULT 11
CCAH_HUMAN
ID   CCAH_HUMAN      STANDARD;     PRT;   2353 AA.
AC   O95180; O95802; Q8WWI6; Q96QI6; Q96RZ9; Q9NYY4; Q9NYY5;
DT   15-JUL-1999 (Rel. 38, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated
DE   calcium channel alpha1 3.2 subunit).
GN   Name=CACNA1H;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Heart;
RX   MEDLINE=98333998; PubMed=9670923;
RA   Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N.,
RA   Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.;
RT   "Cloning and characterization of alpha1H from human heart, a member of
RT   the T-type Ca2+ channel gene family.";
RL   Circ. Res. 83:103-109(1998).
RN   [2]
RP   REVISIONS.
RA   Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Thyroid carcinoma;
RX   MEDLINE=99127945; PubMed=9930755;
RA   Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F.,
RA   Prodanovich P., Harpold M.M., Stauderman K.A.;
RT   "structure and functional characterization of a novel human low-
RT   voltage activated calcium channel.";
RL   J. Neurochem. 72:791-799(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=21096910; PubMed=11157797;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Testis;
RX   MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200;
RA   Jagannathan S., Punt E.L., Gu Y., Arnoult C., Sakkas D., Barratt C.L.,
RA   Publicover S.J.;
RT   "Identification and localization of T-type voltage-operated calcium
RT   channel subunits in human male germ cells. Expression of multiple
RT   isoforms.";
RL   J. Biol. Chem. 277:8449-8456(2002).
RN   [6]
RP   SEQUENCE OF 86-817 FROM N.A.
RA   Cobley V.E.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).
RA   Mittman S., Agnew W.S.;
RL   "Organization and alternative splicing of CACNA1H.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1H
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=A1H-a;
CC         IsoId=O95180-1; Sequence=Displayed;
CC       Name=2; Synonyms=A1H-b;
CC         IsoId=O95180-2; Sequence=VSP_000949;
CC   -!- TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.
CC       Isoform 2 seems to be testis-specific.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown
CC       in this entry. The additional 20 amino acids found in the Ref.4
CC       and Ref.6 sequences are due to a misunderstanding of the real type
CC       of splicing mechanism involved.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF051946; AAC67239.3; -.
DR   EMBL; AF073931; AAD17668.1; -.
DR   EMBL; AE006466; AAK61268.1; ALT_SEQ.
DR   EMBL; AJ420779; CAD12646.1; -.
DR   EMBL; AL031703; CAC42094.1; ALT_SEQ.
DR   EMBL; AF223562; AAF60162.1; -.
DR   EMBL; AF223563; AAF60163.1; -.
DR   Genew; HGNC:1395; CACNA1H.
DR   MIM; 607904; -.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.
DR   GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.
DR   GO; GO:0006936; P:muscle contraction; TAS.
DR   GO; GO:0007520; P:myoblast fusion; TAS.
DR   GO; GO:0008016; P:regulation of heart rate; TAS.
DR   GO; GO:0006810; P:transport; TAS.
DR   InterPro; IPR001682; Ca/Na pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
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KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Repeat; Transmembrane; Voltage-gated channel.
FT   REPEAT        87    779   I.
FT   REPEAT       422   1018   II.
FT   REPEAT      1281   1558   III.
FT   REPEAT      1602   1863   IV.
FT   DOMAIN         1    100   Cytoplasmic (Potential).
FT   TRANSMEM     101    119   S1 of repeat I (Potential).
FT   DOMAIN       120    139   Extracellular (Potential).
FT   TRANSMEM     140    160   S2 of repeat I (Potential).
FT   DOMAIN       161    169   Cytoplasmic (Potential).
FT   TRANSMEM     170    184   S3 of repeat I (Potential).
FT   DOMAIN       185    193   Extracellular (Potential).
FT   TRANSMEM     194    212   S4 of repeat I (Potential).
FT   DOMAIN       213    232   Cytoplasmic (Potential).
FT   TRANSMEM     233    253   S5 of repeat I (Potential).
FT   DOMAIN       254    394   Extracellular (Potential).
FT   TRANSMEM     395    419   S6 of repeat I (Potential).
FT   DOMAIN       420    793   Cytoplasmic (Potential).
FT   TRANSMEM     794    814   S1 of repeat II (Potential).
FT   DOMAIN       815    827   Extracellular (Potential).
FT   TRANSMEM     828    849   S2 of repeat II (Potential).
FT   DOMAIN       850    855   Cytoplasmic (Potential).
FT   TRANSMEM     856    874   S3 of repeat II (Potential).
FT   DOMAIN       875    882   Extracellular (Potential).
FT   TRANSMEM     883    906   S4 of repeat II (Potential).
FT   DOMAIN       907    917   Cytoplasmic (Potential).
FT   TRANSMEM     918    938   S5 of repeat II (Potential).
FT   DOMAIN       939    990   Extracellular (Potential).
FT   TRANSMEM     991   1015   S6 of repeat II (Potential).
FT   DOMAIN      1016   1290   Cytoplasmic (Potential).
FT   TRANSMEM    1291   1313   S1 of repeat III (Potential).
FT   DOMAIN      1314   1331   Extracellular (Potential).
FT   TRANSMEM    1332   1352   S2 of repeat III (Potential).
FT   DOMAIN      1353   1362   Cytoplasmic (Potential).
FT   TRANSMEM    1363   1382   S3 of repeat III (Potential).
FT   DOMAIN      1383   1396   Extracellular (Potential).
FT   TRANSMEM    1397   1418   S4 of repeat III (Potential).
FT   DOMAIN      1419   1428   Cytoplasmic (Potential).
FT   TRANSMEM    1429   1452   S5 of repeat III (Potential).
FT   DOMAIN      1453   1529   Extracellular (Potential).
FT   TRANSMEM    1530   1555   S6 of repeat III (Potential).
FT   DOMAIN      1556   1616   Cytoplasmic (Potential).
FT   TRANSMEM    1617   1637   S1 of repeat IV (Potential).
FT   DOMAIN      1638   1651   Extracellular (Potential).
FT   TRANSMEM    1652   1673   S2 of repeat IV (Potential).
FT   DOMAIN      1674   1680   Cytoplasmic (Potential).
FT   TRANSMEM    1681   1699   S3 of repeat IV (Potential).
FT   DOMAIN      1700   1713   Extracellular (Potential).
FT   TRANSMEM    1714   1737   S4 of repeat IV (Potential).
FT   DOMAIN      1738   1751   Cytoplasmic (Potential).
FT   TRANSMEM    1752   1772   S5 of repeat IV (Potential).
FT   DOMAIN      1773   1835   Extracellular (Potential).
FT   TRANSMEM    1836   1863   S6 of repeat IV (Potential).
FT   DOMAIN      1864   2353   Cytoplasmic (Potential).
FT   DOMAIN       520    530   Poly-His.
FT   DOMAIN      1107   1110   Poly-Ser.
FT   DOMAIN      1583   1586   Poly-Arg.
FT   SITE         378    378   Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE         974    974   Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE        1504   1504   Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE        1808   1808   Calcium ion selectivity and permeability
FT                             (By similarity).
FT   CARBOHYD     192    192   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     271    271   N-linked (GlcNAc...) (Potential).
```

```
Qy     7  GAGAEESGQP-RSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVFFYLS   65
             ::|  ::|: :||||
Db    27  GASPESPGAPGREAERGSEL-GVSPSESP-AAERGAELGADEEQRVPYPALAATVFFCLG   84

Qy    66  QDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF  125
             ||:||||||| :|||||||:|||||:|||||||||||||| :.|.|.|:|||:||.|||
Db    85  QTTRPRSWCLRLVCNPWFEHVSMLVIMLNCVTLGMFRPCEDVECGSERCNILEAFDAFIF  144

Qy   126  AFFAVEMVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL  185
            ||||||| :||||||:||:||||||||||||||||:|||:||||| :||:|||:||||||
Db   145  AFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVAGMFEYSLDGHNVSLSAIRTVRVL  204

Qy   186  RPLRAINRVPSMRILVTILLDTLPMLGNVLLCFVFFIFGIVGVQLWAGLLRNRCFLPE  245
            ||||||||||||||||||:|||||||||||||||||||||:|||||||||||||||:|:
Db   205  RPLRAINRVPSMRILVTLLLDTLPMLGNVLLCFVFFIFGVGVQLWAGLLRNRCFLDS  264

Qy   246  NFSLPLSVD-LERYYQTENEDESPFICSQPRENGMRSCRSVP---TLRGDGGGGPPCGLD  301
            .|. .|: : ||||||:||:|:||||||||||||||:|.. .         .  ||.||:
Db   265  AFVRNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHIPGRRELR------MPCTLG  318

Qy   302  YEAYN------SSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLE  354
            :|||       ..  .  |.|||||:|||:|:::|.|||||||||||||||||||||||||
Db   319  WEAYTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE  378

Qy   355  GWVDIMYFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRV  414
            |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   379  GWVDIMYYVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRA  438

Qy   415  RFLSNASTLASFSEPGSCYEELLKLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQ  474
            |.||:.|||||||||||||||||| | :|:||..:|:.| :|  ||..:.         |
Db   439  RHLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLYARWQSRWRKKVDPSAVQGQ  498

Qy   475  ETQPSSSCSRSHRR-LSVHHLV-HHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRL  532
             :   . . |::|:  :.|||||:||||||||||||. .::.    |        ||:|:
Db   499  --GPGHRQRRAGRHTASVHHLVYHHHHHHHHHYHFSHGSPRRPGPEFGACD---TRLIV  551

Qy   533  MLPPSTPALSGAPPGGAESVHSFYHADCHLE--PVRCQAPPPRSPSEASGR-TVGSGKV  589
             . ||| :|||||||.|||||| ||||| ||:   :|::     :...|   | ||..  
Db   552  RAGAPPSPSPGPSPGRGPPDAESVHSIYHADCHIEGPQERARVAHAAATAAASLRIATGLGTM  611

Qy   590  -YPTV------HTSP------PPETLKEKAIVEVAASSGPPTLTSLNIPPGPY  629
             |||:      ||.        ..    :.|: .  ||||.||:|||.    |||
Db   612  NYPTILPSGVGSGKGSTSPGPGKWAGGPPGT----GGHGPLSLNS----PDPY  657

Qy   630  SSMHKLLETQSTGACQS------SCKISSPCLKADSGACGPDSCPYCARA-GAGEVELA  681
             : :    :  . || :        |.  ||||.   |.|  | ||||.|  |:|.|||:
Db   658  EKIPHVVGEHGLGQAPGHLSGLSVPCPLPSP-PAGTLTCELKSCPYCTRALEDPEGELS  715

Qy   682  DREMPDSDSEAVVEFTQDAQHSDLRDP------------HSRQRSLGPDAEPSSV  725
              .  |||| ..|||||||.:|.|  ||            |  ||: :  | ||.|
Db   716  GSESGDSDGRGVVEFTQDVRHGDRWDPTRPPRATDTPGPGPGSPQRRAQQRAAPGEPGWM  775

Qy   726  LAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSL  785
             .|:| || .:|:|||||||||.|||||||||||||||||||||||||||||||||||||:
Db   776  GRLWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGVEYHEQPEELTNALEISNIVFTSM  835

Qy   786  FALEMLLKLLVYGPFGYIKNPYNIFDGVVVISWEIVGQQGGGLSVLRTFRLMRVLKLV  845
            |||||||||| .||:|||:|||||||| :||||||||| .|||||||||||:||||||
Db   836  FALEMLLKLLACGPLGYIRNPYNIFDGIIVVISWEIVGQADGGLSVLRTFRLLRVLKLV  895

Qy   846  RFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRK  904
            ||||||:|||||| |||||||||||||||||||||||||||||| || .:|. |||:||||
Db   896  RFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLFGGCKFSLKTDTGDTVPDRK  955

Qy   905  NFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILV  964
            |||||||||||||||||||||||.||||||||||||||||:|||||||||||||||||||
Db   956  NFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGNYVLFNLLVAILV  1015

Qy   965  EGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGD-------GD  1015
            ||||||                       |||:|||||:.|       |        ||
Db  1016  EGFQAE------------------------GDANRSDTDEDKTSVHFEEDFHKLRELQTTE  1052

Qy  1016  RKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSA  1075
```

```
Query Match          52.2%;  Score 6210;  DB 1;  Length 2353;
Best Local Similarity 56.6%;  Pred. No. 1.1e-277;
Matches 1364; Conservative 216; Mismatches 526; Indels 302; Gaps 59;
```

```
Db  1053 LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATMPTPKSSPFLDAAPSLPDSRRGSSSSGD 1112
         ||| :  |  |   |     || | |     |    || :: |||||  ||  |||
Db  2049 VTQGGSLQSPPRSRPPASVRTRKHTFGQRCVSSRAAPGGE------RAEASDPADEE 2100

Qy  1076 EPGAAHEMKSPPSARSSPHSPWSGAASSWTSRRSSRNSLGRAPSLKRRSPSGEERRSLLSGE 1135
         :  |  |:  ||   |:  |  ||   || |||   |||||||||   |:||| |||||
Qy  2110 LSWISGDLLP------PGQQEEPP---SPRDLKKCYSVRAQSCQRRPTSWLDEQRRHSIA 2160

Db  1113 PP--LGDQKPPASLRSSPCAPWGPGAWSSRRRSWSSLGRAPSLKRRGQCGERESLLSGE 1170
          |    | |  ||| || |  || |  || |||  |||||||||||  | ||||||||
Db  2101 VSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGFLDKP-GRADEQWRPSAE 2159

Qy  1136 GQESQDEESSEEERASPA--GSDHRHRGSLREEAKSSFDLPDTL------QVPGLH-- 1184
          : | |||   | |||    | | : ||| |  | ||   | |        |:|||
Qy  2161 VSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSTIDPP-ESQQPRTPSP--- 2216

Db  1171 GKGSTDDE--AEDGRAAPGPRATPLRRAESLDPRLRPAALPPTKCRDRDGQVVALPSDF 1228
          : |:|||   | |  :     | ||     |   |   |  |  : |   ||  |: |
Db  2160 LGSGEPGEAKAWGPE-----AEP-ALGARRKKKMSPPCISVEPPAEDBGSARPSAAEGG 2212

Qy  1185 --RTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKGERVRAWIRA 1242
           | |||   || :||      |  | | |: |||    ||    | | |
Qy  2217 GICLRRRAPS------SDSKDPL---ASGPPDSMA--ASPSPKKDVLSLSGLSSDPAD 2263

Db  1229 FLRIDSHREDAEELDDDSEDSCCLRLHKVLEPYKP--------------QWCRS 1268
          |  :|  || |  |  ||  |    | | |: |                | | |
Db  2213 STTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGQASCRAEHLTVPSFAFEPLD 2272

Qy  1243 RLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDP 1302
          | : ||:   |                 |||||||||| ||:||||| ||| |||| |||
Qy  2264 L------DP 2266

Db  1269 ------REAWALYLFSPQNRFRVSCQKVITHKMFDHVLVFIFLNCVTIALERPDIDP 1320
                               | |||||||||||| ||:|||||||:|||||||||
Db  2273 LGVPSGDP 2280

Qy  1303 HSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDIL 1362
          ||:||:||: |||||||:|:|||.|||||||  :||| ||.||||:|||||||:|::||:

Db  1321 GSTERVFLSVSNVIFTAIFVAEMVKVVALGLLSGEHAYLQSSWNLLDGLLVLVSLVDIV 1380

Qy  1363 VSMVSDSGTKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAF 1422
          |:|.:: | ||||:||||||||||||||||||||.|||||||:|||:||||||| ||||

Db  1381 VAMASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAF 1440

Qy  1423 FIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVL 1482
          ||||||||||||||||:||:| ||||:| | :|  | ||||| ||||||||||||||||

Db  1441 FIIFGILGVQLFKGKFYYCEGPDTRNISTKAQCRAAHYRWVRRKYNFDNLGQALMSLFVL 1500

Qy  1483 ASKDGWVDIMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHK 1542
          :|||||.|||||||||||||||| :|||||||||||||||| |||||||||||||||||

Db  1501 SSKDGWNIMYDGLDAVGVDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFVGVVVENFHK 1560

Qy  1543 CRQHQEEEARRREEKRLRLLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLD 1596
          ||||||.||||||||||| ||| ||        |: |||:||| |  |:|||||||||

Db  1561 CRQHQEAEEARRREEKRLRLRLERRRRSTFPSPEAQRRPYYADYSPTRRSIHSLCTSHYLD 1620

Qy  1597 LFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRRFFQDR 1656
          ||||  | .|||||:||||:||: |||||| ||| ||::||:|  ||||||||||||:||

Db  1621 LFITFIICVNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVFEAALKLVAFGFRRRFFKDR 1680

Qy  1657 WNQLDIAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLD 1716
          ||||||||||||||||||||||::|:||||||||||||||||||||||||||:.|||||

Db  1681 WNQLDIAIVLLSIMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLD 1740

Qy  1717 TVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLT 1776
          ||:||||||||||||||||||::||||||||| ||| | :|||| |||| || ||||||

Db  1741 TVVQALPQVGNLGLLFMLLFFIYAALGVELFGRLECESEDNPCEGLSRHAFTFSNFGMAFLT 1800

Qy  1777 LFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVAVLM 1833
          |||||||||||||||||||:|    |||| ||||||||||:||| ||||||||||||

Db  1801 LFRVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPVYFVTFVLVAQFVLVNVVAVLM 1860

Qy  1834 KHLEESNKEAKEEAEELEABLELEMKTLSPQHSPLGSPFLWPGVEGPDSP---DSPKPGA 1890
          |||||||||| | |||| |: :| ||                        :|  |||

Db  1861 KHLEESNKEAREDAEELDAEITELEM-------------------AQGPGSARRVDADRP-- 1899

Qy  1891 LHPAHARSASHFSLEHPTMQPHPTELPG---PDLLTVRKSGVSRTHSLPNDSYMCRHG 1946
               : |:  |||  ||: :       |||| :| |||:|||||||||||:|  |

Db  1900 ----------PLPQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV 1937

Qy  1947 STAEGP------LGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSA 1997
                     || | || ||:| ::||||||||:|  | ::| :||   || |||:

Db  1938 VPASAPHPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIP-----LAVSSPA 1989

Qy  1998 PTWGTIPKLPPPG--RSPLAQRPLRRQAAIRTDSLDVQGLGSREDLL--AEVSGPSP--P 2051
           :     |   |   || |  ||| |||:|:|||| ::||| :|    ::||| | |

Db  1990 RSGEPLHALSPRGTARSPSLLSRLLCRQEAVHTDSLBGK-IDSPRDTLDPAEPGEKTPVRP 2048

Qy  2052 LARAYSFWG--QSSTQAQQHSRSHSKISKHMTPPAPCPGEPENWGKGPPETRSSLELDTE 2109
          | : |: |
```

RESULT 12
CCAH_MOUSE

```
ID   CCAH_MOUSE     STANDARD;      PRT;   2365 AA.
AC   O88427; Q9JKU5;
DT   15-JUL-1999 (Rel. 38, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.2).
GN   Name=Cacna1h;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Mittman S.;
RT   "Exon organization of mouse Cacna1h.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1823-1952 FROM N.A.
RC   STRAIN=C57Bl/6J;
RA   Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1H
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AF226868; AAK21607.2; -.
DR   EMBL; AY026385; AAK21607.2; JOINED.
DR   EMBL; AF051947; AAC67240.1; -.
DR   MGD; MGI:1928842; Cacna1h.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCALPHA1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW   Multigene family; Phosphorylation; Repeat; Transmembrane;
KW   Voltage-gated channel.
```

FT	REPEAT	87	422	I.
FT	REPEAT	776	1015	II.
FT	REPEAT	1292	1569	III.
FT	REPEAT	1613	1874	IV.
FT	DOMAIN	1	100	Cytoplasmic (Potential).
FT	TRANSMEM	101	119	S1 of repeat I (Potential).
FT	DOMAIN	120	139	Extracellular (Potential).
FT	TRANSMEM	140	160	S2 of repeat I (Potential).
FT	DOMAIN	161	169	Cytoplasmic (Potential).
FT	TRANSMEM	170	184	S3 of repeat I (Potential).
FT	DOMAIN	185	193	Extracellular (Potential).
FT	TRANSMEM	194	212	S4 of repeat I (Potential).
FT	DOMAIN	213	232	Cytoplasmic (Potential).
FT	TRANSMEM	233	253	S5 of repeat I (Potential).
FT	DOMAIN	254	394	Extracellular (Potential).
FT	DOMAIN	395	419	S6 of repeat I (Potential).
FT	TRANSMEM	420	790	Cytoplasmic (Potential).
FT	DOMAIN	791	811	S1 of repeat II (Potential).
FT	DOMAIN	812	824	Extracellular (Potential).
FT	TRANSMEM	825	846	S2 of repeat II (Potential).
FT	DOMAIN	847	852	Cytoplasmic (Potential).
FT	DOMAIN	853	871	S3 of repeat II (Potential).
FT	TRANSMEM	872	879	Extracellular (Potential).
FT	TRANSMEM	880	903	S4 of repeat II (Potential).
FT	DOMAIN	904	914	Cytoplasmic (Potential).
FT	TRANSMEM	915	935	S5 of repeat II (Potential).
FT	DOMAIN	936	987	Extracellular (Potential).
FT	DOMAIN	988	1012	S6 of repeat II (Potential).
FT	TRANSMEM	1013	1301	Cytoplasmic (Potential).
FT	DOMAIN	1302	1324	S1 of repeat III (Potential).
FT	TRANSMEM	1325	1342	Extracellular (Potential).
FT	DOMAIN	1343	1363	S2 of repeat III (Potential).
FT	DOMAIN	1364	1373	Cytoplasmic (Potential).
FT	TRANSMEM	1374	1393	S3 of repeat III (Potential).
FT	DOMAIN	1394	1407	Extracellular (Potential).
FT	TRANSMEM	1408	1429	S4 of repeat III (Potential).
FT	DOMAIN	1430	1439	Cytoplasmic (Potential).
FT	DOMAIN	1440	1463	S5 of repeat III (Potential).
FT	TRANSMEM	1464	1540	Extracellular (Potential).
FT	DOMAIN	1541	1566	S6 of repeat III (Potential).
FT	DOMAIN	1567	1627	Cytoplasmic (Potential).
FT	TRANSMEM	1628	1648	S1 of repeat IV (Potential).
FT	DOMAIN	1649	1662	Extracellular (Potential).
FT	DOMAIN	1663	1684	S2 of repeat IV (Potential).
FT	TRANSMEM	1685	1691	Cytoplasmic (Potential).
FT	DOMAIN	1692	1710	S3 of repeat IV (Potential).
FT	DOMAIN	1711	1724	Extracellular (Potential).
FT	TRANSMEM	1725	1748	S4 of repeat IV (Potential).
FT	DOMAIN	1749	1762	Cytoplasmic (Potential).
FT	DOMAIN	1763	1783	S5 of repeat IV (Potential).
FT	TRANSMEM	1784	1846	Extracellular (Potential).
FT	DOMAIN	1847	1874	S6 of repeat IV (Potential).
FT	TRANSMEM	1875	2365	Cytoplasmic (Potential).
FT	DOMAIN	521	531	Poly-His.

FT	DOMAIN	1594	1597	Poly-Arg.
FT	SITE	378	378	Calcium ion selectivity and permeability (By similarity).
FT	SITE	971	971	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1515	1515	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1819	1819	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	1477	1477	N-linked (GlcNAc...) (Potential).
FT	CONFLICT	1823	1825	GIM -> ARG (in Ref. 2).
FT	CONFLICT	1914	1914	D -> E (in Ref. 2).
FT	CONFLICT	1945	1947	APA -> LLQ (in Ref. 2).
FT	CONFLICT	1952	1952	S -> A (in Ref. 2).
FT	CONFLICT	1953	2351	Missing (in Ref. 2).
SQ	SEQUENCE	2365	AA;	261944 MW; 9A8A17570C210596 CRC64;

```
Query Match             51.9%;  Score 6176.5;  DB 1;  Length 2365;
Best Local Similarity   56.6%;  Pred. No. 4e-276;
Matches 1365;  Conservative 235;  Mismatches 528;  Indels 285;  Gaps 61;
```

```
Qy      2 DEEEDGAGAEESGQPRSFMRLNDLS-GAGGRP---GPGS---AEKDPGS---AD---SEA 48
                  : :: :||::: ||||.:  :   |.|      :||
Db      9 DEVRVPLGAGPSA--PAAPVRASPASPGVPGREEQRGSGSSVLAPESPGTECGADLGADEE 67

Qy     49 EGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIA 108
             :::||||||||.||||||||.|||||||||||||||||||.||||||||||||||||:
Db     68 QPVPYPALAATVFFCLGQTTRPRSWCLRLVCNPWFEHISMLVIMLNCVTLGMFRPCEDVE 127

Qy    109 CDSQRCRILQAFDDIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYS 168
             ::|:||.|||.|||||||||||||.|.||||.|::||||||||||||||||||.:.:|
Db    128 CRSERCSILEAFDDTFTFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVMAGMMEYS 187

Qy    169 LDLQNVSFSAVRTVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFGIV 228
             ||||||:||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 LDGHNVSLSAIRTVRVLRPLRAINRVPSMRIIVTLLLDTLPMLGNVLLCFFVFFIFGIV 247

Qy    229 GVQLWAGLLRNRCFLPENFSLPLSVD-LERYYQTENEDESPFICSQPRENGMRSCRSVPT 287
             |||||||||||||||||||||||:||     .:|::|:.:|||...|:.||:...||:
Db    248 GVQLWAGLLRNRCFLDSAFVRNNLTFLRPYYQTEEGENPFICSSRRDNGMQXCSHIPS 307

Qy    288 ---LRGDGGGGPPCGLDYEAY------NSSNTTCVNWNQYYTNCSAGEHNPFKGAINF 337
                  : |::...: :||                :::|.: .|.: . :.||.||||
Db    308 RRELR------VQCTLGWEAYGQPQAEDGGAGRNACINWNQYYNVCRSGEFNPHNGAINF 361

Qy    338 DNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQ 397
             ||||||||||||||||||||||||.|||||||||||||||||||||||||||||||||||
Db    362 DNIGYAWIAIFQVITLEGWVDIMYYVMDAHSFYNFIYFILLIVGSFFMINLCLVVIATQ 421

Qy    398 FSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKLVLVYIILRKAARRLAQVSRA 457
             ||||||||||||||||.|||:||||||||||||||||||||||:|||||||||||||:||||
Db    422 FSETKQRENQLMREQRARYLSNDSTLASFSEPGSCYEELLKKVVGHIFRKVRRSLRLVAR 481

Qy    458 AGVRVGLLSSP-APLGGGETQPSSSCSRSHRR-LSVHHLV-HHHHHHHYHLGNGTLRA 514
             |.: :||.||   ||.|.|..:|  |:. : :  :|:|:. ::::::::|:
Db    482 WQSRWRKKVDPSSTLHGQ--GPRRRPRRAGRRTASVHHLVYHHHHHHHYHFSHGGPRR 539

Qy    515 PRASPEIQDRDANGSRRLM--LPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPP 572
             |.|||: .:|  |.    :     |..|:..|.| |..  :||..:|:|   .|  .||
Db    540 P--SPE----PGAGDTRLVRACVPPSPSPGHGPP-DESVHSIYHADCHVEGPQERARV 592

Qy    573 PRSPSEASGRTVGSG---KVYPTV------------HTSPPPETLKEKALVEVAASSGPPTL 619
             |.|||:|:||.|.||      :|.             .|:|||:|||:|.||:|:::.:|.:
Db    593 AHTIATAASLKLASGLGTMNYPTLPSGAVNSKGSTSSRPKGLR------SAGTPGA 643

Qy    620 TS---LNI-PPGPYSSMHKLLETQSTGACQS-------SCKISSPCLKADSGACGPDSCP 668
             ||     : |||||::|||:||:||||||.:           :.:|.||.||||||.:||
Db    644 TAHSPLSLGSPSPYEKIQHVVGEQGLGRASSHLSGLSVPCPLPSP--QAGTLTCELKSCP 701

Qy    669 YCARA-GAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDP------------HSRRQR 714
             |||.:  |.|                                           ||::.|
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Db   702 YCASALEDPEFEFSGSESGSDAHGVYEFTQDVVRHGDCRDPVQQPHEGGTPGHGNERWRP  761

Qy   715 SLGPDAEPSSVLAFWRLICDTFPRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNA  774
            ::          |||||| :|||||||:||||||  |||||||||||||:|||| |||||
Db   762 PLRTASQPGGLGRLWASFSSKLRRIVDSKYFNRGIMAAILVNTLSMGVEYHEQPDELTNA  821

Qy   775 LEISNIVFTSLFALEMLLKLLVVGPFGYIKNPYNIFDGVIVVISWEIVGQQGGLSVLR  834
            |||||||| | |||||||||| ||| ||:||||||||:|||||||||||| :||||||
Db   822 LEISNIVFISMFALEMLLKLLACGPLGYIRNPYNIFDGIVVVISWEIVGQADGGLSVLR  881

Qy   835 TFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASE  894
            |||| |||||||||||| |||||||:||||||||||||||||||||||||||||||||:
Db   882 TFRLLRVLKLVRFLPALRRQLVVLMRTMDNVATFCMLLMLFIFIFSILGMHLFGCKFSLK  941

Qy   895 RD-GDTLPDRKNFDSLLWAIVTVFQILITQEDWNKVLYNGMASTSSWAALYFIALMTFGNY  953
               |||:||||||||||||||||||||||||||| ||||||||||||||||||:||||||
Db   942 TDSGDTVPDRKNFDSLLWAIVTVFQILITQEDWNVVLYNGMASTSSWAALYFVALMTFGNY 1001

Qy   954 VLFNLLVAILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGD 1013
            |||||||||||||||||                      |||| | : |:   ::
Db  1002 VLFNLLVAILVEGFQAE---------GDATRSDTDEDKTSTHLEED                1038

Qy  1014 GDRKK----------CLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGRALG 1063
                          | ||:| |:   | :|  |||:||||||||| | ||  ||||:|
Db  1039 FDKLRDVRATEMKMYSLAVTPNG-HLEGRGSLPPPLLITHTAATPMPTPKS-SPHLDMAHT 1096

Qy  1064 PASRRTSSSGSGAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSSNSLGRAPSLKRRS 1123
             | || | |  :    :     || : |||  : ||  ||| ||| | ||||||||||||
Db  1097 LLDSRRSRSSSSGSVDPQLG-DQKSLASLRSSPCAPWGPNSAGSSRRSSWNSLGRAPSLKRRS 1155

Qy  1124 PSGERRSLLSGEGQESQDEE-ESSEEERASPAGSDHRHRGSLEREA------KSSFDL-   1174
             | |||||||||::|:|:|  | |||| || |    : :   |:        |||:|
Db  1156 QCGERESLLSGEGKGSTDDEAEDSRPNSGTHPGASPGPRATPLRRRABESLGHRSTMDLCPP 1215

Qy  1175 -PDTLQVPGLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDDADDEGNLSKG 1233
                                     | :|                |:||    |   :
Db  1216 -----TKFRDCNGQMVALPSEFFLRIDSHKEDAAEFDDDIEDSCC                 1262

Qy  1234 ERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITI 1293
            :|  :|:  :  |   ||| |||| ||||:| | | ||: |||||||||||| |||||||
Db  1263 FRLHKVLEPYAPQWCSSRESWALYLFPPQNRLRVSCQKVIAHKMFDHVVLVFIFLNCITI 1322

Qy  1294 AMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLL 1353
            |:|||:||| ::|| || :||||||| | .||:|||||||  |||:|||:|||||||||
Db  1323 ALERPDIDPGSTERAFLSVSNYIFTAIFVVEMMVKVVALGLLWGEHAYLQSSWNVLDGLL 1382

Qy  1354 VLISVIDILVSMVSDSGTKIIGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIG 1413
            || |:||| |:: ::  |:|:|:|||||||||||||||||||  ||||||||:||:|||
Db  1383 VLVSLVDIIVASAGGAKILGVLRVLRLLRTLRPLRVISRAPGLKLVVETLISSLRPIG   1442

Qy  1414 NIVVICCAFFIIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLG 1473
            |||:||||||||||||||||||||| | ||:||||| | :|  |.|||||:|||||||
Db  1443 NIVLICCAFFIIFGILGVQLFKGKFYYCEGTDTRNITTKAECHAAHYRWVRRKYNFDNLG 1502

Qy  1474 QALMSLFVLASKDGWVDIMYGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFV 1533
            ||||||||| |||||| ||| |||||:||||: ||||||||||||||||.|||||||||
Db  1503 QALMSLFVLSSKDGWVNIMYDGLDAVGIDQQPVQNHNPWMLLYFISFLLIVSFFVLNMFV 1562

Qy  1534 GVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRR------KAQCKPYYSDYSRFRLLVH 1587
            |||||||||||||||   |||||||||||||::||       :||:|||:||| :  :|
Db  1563 GVVVENFHKCRQHQEAEEARRREEKRLRRLERRRRSTFPNPEAQRRPYYADYSHTRRSIH 1622

Qy  1588 HLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAF 1647
             ||||||||||||  | |||||:| ||| ||: ||||||:|||:|||||| |: ||||||
Db  1623 SLCTSHYLDLFITFIICLNVVTMSMEHYNQPKSLDEALKYCNYVFTVIFVFEAALKLVAF 1682

Qy  1648 GFRRFFQDRWNQLDLAIVILLSIMGITLEEIEVNASLPINPTIIRMRVLRIARVLKLLKM 1707
            |||||| ||||||||||| |||||| ||||| :|| |||| :|||:|||||||||||||
Db  1683 GFRRFFKDRWNQLDLAIVLLSIMGIALEEIEMNAALPINPIIIRIMRVLRIARVLKLLKM 1742

Qy  1708 AVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATF 1767
            | ||||||||| ||||||||||||||||| | |||||||||||| |  ||||| ||||
Db  1743 ATGMRALLDTVQALPQVGNLGLLFMLLFIYAALGVELFGRLECSEDNPCEGLSRHATF   1802
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Qy  1768 RNFGMAFLTLFRVSTGDNWNGIMKDTLRDC---DQESTCYNTVISPIYVSFVLTAQFVL 1824
            :|||||||||||||||||||||||||||   | :: ||| :||| ::|| ||||||
Db  1803 TNFGMAFLTLFRVSTGDNWNGIMKDTLRECTREDKHCLSYLPALSPVYFVTFVLVAQFVL 1862

Qy  1825 VNVVIAVLMKHLEESNKEAKEEAELEAELELEM-KTLSPQHSPLGSPFLWPGVEGPDSP 1883
            ||||:||||||||||||||:||||:| || :   || |  || | |    || | :
Db  1863 VNVVVAVLMKHLEESNKEAREDAEMDAEIELEIAQGSTAQPPSTAQES-----QGTD-P 1915

Qy  1884 DSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPNDSYMC 1943
            :|                     ::|          ||     | : : |  ||||||
Db  1916 DT---------------------------------------PNLLVVRKVSVSRMLSLPNDSYMF 1941

Qy  1944 RHGSTAEGPLGHRGWGLP------KAQSGGVLSVHSQPADTSYIIQLPKDAPHLLQPHSA 1997
              |    | | | | |         | : | :::|  || || : |  :| ::  ||
Db  1942 RPVAPAAAPHSH------PLQEVEMETYTGPVTSAHSPSLEPRTSFQVPSAASSPARA-SD 1995

Qy  1998 PTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYS 2057
            |   |  :|   ||| |               :  |: ||  |    |  | | |
Db  1996 PLCALSPRDTP--RSLSLSRILYRQEAMHAESLEGQIDDAGEDGIPDYTEPAENISMSQA 2053

Qy  2058 FWG----------QSSTQAQQHSRSHSKISKHMTPPAPCPGPEENWGKGPPETRSSLELD 2107
            | |          ||| :|   :| :|:| :    |:: |   |  | :| :|: |
Db  2054 PLGTLRSPPCSPRPASVRTRKHTFGQHCISSR--PPT------------LGGDDAEAADPAD 2101

Qy  2108 TELSWISGDLLP----------PGGQEEP-------SPRDLKKCYSVEAQSCQRRPTSWLD 2152
            || :: ||:|            ||          || :   | :  | :|    | ||
Db  2102 EEVSHITSSAHPWPATEPHSPEASPTASPAKGTVGSGRDPHRFCSVDAQSFLDKP-GRPD 2160

Qy  2153 EQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPL-GGPGSRPKKKLSPPSITIDPP-ESQGP 2210
            :|                 :|  |::|       | |  |       ||  :|  | ||
Db  2161 AQRWSSVE---LDNG-DGHLESGEVRARASELEPALGARRKKKMSPPCISIDPPTEDEGS 2216

Qy  2211 RTPPSP---GICLRRRAPSSDSK-----------DPLASGPPDSMAASPSPKKDV 2251
            | ||:      | :| |  ::|            :|| |||| |  |: |  |:
Db  2217 SRPPAAEGGNTTLRRRTPSCEAALHRDCPESTEGPGTGDPVAKGERWGQA---SCRAEH 2273

Qy  2252 LSLSGLSSDPADL 2264
             | | |:  |  :
Db  2274 LTVPNFAFEPLDM 2286
```

RESULT 13
CCAI_HUMAN
ID   CCAI_HUMAN   STANDARD;   PRT;   2223 AA.
AC   Q9P0X4; O95504; Q7Z6S9; Q8NFX6; Q9NZC8; Q9UH15; Q9UH30; Q9ULJ9;
AC   Q9UNE6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).
GN   Name=CACNA1I; Synonyms=KIAA1120;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Brain;
RX   MEDLINE=99381950; PubMed=10454147;
RA   Mittman S., Guo J., Emerick M.C., Agnew W.S.;
RT   "Structure and alternative splicing of the gene encoding alphaII, a
RT   human brain T calcium channel alphaI subunit.";
RL   Neurosci. Lett. 269:121-124(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Brain;
RX   MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200;
RA   Monteil A., Chemin J., Leuranguet V., Altier C., Mennessier G.,
RA   Bourinet E., Lory P., Nargeot J.;
RT   "Specific properties of T-type calcium channels generated by the human
RT   alphaI subunit.";

```
RL   J. Biol. Chem. 275:16530-16535(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.
RC   TISSUE=Brain;
RX   MEDLINE=22074770; PubMed=12080115;
RA   Gomora J.C., Murbartian J., Arias J.M., Lee J.-H., Perez-Reyes E.;
RT   "Cloning and expression of the human T-type channel Ca(v)3.3: insights
RT   into prepulse facilitation.";
RL   Biophys. J. 83:229-241(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA   Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA   Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA   Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA   Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA   Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA   Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA   Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA   Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA   Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA   Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA   Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA   Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA   Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA   Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA   Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA   Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA   Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA   Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA   Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA   Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA   Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA   Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA   Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA   Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Do T.,
RA   Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA   Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA   Lewis J., Lewis S., Lin S., Loh P., Malaj E., Nguyen T., Pan H.,
RA   Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA   Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA   Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA   Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA   Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA   Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA   Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA   Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA   Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA   Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA   Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA   Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA   O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA   Khan A.S., Lane L., Tilahun Y., Wright H.;
RT   "The DNA sequence of human chromosome 22.";
RL   Nature 402:489-495(1999).
RN   [5]
RP   SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA   Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
-!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. Isoform alpha-1I
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes. Gates in voltage ranges
CC       similar to, but higher than alpha 1G or alpha 1H (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=Delta36b;
CC         IsoId=Q9P0X4-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9P0X4-2; Sequence=VSP_000951;
CC       Name=3; Synonyms=Alpha1I-a;
CC         IsoId=Q9P0X4-3; Sequence=VSP_000950, VSP_000951;
CC       Name=4;
CC         IsoId=Q9P0X4-4; Sequence=VSP_000950;
-!- TISSUE SPECIFICITY: Brain specific.
-!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
-!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II (By similarity).
-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
-!- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to
CC       erroneous gene model prediction.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF129133; AAD45251.1; -.
DR   EMBL; AF142567; AAF25722.1; -.
DR   EMBL; AF211189; AAF44626.1; -.
DR   EMBL; AF393329; AAM67414.1; -.
DR   EMBL; AL008716; CAA15494.1; -.
DR   EMBL; AL022312; CAB62988.1; -.
DR   EMBL; AL022319; CAB62996.1; ALT_SEQ.
DR   EMBL; AL022319; CAD92536.1; -.
DR   EMBL; AB032946; BAA86434.1; -.
DR   Genew; HGNC:1396; CACNA1I.
DR   MIM; 608230; -.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.
DR   GO; GO:0008332; F:low voltage-gated calcium channel activity; NAS.
DR   GO; GO:0006816; P:calcium ion transport; NAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR01629; TVDCCALPHA1.
DR   PRINTS; PR01629; CACHANNEL.
KW   Alternative splicing; Calcium; Calcium channel; Calcium-binding; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Polymorphism; Repeat; Transmembrane; Voltage-gated channel.
FT   REPEAT         66    401       I.
FT   REPEAT        626    865       II.
FT   REPEAT       1157   1434       III.
FT   REPEAT       1472   1733       IV.
FT   DOMAIN          1     78       Cytoplasmic (Potential).
FT   TRANSMEM       79     99       S1 of repeat I (Potential).
FT   DOMAIN        100    120       Extracellular (Potential).
FT   TRANSMEM      121    141       S2 of repeat I (Potential).
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FT   DOMAIN     142   148   Cytoplasmic (Potential).
FT   TRANSMEM   149   169   S3 of repeat I (Potential).
FT   DOMAIN     169   173   Extracellular (Potential).
FT   TRANSMEM   174   191   S4 of repeat I (Potential).
FT   DOMAIN     192   211   Cytoplasmic (Potential).
FT   TRANSMEM   212   232   S5 of repeat I (Potential).
FT   DOMAIN     233   377   Extracellular (Potential).
FT   TRANSMEM   378   398   S6 of repeat I (Potential).
FT   DOMAIN     399   640   Cytoplasmic (Potential).
FT   TRANSMEM   641   661   S1 of repeat II (Potential).
FT   DOMAIN     662   676   Extracellular (Potential).
FT   TRANSMEM   677   697   S2 of repeat II (Potential).
FT   DOMAIN     698   702   Cytoplasmic (Potential).
FT   TRANSMEM   703   721   S3 of repeat II (Potential).
FT   DOMAIN     722   729   Extracellular (Potential).
FT   TRANSMEM   730   753   S4 of repeat II (Potential).
FT   DOMAIN     754   764   Cytoplasmic (Potential).
FT   TRANSMEM   765   785   S5 of repeat II (Potential).
FT   DOMAIN     786   841   Extracellular (Potential).
FT   TRANSMEM   842   862   S6 of repeat II (Potential).
FT   DOMAIN     863  1166   Cytoplasmic (Potential).
FT   TRANSMEM  1167  1187   S1 of repeat III (Potential).
FT   DOMAIN    1188  1209   Extracellular (Potential).
FT   TRANSMEM  1210  1230   S2 of repeat III (Potential).
FT   DOMAIN    1231  1244   Cytoplasmic (Potential).


Query Match             46.2%;  Score 5496.5;  DB 1;  Length 2223;
Best Local Similarity   51.3%;  Pred. No. 8.2e-245;
Matches 1241;  Conservative 217;  Mismatches 527;  Indels 435;  Gaps 60;

Qy    31  RPGPGSAEKDPGSADSEAEG---LPYPALAPVFVFFYLSQDSRPRSWCLRTVCNPWFERI   86
          ::||| :| |.||     |    : |:|||| :.|| |  : :::||| ||||.||||| |
Db    25  QPGPRSPPSSPPGLEEPLDGADPHVPDLAPIAFFCLRQTTSPRNWCIKMVCNPWFECV   84

Qy    87  SMLVILLNCVTLGMFRPCEDIACDSQRCRIIQAFDDFIFAFFAVEMVKMVALGIFGKKC  146
          ||||||||||| ||  ||  :.|.| :|  :||.|||||| ||| |||.|||||||||||
Db    85  SMLVILLNCVTIGMYQPCDDMDCLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKC  144

Qy   147  YLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLLD  206
          |||||||||||||| |||:|||||||| . ||:||||||||:|||||||||||| ||||
Db   145  YLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTVRLRPLKAINRVPSMRILVNLLLD  204

Qy   207  TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE  266
          |||||||||||||||||||||||||||||||||||| ||| |.. :.|| |||| |. ||
Db   205  TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLEENFTIQGDVALPYYQPEDDE  264

Qy   267  SPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL-----DYEAYNSSSNTT--CVNWNQ  318
          .|||| .   ||: .|  : | |.     .||      |   |.:. | ...|||||:
Db   265  MPFICSLSGDNGIMGCHEIPPLKEQ--GRECLSKDDVYDFGAGRQDLNASGLCVNWNR  321

Qy   319  YYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFWMDAHSYFNFIYFILL  378
          || .| :| .|.|||||||||||||||.||||||||||||||| .||||| ||||||||
Db   322  YYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVDIMYYVMDAHSFYNFIYFILL  381

Qy   379  IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLK  438
          |||||||||||||||||||||||||||.:|| ||| ::| ..||..|..|| .|||:: .
Db   382  IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEEIFQ  440

Qy   439  YLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCRSHRRLSVHHLVHHH  498
          |:. ||||| .:         | :. | | |:    : :.:    | ::.|.||.|.
Db   441  YVCHILRKAKR-----RALGLYQALQSRRQALGPEAPAKP---------------GPH  480

Qy   499  HHHHHHYH--LGNGTLRAPPASPEIQDRDAN-GSRRLM-LPPPSTPALGSGAPPGGAESV  553
          ||| |.|   | |.  ..   : |  .. ..  |.|: .|:||     ||: |      .
Db   481  AKEPRHYHGKTKGQG--------DEGRHLGSRHCQTLHGPASP--GNDHSGRE--  523

Qy   554  HSFYHADCHLEPVRCCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAAS  613
          |  | | | |    |.      .| .      |    : | .:     |          |
Db   524  ------------LC--PQHSPLDATPHTL----------VQPIPATL  546

Qy   614  SGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-  672
          :      :     | |:: :        | | |.|  |||   ||.||| | .||.|
Db   547  -------------------------ASDPASCPCCQHE  559

Qy   673  -----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL-  726
               .|.| |   | . .| |.  |  |.    ::. |  .  ::||||||  ||. .
Db   560  DGRRPSGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEEEQAD  616

Qy   727  ------AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISN  779
                | | |.|  ||.|||||||| |||||.|||||.|||||:||||||| |:||.||
Db   617  GAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPELTNILEICN  676

Qy   780  IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQQGGGLSVLRTFRLM  839
          :|||| ||||| :||  :| | | :||||||| :||:||.|||||  .|||||||||||
Db   677  VVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLL  736

Qy   840  RVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GD  898
          ||||||||:|||.|||||||||||||||||||||||||||||||||||:|||| | | ||
Db   737  RVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGD  796

Qy   899  TLPDRKNFDSLLWAIVTFVFQILTQEDWNKVLYNGMASTSWAALYFIALMTFGNYVLFNL  958
          |:||||||||||||||||||||||||||| ||||||||| ||:|||:|||||||.|||||
Db   797  TVPDRKNFDSLLWAIVTFVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNVLFNL  856

Qy   959  LVAILVEGFQAEEISKREDASGQLSCIQLPVDSQGQDANKSESEPDFFSPS--------  1009
          |.|||||||||                   |.|.:.   ||:|.|  :.
Db   857  ------------GDANRSYSDEDQSSSNIEBFDKLQE  893

Qy  1010  -LDGDGDRKKCLALVSLGEHPELRKSLLPLLPLIIHTAATPMSLPKSTSTGLGEALGPASRR  1068
           |.|.||   | |:.|.         ||  ||:               .|:| | ||  .| |
Db   894  GLDSSGDPKLCPIPMTPNGH--------SLPLGGHLGPAGAGPAPRL  936

Qy  1069  T---------------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGR  1115
                           ||..  :.:   : .|  :::::.||.|:||.  .|:||||.||.
Db   937  SLQPDPMLVALGSRKSSVMSLGRMSYDQRSLSSSRSSYYGPWGRSAAWASRRSSWN----  992

Qy  1116  APSLKRRSPSGERRSLLSGE-GQESQDEEESSE--ERASPAGSDH  1158
            |::|. ..|  .|||.|.  |:  .  ..:::  |.|||. .|:
Db   993  --SLKHKPSAEHESLLSAERGGGARVCEVAADEGPPRAAPLHTPHAHHIHHGPHLAHRH  1050

Qy  1159  -RHRGSLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRLARALRPD  1215
           ||:  .||.|    ||.. |:..|.| .||     |:.||:||||: |::   |  |
Db  1051  RHHRRTLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAGHEDCNGRMPSIAKDVFTKMG  1110

Qy  1216  DPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITH  1275
          | .| | |.|:.| :..||.::. :  .:   ||::||| ||:| |:.||.:||  |: |
Db  1111  DRGDRGED--EEEIDYTLCFRVRKMIDVVKPDWCEVREDWSVYLFSPENRFRVLCQTIIAH  1169

Qy  1276  KMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWC  1335
          |:||.||| .|||||||||:||| |: | :.|||||.|||||||.|.||||.||| ||. 
Db  1170  KLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLY  1229

Qy  1336  FGEQAYLRSSWNVLDGLIVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLRVISRA  1395
          |||||||||||||||| ||::|:||| ||:.|:.| |||| |||||||||||||||||||
Db  1230  FGEQAYLRSSWNVLDGFIVFVSIIDIVVSLASAGGAKILGVLRVLRLLRTLRPLRVISRA  1289

Qy  1396  QGLKLVETLMSSLKPIGNIVVICCAFFIIFGLGVQLFKGKFFVCQGEDTRNITNKSDC  1455
           ||||||||:|||||||||| |||||||||| ||||||||| .| |.|||||||:|||
Db  1290  PGLKLVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDC  1349

Qy  1456  AEASYRRVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGWDQQPIMNHPWMLL  1515
           .|.||.||.||||||||||||||||||||||||:||| ||||| . |.|| |||||||
Db  1350  MAANYRMVVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVADVDQQPVTNHPWMLL  1409

Qy  1516  YFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEARRREEKRLRLEKKRRKAQCKPY  1575
          |||||||||:||||||||||||||||||||||||. ||||||||||||||||||. ||
Db  1410  YFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREEKRLRLEKKRRKAQRLPY  1469

Qy  1576  YSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVI  1635
          |: |  .||| | :||||||| |||  | |||||||::|||:|  ||:| |||||:||.:
Db  1470  YATYCHTRLLIHSMCTSHYLDIFITFFICLNVVTMSLEHYNQPTSLETALYCNYMFTTV  1529

Qy  1636  FVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRV  1695
          ||||:| |||||| |||| ||||||||||||||:||||||||| ||:||||||| ||||
Db  1530  FVLEAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIRIRMRV  1589
```

```
Qy   1696  LRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDET  1755
                 ||||||||||||  ||||||||||  ||||||||||||||||||  ||||||
Db   1590  LRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKIVCNDE  1649

Qy   1756  HPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIY  1812
                 ||||:  ||||||||||||||||||:||||||||||||||:  :|||::  |||
Db   1650  NPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVSPLY  1709

Qy   1813  FVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEABLEEM-KTLSPQPHSPLGSP   1871
                 |||||||||||||||||||||||:  |:|:||||:|| : |:||||||||||||
Db   1710  FVSFVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRLPTGSP  1769

Qy   1872  FLMPGVEGPD------------------------------SP----------------DSPKPG  1889
                 ::                                      :
Db   1770  GA--PG-RGPGGAGGGDTBGGLCRRCYSPAQENLWLDSVSLIIKDSLBGELTIIDNLSGS  1827

Qy   1890  ALH----PAA------------------------------HARSAS------HRSLEHPTMQP------H  1913
                 :|||                                         ||||
Db   1828  IFHHYSSPAGCKKCHHDKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPTACPFGRKDS  1887

Qy   1914  PTELPGPDLLTVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGS  1967
                 ::                   :::::|                        |||
Db   1888  KGELDPPEPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQ  1943

Qy   1968  VLSVHSQPADTSYILQLPKDAPH-----LLQPHSAPTWCTIPKLPPPG-----RSPLAQ  2016
                 ||                            :||                         |||
Db   1944  APPSPFSPDASSPLLPMPAEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLRSPRVN  2003

Qy   2017  RPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPLARAYSFWGQSSTQAQQHSRSHSKI  2076
                 |:                            :||
Db   2004  CTLLRQATGSDTSLD------------------ASPSSSAGSLQTTLEDSLTLSDSPRRA-----  2045

Qy   2077  SKHMTPPAPCPGPEPNWGKGPPEIRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCY  2136
                 |||                                                 |||
Db   2046  ---LGPPAPAPGPRAGLS------PAARRRLSL------------------RGRGLFSLR  2078

Qy   2137  SVEAQSCQRRPTSWLDEQRHSIAVSCLDSGSQPHLGTDPSN---LGGQPLGGPGSGRPKK  2193
                 |||                                        |||
Db   2079  ----------HQRSHSSGGS-TSPGCTHHDSMDFPSDEBGRGGAGGGGAGSEHSE  2125

Qy   2194  KLSPPSIT---IDPPESQGPRTPPSPGICLRRRAPSSDS----KDPLASGPPDSMAASPS  2246
                 |||                                         |:|  |
Db   2126  TLSSLSTSLFCPPP-----PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPS  2179

Qy   2247  PKKDVLSLSGLSSDPADLDP  2266
                 ||
Db   2180  WAAD------RSKDPPGRAP  2193
```

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RESULT 14
CCAI_RAT
ID   CCAI_RAT     STANDARD;     PRT;   1835 AA.
AC   Q92Q78; Q9EQ59;
DT   30-MAY-2000 (Rel. 39, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-
DE   gated calcium channel alpha subunit Cav3.3) (CaVT.3).
GN   Name=Cacnali;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=99165796; PubMed=10066244;
RA   Lee J.-H., Daud A.N., Cribbs L.L., Lacerda A.E., Pereverzev A.,
RA   Kloeckner U., Schneider T., Perez-Reyes E.;
RT   "Cloning and expression of a novel member of the low voltage-activated
RT   T-type calcium channel family.";
RL   J. Neurosci. 19:1912-1921 (1999).
RN   [2]
```

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REVISIONS TO 345; 1656 AND 1737.
RA   Perez-Reyes E.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA   McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,
RA   Baillie D.L., Stea A., Snutch T.P.;
RT   "Molecular and functional characterization of a family of rat brain T-
RT   type calcium channels.";
RL   J. Biol. Chem. 276:3999-4011(2001).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. Isoform alpha-1I
CC       gives rise to T-type calcium currents. T-type calcium channels
CC       belong to the "low-voltage activated (LVA)" group and are strongly
CC       blocked by nickel and mibefradil. A particularity of this type of
CC       channels is an opening at quite negative potentials, and a
CC       voltage-dependent inactivation. T-type channels serve pacemaking
CC       functions in both central neurons and cardiac nodal cells and
CC       support calcium signaling in secretory cells and vascular smooth
CC       muscle. They may also be involved in the modulation of firing
CC       patterns of neurons which is important for information processing
CC       as well as in cell growth processes. Gates in voltage ranges
CC       similar to, but higher than alpha 1G or alpha 1H.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- PTM: In response to raising of intracellular calcium, the T-type
CC       channels are activated by CaM-kinase II (By similarity).
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF086827; AAD17796.2; -.
DR   EMBL; AF290214; AAG35188.1; -.
DR   InterPro; IPR001682; Ca/Na pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005445; TVDCCAlpha1.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01629; TVDCCALPHA1.
KW   Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW   Ionic channel; Multigene family; Phosphorylation; Repeat;
KW   Transmembrane; Voltage-gated channel.
FT   REPEAT        64    399       I.
FT   REPEAT       584    823       II.
FT   REPEAT      1116   1393       III.
FT   REPEAT      1431   1692       IV.
FT   DOMAIN         1     76       Cytoplasmic (Potential).
FT   TRANSMEM      77     97       S1 of repeat I (Potential).
FT   DOMAIN        98    115       Extracellular (Potential).
FT   TRANSMEM     116    137       S2 of repeat I (Potential).
FT   DOMAIN       138    146       Cytoplasmic (Potential).
FT   TRANSMEM     147    166       S3 of repeat I (Potential).
FT   DOMAIN       167    171       Extracellular (Potential).
```

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FT   TRANSMEM    172    189    S4 of repeat I (Potential).
FT   DOMAIN      190    209    Cytoplasmic (Potential).
FT   TRANSMEM    210    230    S5 of repeat I (Potential).
FT   DOMAIN      231    371    Extracellular (Potential).
FT   TRANSMEM    372    396    S6 of repeat I (Potential).
FT   DOMAIN      397    598    Cytoplasmic (Potential).
FT   TRANSMEM    599    619    S1 of repeat II (Potential).
FT   DOMAIN      620    632    Extracellular (Potential).
FT   TRANSMEM    633    654    S2 of repeat II (Potential).
FT   DOMAIN      655    660    Cytoplasmic (Potential).
FT   TRANSMEM    661    679    S3 of repeat II (Potential).
FT   DOMAIN      680    687    Extracellular (Potential).
FT   TRANSMEM    688    711    S4 of repeat II (Potential).
FT   DOMAIN      712    722    Cytoplasmic (Potential).
FT   TRANSMEM    723    743    S5 of repeat II (Potential).
FT   DOMAIN      744    795    Extracellular (Potential).
FT   TRANSMEM    796    820    S6 of repeat II (Potential).
FT   DOMAIN      821   1125    Cytoplasmic (Potential).
FT   TRANSMEM   1126   1148    S1 of repeat III (Potential).
FT   DOMAIN     1149   1166    Extracellular (Potential).
FT   TRANSMEM   1167   1187    S2 of repeat III (Potential).
FT   DOMAIN     1188   1197    Cytoplasmic (Potential).
FT   TRANSMEM   1198   1217    S3 of repeat III (Potential).
FT   DOMAIN     1218   1231    Extracellular (Potential).
FT   TRANSMEM   1232   1253    S4 of repeat III (Potential).
FT   DOMAIN     1254   1263    Cytoplasmic (Potential).
FT   TRANSMEM   1264   1287    S5 of repeat III (Potential).
FT   DOMAIN     1288   1364    Extracellular (Potential).
FT   TRANSMEM   1365   1390    S6 of repeat III (Potential).
FT   DOMAIN     1391   1445    Cytoplasmic (Potential).
FT   TRANSMEM   1446   1466    S1 of repeat IV (Potential).
FT   DOMAIN     1467   1480    Extracellular (Potential).
FT   TRANSMEM   1481   1502    S2 of repeat IV (Potential).
FT   DOMAIN     1503   1509    Cytoplasmic (Potential).
FT   TRANSMEM   1510   1528    S3 of repeat IV (Potential).
FT   DOMAIN     1529   1542    Extracellular (Potential).
FT   TRANSMEM   1543   1566    S4 of repeat IV (Potential).
FT   DOMAIN     1567   1580    Cytoplasmic (Potential).
FT   TRANSMEM   1581   1601    S5 of repeat IV (Potential).
FT   DOMAIN     1602   1664    Extracellular (Potential).
FT   TRANSMEM   1665   1692    S6 of repeat IV (Potential).
FT   DOMAIN     1693   1835    Cytoplasmic (Potential).
FT   SITE        355    355    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE        779    779    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE       1339   1339    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   SITE       1637   1637    Calcium ion selectivity and permeability
FT                             (By similarity).
FT   CARBOHYD    171    171    N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    242    242    N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    309    309    N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   1301   1301    N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   1304   1304    N-linked (GlcNAc...) (Potential).
FT   CONFLICT    193    193    M -> L (in Ref. 3).
FT   CONFLICT    291    291    C -> V (in Ref. 3).
FT   CONFLICT    394    394    V -> L (in Ref. 3).
FT   CONFLICT    406    406    E -> N (in Ref. 3).
FT   CONFLICT    485    485    C -> S (in Ref. 3).
FT   CONFLICT    512    512    D -> Y (in Ref. 3).
FT   CONFLICT    558    558    S -> R (in Ref. 3).
FT   CONFLICT    683    683    G -> S (in Ref. 3).
FT   CONFLICT    691    691    F -> S (in Ref. 3).
FT   CONFLICT    739    740    MH -> ID (in Ref. 3).
FT   CONFLICT    833    833    C -> Y (in Ref. 3).
FT   CONFLICT    846    846    F -> L (in Ref. 3).
FT   CONFLICT    856    856    S -> R (in Ref. 3).
FT   CONFLICT    905    905    L -> R (in Ref. 3).
FT   CONFLICT    913    913    M -> YW (in Ref. 3).
FT   CONFLICT    936    936    W -> G (in Ref. 3).
FT   CONFLICT    996    996    A -> R (in Ref. 3).
FT   CONFLICT   1060   1060    I -> M (in Ref. 3).
FT   CONFLICT   1094   1094    D -> CC (in Ref. 3).
FT   CONFLICT   1197   1198    SS -> TD (in Ref. 3).
FT   CONFLICT   1229   1231    Missing (in Ref. 3).
FT   CONFLICT   1422   1422    K -> Y (in Ref. 3).
FT   CONFLICT   1623   1625    FGM -> SAR (in Ref. 3).
FT   CONFLICT   1656   1656    S -> T (in Ref. 3).
FT   CONFLICT   1737   1737    P -> A (in Ref. 3).
SQ   SEQUENCE  1835 AA;  205348 MW;  E6025E0F1B80CCA CRC64;
```

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Query Match             45.2%;  Score 5383;  DB 1;  Length 1835;
Best Local Similarity   56.9%;  Pred. No. 1.1e-239;
Matches  1139;  Conservative  184;  Mismatches  344;  Indels  336;  Gaps  38;

Qy     27  GAGGRPGPGSAEKDPGSADSEAEG---LPYPALAPVFFYLSQDSRPRSWCLRTVCNPW   82
           :|  ||||    |       |  :|:| ||: |  ||  : :||:   .|::||| ||||
Db     19  GITEQPGPRSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIRMVCNPW   78

Qy     83  FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIF  142
           ||| |||||||||||||||: | |  |: |  |::|||||||::||:||||||||| :||||
Db     79  FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIF  138

Qy    143  GKKCYLGDTWNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVT  202
           ||||||||||||||||||||| ||||||||:::|||||:||||||||||||||:||||||||
Db    139  GKKCYLGDTWNRLDFFIVAGMVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVN  198

Qy    203  LLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLLERYYQTE  262
           |||||||||||||||||||||||||:||||||||||||||:  |  ||:|  |:  |||:|||
Db    199  LLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPPYYQPE  258

Qy    263  NEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL---DYBAYNSSSNTT--CV  314
           |::|  |||  |  |  |.  :           |  ||    ..  ::   |  |  :|
Db    259  EDDEMPFICSLTGDNGIMGCHEIPLPKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCV  315

Qy    315  NWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYVMDAHSFYNFIY  374
           ||| |||:||:| ||| |||||||||||||.|:|||||||||:||:|||||||||||:|
Db    316  NWNRYYNVCRTGNANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFIY  375

Qy    375  FILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYE  434
           ||||||||||||:|||||||||||||||||:||||||||| ||  :| |||: |  |||||
Db    376  FILLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASVAEPGDCYE  434

Qy    435  ELKLYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHL  494
           ||:|   | |||:::| | ::  |                              :| :|:
Db    435  EIFQYVCHLRKAKRRALGLYQALQNR-----------------------------------  461

Qy    495  VHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVH  554
           |: :               . :    |:    |  ||  |  |  | |   |    |
Db    462  ----------------------------RQAMG----------PGTPA--PAKPGP-----  477

Qy    555  SFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASS  614
           |.  | ||   :|  :| :|
Db    478  ---HAK---EPSHCKLCPRHSPLD-------------------------------------  504

Qy    615  GPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-  672
            |:    |:    |  : ||| : |||
Db    505  ------------------------------ISAILASD-----PSSCPHCQHEA  523

Qy    673  ---AGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRSLGPDABPSSVLA-  727
              | |   : :|   |   |  |       |   : |::  |:|    | | | |  :|
Db    524  GRRPSGLGSTD-SGQEGSGSGSAEAEANGDG---LQSSEDGVSSDLGKEEQEDGAAR  578

Qy    728  ----FWRLICDTFRKIVDSKYFGRGIMAILIVNTLSMGIEYHEQPELTNALEISNTVFT  783
               |  || |  || |:|||||  || |  :  |:|   | |||| | |   :|:  ||
Db    579  LCGDVWRETRKKLRGIVDSKYFNRGIMALLVNTVSMGIEHHEQPELTNILEICNVVFT  638

Qy    784  SLFALEMLLKLLVYGPFGYIKNPYNIIFDGVIVISVWEIVGQQGGGLSVLRTFRLMRVLK  843
           |:||||:|||| |||| |:|||||||:||| ||:|:|||||| | | |||||||| :|:||
Db    639  SMFALEMILKLAAFGFLDYLRNPYNIFDSIIVIISIWEIVQADGGGLSVLRTFRLLRVLK  698

Qy    844  LVRFLPALQRQLVLMKTDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPD  902
           ||||:|||:|:|| |||||||||||||||||||||||||||||||||   || |||:|||
Db    699  LVRFMPALRRQLVVLMKTDNVATFCMLLMLFIFIFSILGMHLFGCKFSLRTDGDTVPD  758
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Db    1748  APGRGSGGAGAGG-DTESHLCRH 1769
            |||:||    |:||:|||

RESULT 15
Q7Z6S8
ID   Q7Z6S8      PRELIMINARY;      PRT;   1994 AA.
AC   Q7Z6S8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   DJ172B20.1 (Calcium channel, voltage-dependent, alpha 1I subunit)
DE   (Fragment).
GN   Name=CACNA1I;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Theria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Phillips S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL022319; CAD92537.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na pore.
DR   InterPro; IPR002111; Cat_channel TrpL.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
KW   Ion transport; Ionic channel; Transmembrane; Transport.
FT   NON_TER       1          1
SQ   SEQUENCE   1994 AA;  220004 MW;  A5EFAE5FA32DCF76 CRC64;

Query Match            40.6%;  Score 4836;  DB 2;  Length 1994;
Best Local Similarity  49.8%;  Pred. No. 2e-214;
Matches 1117;  Conservative 188;  Mismatches 484;  Indels 456;  Gaps 55;
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Qy   903  RKNFDSLLWAIVTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAI  962
              ||||||||||||||||||||||| ||||||||||   |:||: |||||:||||||||||
Db   759  RKNFDSLLWAIVTVFQIILTQEDWNVVLYNGMASTTPWASLYFVALMTFGNYVLFNLLVAI  818

Qy   963  LVEGFQAEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPS----------LDG  1012
              |||||||        : :
Db   819  LVEGFQAE------------------GDANRSCSDEDQSSSNLEEFDKLPEGLDN  855

Qy  1013  DGRKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEAIGPA-SRRTSS  1071
              |||            |: ||
Db   856  SRDLKLCPIPMTPNGH------SLP-------LGAHLGPAGTMGTAP  892

Qy  1072  SGSAEPG-------------------AAHEMKSPPSARSSPHSPWSAASSWTSRSSRNSL  1113
                    : :  :|  : :|||| | :
Db   893  RLSLQPDPVLVALDSRKKSVSMSLGRMSYDQRSLSSSRSSYYGPWGRSGTWASRRSSWN--  950

Qy  1114  GRAPSLKRRSPSGERRSLLSGEGQESQDEE-ESSEEE----RASPAGSDH----------  1158
                 |:||| : : : | | |
Db   951  --SLKHKPPSAEHESLLSGEGGGSCVRACEGAREEAPTRTAPLHAPHAHHAHHGPHLA  1006

Qy  1159  ---RHRGSLEREAKSSFDLPDTLQVPGLHRTAS--GRGSASEHQDCNGKSASGRLARAL  1212
                  |||:||         |  |  ||||:|||   :|:|  ||   |: :|:|| ||
Db  1007  HRHRHHRRTLSLDTRDSVDLGELVPVGAHSRAAWRGAGQAPGHEDCNGRMPNIAKDVFT  1066

Qy  1213  RPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI  1272
              ||          :  |      |  |:|  |:
Db  1067  KMDDRRDRGBD-EEEIDYTLCFRVRKMIDVYKPDWCEVREDWSVVLFSPENKFRILCQTI  1125

Qy  1273  ITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERRIFLTLSNYIFTAVFLAEMTVKVVAL  1332
              | ||:|||:|:|||||||:|||||||||||||  |:|:|:|||||||| |:|:|:| :||
Db  1126  IAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERRIFLTVSNYIFTAIFVGEMTLKVVSL  1185

Qy  1333  GWCFGEQAYLRSSWNVLDGLLVLVLISVIDIILSMVSDSGTKILGMLRVLRLLRTLRPLRVI  1392
              ||:|||||||||||||||||:| |  ||||||:|||||:|||||:|||:|||||||||||||
Db  1186  GLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSVASAGGAKILGVLRVLRLLRTLRPLRVI  1245

Qy  1393  SRAQGLKLVVETIMSSLKPIGNIVIVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK  1452
              |||:|||||||| ||||||||||||| :|||||||||||||||||||||  ||||||||||
Db  1246  SRAPGLKLVVETLISSLKPIGNIVLVICCAFFIIFGIIGVQLFKGKFYHCLGVDTRNITNR  1305

Qy  1453  SDCAEASYRWRHKYNFDNLGQALMSLFVLASKDGWVDIMYDLGLDAVGVDQQPIMNHNPW  1512
              |||  ||||| ||:|||||||||||||||||||||||:| | | |: | |:||| |||||
Db  1306  SDCVAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHNPW  1365

Qy  1513  MLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRRLEKKRRKAQC  1572
              |||||:||||:||||||||||||||||||||||||| ||||||||||||||||||||:
Db  1366  MLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEEAEARRREEKRLRRLEKKRRKAQR  1425

Qy  1573  KPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIF  1632
              ||                         |  | ||  ||  : :    :|| ||:|| |||
Db  1426  LPYYATYCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMF  1485

Qy  1633  TVIFVLESVFKLVAFGFRRFFQDRWNQLDIAIVLLSIMGITLEEIEVNASLPINPTIIRI  1692
              |::||||:||||||:||||||||||||||||||||||||||||||||| |||||||||||
Db  1486  TTVFVLEAVLKLVAFGFGRLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRI  1545

Qy  1693  MRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLEC  1752
              |||||||||||||: |   :|||||:|||||||||||||||||||:|  |||||| |||:
Db  1546  MRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKLVC  1605

Qy  1753  DETHPCRGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS  1809
              :  | |||:|||||||||||||||||||||||||||||||||||| |||:||   |:|:|
Db  1606  NDENPCRGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQFVS  1665

Qy  1810  PIYFVSFVLTAQFVLNVVIAVLMKHLEBSNKEAKEAEBLEAELELEM-KTLSPQPHSPL  1868
              ||||||||| ||||| |||| ||||    |:| :::  | |:  | |   |     |   |
Db  1666  PLYFVSFVLTAQFVLNVVVAVLMKHLDDSNKEAQEDAEMDAEIELEMAHGLGPCP----  1721

Qy  1869  GSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTV---  1925
                                    |:|   | ||   |   |     |
Db  1722  -------GPCPG-----------------PCPCPCPCPGPRLIPTSSPG  1747

Qy  1926  ---RKSGVSRTHSLPNDSYMCRH  1945
              ||:|  |:|||||||:||||
Db  1748  APGRGSGGAGAGG-DTESHLCRH  1769
```

```
Db              ||||||||||||||||||||||||||||||||||||||||:|||||| ||||::|||||||
Db   1356 RIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVELFGKL 1415

Qy   1751 ECDETHPCEGLGRHATFRNFGMAFLTLFRYSTGDNWNGIMKDTLRDC-DQESTCYNTV-- 1807
                :||::|||||| :|||||:|||||||||:|||||||||||||||||| :::
Db   1416 VCNDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSSLQF 1475

Qy   1808 ISPIYFVSFVLTAQFVLVNVIAVLMKHLLESNKEAKEABAELEABELEM-KTLSPQPHS 1866
           :|||||||||||||||:|||:||||||||:|||||:|::|:|:|:|||| :::
Db   1476 VSPLYFVSFVLTAQFVLINVVVAVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGPRL 1535

Qy   1867 PLGSPFLWPGVEGPD------------SP------------------------------D 1884
           |:|||      |||
Db   1536 PTGSPGA-PG-RGPCGAGGGDTEGGLCRRCYSPAQENLWLDSVSLIIKDSLEGELTIID 1593

Qy   1885 SPKPGALH-----PAA--------------------HARSAS-----HFSLEHPTMQP- 1912
           :|:|||   :||
Db   1594 NLSGSIFHHYSSPAGCKKCHHDKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDTACPP 1653

Qy   1913 ----HPTELPGPDLLTVRKSG------VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPK 1962
               |:|:|     :      :: ::
Db   1654 GRKDSKGELDPPEPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LK 1709

Qy   1963 AQGGSVLSVHSQPADTSYILQLPKDAPH------LLQPHSAPTWGTIPKLPPPG-----R 2011
            :|:  :|:|::|||| :||:|||||      |||
Db   1710 HDSSQAPPSPFSPDASSPLLPMPAEFFHPAVSASQKGPEKGTGTGTLPKIALQGSWASLR 1769

Qy   2012 SPLAQRPLRRQAAIRTDSLDVQGLGSREDLLAEVSGPSPPLARAYSFWGGSSTQAQQHSR 2071
           ||:  ||||||| |||||:
Db   1770 SPRVNCTLLRQATGSDTSLD-----------------ASPSSSAGSLQTTLEDSLTLSDSPPR 1815

Qy   2072 SHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEPPSPRD 2131
           :    :   |:|||||  ::
Db   1816 A------LGPPAPAGPPRAGLS------PAARRRLSL------------RGRG 1844

Qy   2132 LKKCYSVEAQSCCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSN---LGGQPLGGPG 2188
           |:                :|:|
Db   1845 LFSLRGLRA-------------HQRSHSSGGS-TSPGCTHHDSMDPSDEEGRGGAGGGGAG 1891

Qy   2189 SRPKKKLSPPSIT---IDPPESQGPRTPPSPGICLRRRAPSSDS----KDPLASGPPDSM 2241
           |   :::     :::
Db   1892 SEHSETLSSLSLTSLFCPPP------PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGL 1945

Qy   2242 AASPSPKKDVLSLSGLSSDPADLDP 2266
            |::|
Db   1946 ARSPSWAAD-------RSKDPPGRAP 1964

Search completed: November 18, 2004, 13:32:35
Job time : 265.833 secs
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Qy    669 YCAR------AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEP 722
           :|||      :|:   ::
Db    326 CCQHEDGRRPSGLLGSTD-SGQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEE 382

Qy    723 SSVL------AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNA 774
           :||:       ||  |||| :|||||||| ||||:||||||:|||||:|||||||||:
Db    383 EEQADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMALLVNTVSMGIBHHEQPEELTNI 442

Qy    775 LEISNIVFTSLFALEMLKLLVVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLR 834
           ||| |:|||:||||||:||   ||:||::|||||||:|||:||:|||||| ||||||
Db    443 LEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLR 502

Qy    835 TFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASE 894
           |||:|||||||||:|||:|||||||||||||||||||||||||||||||||||:||||:
Db    503 TFRLLRVLKLVRFMPALRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLR 562

Qy    895 RD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMAST5SWAALYFIALMTFGNY 953
           :| |||:||||||||||:|||||||||||||||:|||||||||:||:|||:||||||||
Db    563 TDTGDTVPDRKNFDSLLMAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNY 622

Qy    954 VLFNLLIVAILVEGFQAEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS---- 1009
           |||||||||||||||||               :: :||:||||
Db    623 VLFNLLIVAILVEGFQAE--------------GDANRSYSDEDQSSSNIEEF 659

Qy   1010 ------LDGDGDRKKCLAIVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALG 1063
                 :|| |  |  |
Db    660 DKLQEGLDSSGDPKLCPIPMTPNGH--------LDP------SLPLGGHLGPAGAAG 702

Qy   1064 PASRRT------SSSGSAEPGAAHEMKSPPSARSSPHSPWSAASWTSRRSSR 1110
           ||:|       :: :  |  :|       |:  |||     ||:|||||
Db    703 PAPRLSLQPDPMIVALGSRKSSVMSLGRMSYDQRSLSSSRSSYGPWGRSAAWASRRSSW 762

Qy   1111 NSLGRAPSLKRRSPSGERRSLLSGE-GQESQDEEESEE--ERRASPAGSDH------ 1158
           |   :  |:|  | ||:|| ||:||  ::   ::
Db    763 N------SLKHKPPSAEHESLLSAERGGARVCEVAADEGPPRAAPLHTPHAHHITHHGPH 816

Qy   1159 -----RHRGSLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRLAR 1210
                 :|:   |      : :|    |     |:    ||::|:|||||
Db    817 LAHRHRHRHRRTLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDV 876

Qy   1211 ALRPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFLLCH 1270
           :     :  || ::|  :||:|| | |:::|:    |   | |||:|:|||||||||||
Db    877 FTKMGDRGDRGED-EEEIDYTLCFRVRKMIDVYKPDWCEVRRDWSVVLFSPENRFRVLCQ 935

Qy   1271 RIITHKMFDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVV 1330
           |:|:||:||:|||. |||||||:| ||||||  |||||||||||||||:|:.|||:|||
Db    936 TIIAHKLFDYVVLAFIFLNCITTIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVV 995

Qy   1331 ALGWCFGEQAYLRSSWNVLDGLLVLLSVIDILVSMVSDSGTKILGMLRVLRLLRTLRPLR 1390
            ||:.|||||||||||||||| |||.|:||::||:::: :||||:||||||||||||||||
Db    996 SLGLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSLASAGGAKILGVLRVLRLLRTLRPLR 1055

Qy   1391 VISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNIT 1450
           |||||:|||||||||:|||||||||||:|||||||||||||||||||||:| |||||||
Db   1056 VISRAPGLKLVVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNIT 1115

Qy   1451 NKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPIMNHN 1510
           |:|||.|| ||||:||||||||||||||||||||||||||:|||:|||||.||||:.|||
Db   1116 NRSDCMAANYRWVHHKYNFDNLGQALMSLFVLASKDGWVNIMYNGLDAVAVDQQPVTNHN 1175

Qy   1511 PWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCROHQEEEEARRREKRLRLEKKRRKA 1570
           |||||||||||||||:|||||||||||||||||||||||   |||||:|||||||||||
Db   1176 PWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRQHQEAEARRREEKRLRLEKKRRKA 1235

Qy   1571 QCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNY 1630
           | :||| .| ||||:|| |||||||||||| :| ||||||::|||.||::|||||:.|||
Db   1236 QRLPYYATYCHTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNY 1295

Qy   1631 IFTVIFVLESVFKLVAFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTII 1690
           :||.:||||:|.||||||:|||||||||||||||||||::|||||||::||:|||||||
Db   1296 MFTTVFVLEAVLKLVAFGLRRFFKDRWNQLDLAIVLLSVWGITLEEIEINAALPINPTII 1355

Qy   1691 RIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDL 1750
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.3132 Seconds
(without alignments)
3727.727 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEEDGAGAEESGQPRSFM.........PKKDVLSLSGLSSDPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5	Sequence 5, Appli
2	6315.5	53.1	1207	3	US-09-398-522-52	Sequence 52, Appl
3	6211	52.2	2353	3	US-08-984-709A-50	Sequence 50, Appl
4	5492.5	46.1	2175	3	US-09-404-650-2	Sequence 2, Appl
5	5492.5	46.1	2175	3	US-09-935-541-2	Sequence 2, Appli
6	5484	46.1	2188	3	US-09-404-650-4	Sequence 4, Appli
7	5484	46.1	2188	4	US-09-935-541-4	Sequence 4, Appli
8	5366	45.1	1835	3	US-09-404-650-5	Sequence 5, Appli
9	5366	45.1	1835	4	US-09-935-541-5	Sequence 5, Appli
10	1750.5	14.7	2343	3	US-09-268-163-4	Sequence 4, Appli
11	1749	14.7	2337	3	US-08-713-118-2	Sequence 2, Appli
12	1749	14.7	2337	3	US-09-452-007-2	Sequence 2, Appl
13	1748.5	14.7	2339	1	US-08-455-543A-47	Sequence 47, Appl
14	1748.5	14.7	2339	3	US-08-223-305C-47	Sequence 47, Appli
15	1746.5	14.7	2339	3	US-09-268-163-6	Sequence 6, Appli
16	1743	14.6	2237	1	US-08-455-543A-48	Sequence 48, Appl
17	1743	14.6	2237	2	US-08-223-305C-48	Sequence 48, Appl
18	1741	14.6	2237	3	US-09-268-163-8	Sequence 8, Appli
19	1722	14.5	2336	3	US-09-268-163-10	Sequence 10, Appli
20	1632.5	13.7	1873	1	US-08-435-675B-4	Sequence 4, Appl
21	1622.5	13.6	1873	3	US-08-336-257A-7	Sequence 7, Appl
22	1619.5	13.6	1984	3	US-08-836-325-10	Sequence 10, Appl
23	1619.5	13.6	1984	4	US-09-457-571-10	Sequence 10, Appl
24	1619.5	13.6	1985	4	US-09-495-714C-6	Sequence 6, Appli
25	1616	13.6	1872	6	5386025-6	Patent No. 5386025
26	1615.5	13.6	1989	3	US-08-836-325-12	Sequence 12, Appl
27	1615.5	13.6	1989	4	US-09-457-571-12	Sequence 12, Appl
28	1607.5	13.5	2516	3	US-08-374-077C-2	Sequence 2, Appli
29	1607.5	13.5	2516	3	US-08-895-590-2	Sequence 2, Appli
30	1607.5	13.5	2516	4	US-09-539-879A-2	Sequence 2, Appli
31	1601	13.4	1977	4	US-09-495-714C-4	Sequence 4, Appli
32	1601	13.4	2509	2	US-08-149-097D-35	Sequence 35, Appli
33	1587	13.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
34	1587	13.3	2016,	4	US-09-896-994-2	Sequence 2, Appli
35	1586	13.3	1969	3	US-08-836-325-16	Sequence 16, Appli
36	1586	13.3	1969	4	US-09-457-571-16	Sequence 16, Appl
37	1586	13.3	2016	3	US-09-634-920-4	Sequence 4, Appl
38	1586	13.3	2016	4	US-09-840-125-4	Sequence 4, Appli
39	1583	13.3	1977	4	US-09-976-594-757	Sequence 757, App
40	1583	13.3	1977	4	US-09-919-039-367	Sequence 367, App
41	1573.5	13.2	1912	4	US-09-495-714C-2	Sequence 2, Appli
42	1569.5	13.2	1968	1	US-08-455-543A-45	Sequence 45, Appl
43	1569.5	13.2	1968	2	US-08-223-305C-45	Sequence 45, Appl
44	1560.5	13.1	2161	1	US-08-455-543A-51	Sequence 51, Appl
45	1560.5	13.1	2161	2	US-08-223-305C-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
;
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match   99.7%; Score 11862.5; DB 3; Length 2273;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 2260; Conservative 4; Mismatches 2; Indels 7; Gaps 1;

Qy   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MDEEEDGAGAEESGQPRSFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

Qy   181 TVRVLRPLRAINRVPSMRIILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TVRVLRPLRAINRVPSMRIILVTLLLDTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR 240

Qy   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL 300

Qy   301 DYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360
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Qy   361 YFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420
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Db   361 YFVMDAHSFYNFIYFILLIIVGSFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNA 420

Qy   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGGETQPSS 480
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Db   421 STLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGGETQPSS 480

Qy   481 SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQRDANGSRRLMLPPPSTP 540
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Db   481 SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQRDANGSRRLMLPPPSTP 540

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600

Qy   601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
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Qy   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720
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Db   661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA 720

Qy   721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780

Qy   781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVLSVWEIVGQQGGLSVLRTFRLMR 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVLSVWEIVGQQGGLSVLRTFRLMR 840

Qy   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
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Db   841 VLKLVRFLPALQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900

Qy   901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
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Qy   961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020
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Db   961 AILVEGFQAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020

Qy  1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGAEPGAA 1080
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Qy  1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQOESQ 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQQSQ 1140

Qy  1141 DEEESSEEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHQDCN 1200
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Qy  1201 GKSASGRLARALRPDDPLLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
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Db  1201 GKSASGRLARALRPDDPLLDGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP 1260

Qy  1261 PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 PQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320

Qy  1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 FLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380

Qy  1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 RLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440
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Qy  1441 CQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVG 1500
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Qy  1501 VDQQPIMNNPWMLLYFISFLLIVAFFVLNMFVGVVENFHKCROHQEEEARRREEKRL 1560
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Qy  1561 RRLEKKRR------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVIGLNVVTMAME 1613
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Qy  1614 HYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDDLAIVLLSIMGIT 1673
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Db  1621 HYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRRFFQDRWNQLDDLAIVLLSIMGIP 1680

Qy  1674 LEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFM 1733
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 LEQIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFM 1740

Qy  1734 LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
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Db  1741 LLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1800

Qy  1794 LRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAEAEAEL 1853
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Db  1801 LRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAEAEAEL 1860

Qy  1854 ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH 1913
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Db  1861 ELEMKTLSPQPHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH 1920

Qy  1914 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGSVLSVHS 1973
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGGSVLSVHS 1980

Qy  1974 QPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQ 2033
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Db  1981 QPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQ 2040

Qy  2034 GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGEPNW 2093
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Db  2041 GLGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGEPNW 2100

Qy  2094 GKGPPETRSSLEDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2153
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 GKGPPETRSSLEDTELSWISGDLLPPGGQEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2160

Qy  2154 QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP 2213
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Db  2161 QRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTP 2220

Qy  2214 PSPGICLRRRAPSDSDKDPLASGPPDSMAASPSPKKDVLSLSGLLSSDPADLDP 2266
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Db  2221 PSPGICLRRRAPSDSDKDPLASGPPDSMAASPSPKKDVLSLSGLLSSDPADLDP 2273
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